

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 03:48:23 ; Search time 26813 Seconds  
(without alignments)  
11769.993 Million cell updates/sec

Title: US-08-554-424-7  
Perfect score: 6513  
Sequence: 1 TCTAGACGTTGGCCGCGATAG.....ACGGAGATTAGCTCTAGA 6513

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hc: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6513	100.0	6513	6 125433	Sequence 7
2	6513	100.0	6513	6 125433	Sequence 7
3	6513	100.0	6513	6 125433	Sequence 7
4	6288	96.5	6883	3 DROSODCHA	174672 Sequence 7
5	6209.6	95.3	6527	6 CQ593262	M32078 Drosophila
6	6163.8	94.6	6519	6 ARO28545	CQ593262 Sequence
7	4508.2	69.2	6899	3 MDPARA	AR028545 Sequence
8	4447.8	68.3	6318	3 MDU3813	X96668 M domestica
9	4447.8	68.3	6318	3 ARO28529	U38813 Musca domes
10	4434.2	68.1	6315	6 MDU3814	AR028529 Sequence
11	4434.2	68.1	6315	6 ARO28530	U38813 Musca domes
12	3536.4	54.3	6317	3 AY663385	AR028530 Sequence
13	3425.4	42.6	6304	3 AY663384	AY663385 Aedes aeg
14	2905.8	44.6	6096	3 BGU73584	AY663384 Aedes alb
15	2904.2	44.6	6096	3 BGU73583	U73584 Blatella g
16	2653	40.7	6156	3 AY191155	U73583 Blatella g
17	2649.8	40.7	6156	3 AY191156	AY191155 Pediculus
18	2646.6	40.6	6156	3 AY191157	AY191156 Pediculus
19	2643.6	40.6	6521	3 AB090951	AB090951 Pediculus

20	2431.6	37.3	5068	3 BGU71083	U71083 Blatella g
21	2110.2	32.4	5086	3 AF072493	AF072493 Heliothis
22	1798.8	27.6	2144	3 DYT25843	U25843 Drosophila
23	1512.4	23.2	6648	3 AY259834	AY259834 Varroa de
24	1304.2	20.0	8065	3 AY322171	AY322171 Mesobuthu
25	1237.6	19.0	3599	3 AF134216	AF134216 Boophilus
26	1223	18.8	3262	3 AF114489	AF114489 Lepidoptera
27	1088	16.7	1878	3 AY663383	AY663383 Aedes alb
28	1070.2	16.4	1809	3 AY663382	AY663382 Aedes alb
29	1050.4	16.1	166935	3 AC010920	AC010920 Drosophila
30	1050.4	16.1	304713	3 AE003502	AE003502 Drosophila
31	1047.2	15.7	36569	2 AC014943	AC014943 Drosophila
32	1021.4	15.7	6586	6 AR181360	AR181360 Sequence
33	1019.4	15.7	6007	6 AR181336	AR181336 Sequence
34	1019.4	15.7	6586	10 AF049240	AF049240 Rattus no
35	998.6	15.3	5937	6 AF049617	AF049617 Mus muscu
36	993	15.2	5977	6 AR181335	AR181335 Sequence
37	993	15.2	6556	6 AR181338	AR181338 Sequence
38	993	15.2	6556	10 AF049239	AF049239 Rattus no
39	979	15.0	6458	10 MMU271477	MMU271477 Mus muscu
40	977.2	15.0	7545	10 RATSCAL	RATSCAL Rattus norv
41	974	15.0	6503	4 BTA251721	BTA251721 Bos tauru
42	963	14.8	6394	4 CPAS55547	CPAS55547 Canis fam
43	958.6	14.7	6826	6 AR181339	AR181339 Sequence
44	958.6	14.7	6826	10 RATSCP6A	RATSCP6A Rattus norv
45	952.2	14.6	1728	3 AY663377	AY663377 Aedes aeg

#### ALIGNMENTS

RESULT 1	125433	Sequence 7 from patent US 5550049.	DNA	linear	PAT 07-OCT-1996
LOCUS	125433	Sequence 7 from patent US 5550049.	DNA	linear	PAT 07-OCT-1996
DEFINITION	125433	Sequence 7 from patent US 5550049.	DNA	linear	PAT 07-OCT-1996
ACCESSION	125433	Sequence 7 from patent US 5550049.	DNA	linear	PAT 07-OCT-1996
VERSION	125433.1	GI:1605303	DNA	linear	PAT 07-OCT-1996
KEYWORDS	Unknown.	Unknown.	DNA	linear	PAT 07-OCT-1996
SOURCE	Unknown.	Unknown.	DNA	linear	PAT 07-OCT-1996
ORGANISM	Unknown.	Unknown.	DNA	linear	PAT 07-OCT-1996
REFERENCE	1 (bases 1 to 6513)	Unknown.	DNA	linear	PAT 07-OCT-1996
AUTHORS	Van der Ploeg, L.H.T. and Warmke, J.W.	Unknown.	DNA	linear	PAT 07-OCT-1996
TITLE	Process for identifying para cation channel modulators	Unknown.	DNA	linear	PAT 07-OCT-1996
JOURNAL	Patent: US 5550049-A 7 27-AUG-1996;	Unknown.	DNA	linear	PAT 07-OCT-1996
FEATURES	Location/Qualifiers	Unknown.	DNA	linear	PAT 07-OCT-1996
source	1..6513	Unknown.	DNA	linear	PAT 07-OCT-1996
ORIGIN	/organism="unknown"	Unknown.	DNA	linear	PAT 07-OCT-1996
	/mol_type="unasigned DNA"	Unknown.	DNA	linear	PAT 07-OCT-1996
Query Match	100.0%; Score 6513; DB 6; Length 6513;	Unknown.	DNA	linear	PAT 07-OCT-1996
Best Local Similarity	100.0%; Pred. No. 0;	Unknown.	DNA	linear	PAT 07-OCT-1996
Matches 6513; Conservative	0; Mismatches	0; Indels	DNA	linear	PAT 07-OCT-1996
	0; Gaps	0; Gaps	DNA	linear	PAT 07-OCT-1996
QY	1 TCTAGACGTTGGCCGCGATAGCAATGTCGATCTGATATCTGAGAAGAC	60			
DB	1 TCTAGACGTTGGCCGCGATAGCAATGTCGATCTGATATCTGAGAAGAC	60			
QY	61 GCAGTTTGTTCCTCCCTTTACCGCGAATCATTTGTCGCAATGCAACGCAATGCGG	120			
DB	61 GCAGTTTGTTCCTCCCTTTACCGCGAATCATTTGTCGCAATGCAACGCAATGCGG	120			
QY	61 GCAGTTTGTTCCTCCCTTTACCGCGAATCATTTGTCGCAATGCAACGCAATGCGG	120			
DB	61 GCAGTTTGTTCCTCCCTTTACCGCGAATCATTTGTCGCAATGCAACGCAATGCGG	120			
QY	121 CTGAACATGAAAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180			
DB	121 CTGAACATGAAAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180			
QY	121 CTGAACATGAAAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180			
DB	121 CTGAACATGAAAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180			
QY	181 ATGGTCCAG	240			
DB	181 ATGGTCCAG	240			
QY	181 ATGGTCCAG	240			
DB	181 ATGGTCCAG	240			
QY	241 CACAACCGATCTTACATTTGCAACGAGGTGCGCAATACCTGTTGATTCAGAGGAGCT	300			
DB	241 CACAACCGATCTTACATTTGCAACGAGGTGCGCAATACCTGTTGATTCAGAGGAGCT	300			

Db 241 CACMACCGATCTTACACTTGAA CAGGGTGTCCAA TACCTGTTCAATG CAGGCGACT 300  
QY 301 TCCCGCGGAATTGGGCTCCACTCTCTGAGAGATATCCCTACTACAGCAATGTAC 360  
Db 301 TCCCGCGGAATTGGGCTCCACTCTCTGAGAGATATCCCTACTACAGCAATGTAC 360  
QY 361 TGAATTCTGAGTTGTGAAGCAAGAAAGATATTTTTCGCTTTTCTGCATCAAAAGCA 420  
Db 361 TGAATTCTGAGTTGTGAAGCAAGAAAGATATTTTTCGCTTTTCTGCATCAAAAGCA 420  
QY 421 TGTGAGATCTGAGATCAATCCGATAGCTGTGTGGCCATTTCATTTAGTGCATC 480  
Db 421 TGTGAGATCTGAGATCAATCCGATAGCTGTGTGGCCATTTCATTTAGTGCATC 480  
QY 481 CATTAATTTTCCCTATTCATCATCA CCAATTCCTGTCATCTGATGATATGC 540  
Db 481 CATTAATTTTCCCTATTCATCATCA CCAATTCCTGTCATCTGATGATATGC 540  
QY 541 CGAACACGCCCAAGGTTGAGTCCA CTGAGGTGATTCACCGGAATCTACATTTGAAT 600  
Db 541 CGAACACGCCCAAGGTTGAGTCCA CTGAGGTGATTCACCGGAATCTACATTTGAAT 600  
QY 601 CAGGTGTAAGTATGAGTGAAGGAGTTTCA TTTTATGCGCTTTAGCTATCTAGAGATG 660  
Db 601 CAGGTGTAAGTATGAGTGAAGGAGTTTCA TTTTATGCGCTTTAGCTATCTAGAGATG 660  
QY 661 CATTGAATTTGCTGAGCTTGTAGTAA TTAGCTTTAGCTTTAGCTTTAGAGATG 720  
Db 661 CATTGAATTTGCTGAGCTTGTAGTAA TTAGCTTTAGCTTTAGCTTTAGAGATG 720  
QY 721 TAGGTAATCTAGACGCTTGGAAAGCTTTA GAGGTGCTGCGAGGCTTTAAACCTGAGCA 780  
Db 721 TAGGTAATCTAGACGCTTGGAAAGCTTTA GAGGTGCTGCGAGGCTTTAAACCTGAGCA 780  
QY 781 TTGGCAGAGCTTGAAGACATGCTGCGAG CCGCTCATCGAATCGGTGAAGATCTGCGG 840  
Db 781 TTGGCAGAGCTTGAAGACATGCTGCGAG CCGCTCATCGAATCGGTGAAGATCTGCGG 840  
QY 841 ATGTGATTAATCTGACCATGTTCTCCCTG TCGTGTGCTGATGAGGCTTACATCT 900  
Db 841 ATGTGATTAATCTGACCATGTTCTCCCTG TCGTGTGCTGATGAGGCTTACATCT 900  
QY 901 AATAGGCGGCTGACCGGAGAGTGAATCA AAGAGTTCCGCTGAGAGGCTTCTGAGGCA 960  
Db 901 AATAGGCGGCTGACCGGAGAGTGAATCA AAGAGTTCCGCTGAGAGGCTTCTGAGGCA 960  
QY 961 ATCTGACGAGAGAGATGAGACTATCA CAATGCGCAATGCTCCAAATTTGATTCGAGG 1020  
Db 961 ATCTGACGAGAGAGATGAGACTATCA CAATGCGCAATGCTCCAAATTTGATTCGAGG 1020  
QY 1021 ACGAGGCGATCTCATTTCCGTTATGCGGA TATATCCGCTGCGGAGCAATGCGAGCA 1080  
Db 1021 ACGAGGCGATCTCATTTCCGTTATGCGGA TATATCCGCTGCGGAGCAATGCGAGCA 1080  
QY 1081 ATTACGCTGCTGAGGAGGTTTGGTCCGAAT CCGAATTTAGCTTACACAGCTTCAAT 1140  
Db 1081 ATTACGCTGCTGAGGAGGTTTGGTCCGAAT CCGAATTTAGCTTACACAGCTTCAAT 1140  
QY 1141 CGTTGAGATGAGGCTTCTCTGCTCGGCTTC CGGCTGATGACA CAGGACTTTCGAGAGATC 1200  
Db 1141 CGTTGAGATGAGGCTTCTCTGCTCGGCTTC CGGCTGATGACA CAGGACTTTCGAGAGATC 1200  
QY 1201 TGTACACAGTGTGTGCGCGCGCGGACCA TATGCAATGCTGTCTTTATATGATCA 1260  
Db 1201 TGTACACAGTGTGTGCGCGCGCGGACCA TATGCAATGCTGTCTTTATATGATCA 1260  
QY 1261 TCTTCTGAGTTTCAATTTCTATCTGTGAAT TTTGATTTGAGCTTTGAGCTTTGATG 1320  
Db 1261 TCTTCTGAGTTTCAATTTCTATCTGTGAAT TTTGATTTGAGCTTTGAGCTTTGATG 1320  
QY 1321 ACGAATTCGAAGAGAGCGGAGAGAGAGAG AGAGCTGCGAAGAGAGAGAGAGAG 1380  
Db 1321 ACGAATTCGAAGAGAGCGGAGAGAGAGAG AGAGCTGCGAAGAGAGAGAGAGAGAG 1380

QY 1381 CGGAAGAGCTTCCCGCGCGCGCAAGGCGCA AAGCTTGAAGAGAGGCGCAATGCGAGGCTC 1440  
Db 1381 CGGAAGAGCTTCCCGCGCGCGCGCAAGGCGCA AAGCTTGAAGAGAGGCGCAATGCGAGGCTC 1440  
QY 1441 AGGAGAGAGGAGATGCGGCTGCGCGGAGAG GAGCTGCACTGCATCCGAAATGAGCAAGA 1500  
Db 1441 AGGAGAGAGGAGATGCGGCTGCGCGGAGAG GAGCTGCACTGCATCCGAAATGAGCAAGA 1500  
QY 1501 GTTCCAGCTTATCTTGATCAGCTATGAGCTA TTTTGTGGCGGCGAAGAGGCAACGATG 1560  
Db 1501 GTTCCAGCTTATCTTGATCAGCTATGAGCTA TTTTGTGGCGGCGAAGAGGCAACGATG 1560  
QY 1561 ACAAACAAGAAAGAGATGTCATTCGAGAGG CTGAGGTGAGTCCGAGTCCGTAAGCG 1620  
Db 1561 ACAAACAAGAAAGAGATGTCATTCGAGAGG CTGAGGTGAGTCCGAGTCCGTAAGCG 1620  
QY 1621 TTATACAAAGACACAGACCTTACACAGCA CACCAAGCTTACCAAGTTGCTTAAAGTGA 1680  
Db 1621 TTATACAAAGACACAGACCTTACACAGCA CACCAAGCTTACCAAGTTGCTTAAAGTGA 1680  
QY 1681 GCAAGCATCTTATCTTATCTTACCTGTTCA CCGTTTAACTAGCAGGAGATCAGTATG 1740  
Db 1681 GCAAGCATCTTATCTTATCTTACCTGTTCA CCGTTTAACTAGCAGGAGATCAGTATG 1740  
QY 1741 GCAAGCATCTTATCTTATCTTACCTGTTCA CCGTTTAACTAGCAGGAGATCAGTATG 1800  
Db 1741 GCAAGCATCTTATCTTATCTTACCTGTTCA CCGTTTAACTAGCAGGAGATCAGTATG 1800  
QY 1801 AGCCATTTGATTTGTCACATATCAGATGCT CCAAGACACTTTCCTTATGCCAGACT 1860  
Db 1801 AGCCATTTGATTTGTCACATATCAGATGCT CCAAGACACTTTCCTTATGCCAGACT 1860  
QY 1861 CGAATCCCTGACCCCGATGTCGAAAGAAAT GGGGCGCATATGAGGCGGCTGATATG 1920  
Db 1861 CGAATCCCTGACCCCGATGTCGAAAGAAAT GGGGCGCATATGAGGCGGCTGATATG 1920  
QY 1921 GCAATCTAGGCTCCGACACTCATCTATACCT GCGATCCGCAATATCGTATACCT 1980  
Db 1921 GCAATCTAGGCTCCGACACTCATCTATACCT GCGATCCGCAATATCGTATACCT 1980  
QY 1981 CACATGCGCATCTTACCTGCGGCGATGCGCT GATCGATGATGAGGCGGCGGCA 2040  
Db 1981 CACATGCGCATCTTACCTGCGGCGATGCGCT GATCGATGATGAGGCGGCGGCA 2040  
QY 2041 GCAATTTGCGCAACCGCAACACAGCAATCA TCACTGAGGCGGCGCAATGCGGCGCA 2100  
Db 2041 GCAATTTGCGCAACCGCAACACAGCAATCA TCACTGAGGCGGCGCAATGCGGCGCA 2100  
QY 2101 CCTGCTGACACCAATCAACAGCTGATCTGCA CTATGCAATTTGAGGCTTGCAGAC 2160  
Db 2101 CCTGCTGACACCAATCAACAGCTGATCTGCA CTATGCAATTTGAGGCTTGCAGAC 2160  
QY 2161 CGAGACAGCTGCGCAAGATTTAACTATCAAT CTTTATGAGGCGGCGGCGGCA 2220  
Db 2161 CGAGACAGCTGCGCAAGATTTAACTATCAAT CTTTATGAGGCGGCGGCGGCA 2220  
QY 2221 AAACGCTGTTGATGAAAGATGTGATGCTGTA TGAATGACATCATGCAAGCGGCTG 2280  
Db 2221 AAACGCTGTTGATGAAAGATGTGATGCTGTA TGAATGACATCATGCAAGCGGCTG 2280  
QY 2281 GTGCGCACAGTGGGCGAAGGATGCGGCTGCT CCGTTTACTATTTCCCAACAGAGACG 2340  
Db 2281 GTGCGCACAGTGGGCGAAGGATGCGGCTGCT CCGTTTACTATTTCCCAACAGAGACG 2340  
QY 2341 ATGACAGAGATGAGGCGGAGCTTCAAAAGCA CAGGCACTGCAAGAGATGCTCAAGGCAATG 2400  
Db 2341 ATGACAGAGATGAGGCGGAGCTTCAAAAGCA CAGGCACTGCAAGAGATGCTCAAGGCAATG 2400  
QY 2401 ATGAGTTTGTGTGTGAGAGCTGTTGCTGAG TTTGTTGAAATTTCAAGAGATGAGGTAATG 2460  
Db 2401 ATGAGTTTGTGTGTGAGAGCTGTTGCTGAG TTTGTTGAAATTTCAAGAGATGAGGTAATG 2460

QY 2461 TCATGCTTCGATCCCTTCGAGCTCTTCAATCAAGCTGTGATGTGTCACAGCA 2520  
Db 2461 TCATGCTTCGATCCCTTCGAGCTCTTCAATCAAGCTGTGATGTGTCACAGCA 2520  
QY 2521 TGTTCATGCGATGATCAACATATGAAACAGAGATGAAAGCGCTGCTCAAGATG 2580  
Db 2521 TGTTCATGCGATGATCAACATATGAAACAGAGATGAAAGCGCTGCTCAAGATG 2580  
QY 2581 GCAACTATTTCTCAACGCGCACTTTGTCATGAGGCGCACATGAAGTATGCGCATGA 2640  
Db 2581 GCAACTATTTCTCAACGCGCACTTTGTCATGAGGCGCACATGAAGTATGCGCATGA 2640  
QY 2641 GCCCAAGTACTATTTCCAGAGAGGCTGGAACATCTTCACTTATCTGAGCCCTAT 2700  
Db 2641 GCCCAAGTACTATTTCCAGAGAGGCTGGAACATCTTCACTTATCTGAGCCCTAT 2700  
QY 2701 CGCTATTGGAACCTGAGACTCGAGGGGTGTCAGGGGTCTGTCCGTATGCGTTCCCTTGCAT 2760  
Db 2701 CGCTATTGGAACCTGAGACTCGAGGGGTGTCAGGGGTCTGTCCGTATGCGTTCCCTTGCAT 2760  
QY 2761 TGTTCGCTGATTTCAAACTGCGCAAGTCTTGGCCCACTTAATTTACTCATTTGATTA 2820  
Db 2761 TGTTCGCTGATTTCAAACTGCGCAAGTCTTGGCCCACTTAATTTACTCATTTGATTA 2820  
QY 2821 TGGAGCGCAACCATGAGGCGCTTGGGTAATCTGACATTTGTACTTTGATTAATCTTCA 2880  
Db 2821 TGGAGCGCAACCATGAGGCGCTTGGGTAATCTGACATTTGTACTTTGATTAATCTTCA 2880  
QY 2881 TCTTTGCGGTGATGGAATGCAACTGTTCCGAAAGATATCATGATCAAGAGCGCT 2940  
Db 2881 TCTTTGCGGTGATGGAATGCAACTGTTCCGAAAGATATCATGATCAAGAGCGCT 2940  
QY 2941 TTCCGATGAGGAGCTGCGCGGCTGGAACCTTCACTGATTAATGACAGCTTCAATGATCG 3000  
Db 2941 TTCCGATGAGGAGCTGCGCGGCTGGAACCTTCACTGATTAATGACAGCTTCAATGATCG 3000  
QY 3001 TGTTCGCGGTGATGGAATGCAACTGTTCCGAAAGATATCATGATCAAGAGCGCT 3060  
Db 3001 TGTTCGCGGTGATGGAATGCAACTGTTCCGAAAGATATCATGATCAAGAGCGCT 3060  
QY 3061 ATGCTGCTGATTCCTTCTTCTTGGCCACGTTGTCATCGGCAATCTTGTGATCTTA 3120  
Db 3061 ATGCTGCTGATTCCTTCTTCTTGGCCACGTTGTCATCGGCAATCTTGTGATCTTA 3120  
QY 3121 ACCCTTTCTAGCTTGTGTTTTCATTTGGCTACTATGACTTATCAGCGCGGACTG 3180  
Db 3121 ACCCTTTCTAGCTTGTGTTTTCATTTGGCTACTATGACTTATCAGCGCGGACTG 3180  
QY 3181 CCGATTAAGATAGCAATTAAGTACGAGGCTTCAATGAAATGCGGATTTAAAGTT 3240  
Db 3181 CCGATTAAGATAGCAATTAAGTACGAGGCTTCAATGAAATGCGGATTTAAAGTT 3240  
QY 3241 GGGTAAAGCTAATATGCTGATTTCAATTAATACGTAAACAAATTGCAATCAAA 3300  
Db 3241 GGGTAAAGCTAATATGCTGATTTCAATTAATACGTAAACAAATTGCAATCAAA 3300  
QY 3301 TAAATGATCAACATCAAGTGAAGACCAACAGATCACTGATTTGAGCGAAGAGC 3360  
Db 3301 TAAATGATCAACATCAAGTGAAGACCAACAGATCACTGATTTGAGCGAAGAGC 3360  
QY 3361 ATGTTGACAGCACTGAGCTGAGGCGACGAGATCTTCGCGAGCGCTCATCAAGA 3420  
Db 3361 ATGTTGACAGCACTGAGCTGAGGCGACGAGATCTTCGCGAGCGCTCATCAAGA 3420  
QY 3421 AGGGGATCAAGAGCAGCACTGAGGCTGAGGCTGAGGATGAGGATTTCAAGA 3480  
Db 3421 AGGGGATCAAGAGCAGCACTGAGGCTGAGGCTGAGGATGAGGATTTCAAGA 3480  
QY 3481 TACACGCGCAGATGAAGAACCAAGCGGAAAGATCCAAATATCTAAATTAACCAAGCA 3540  
Db 3481 TACACGCGCAGATGAAGAACCAAGCGGAAAGATCCAAATATCTAAATTAACCAAGCA 3540  
QY 3541 TGAATGCACTCAATTAACCAAGCAATATGATGGAACAGAGCTAAACATAGAG 3600

Db 3541 TGAATGCACTCAATTAACCAAGCAATATGATGGAACAGAGCTAAACATAGAG 3600  
QY 3601 GTTGTCTCTTACAGAGCAGCACTGCGAGCATTAATCTATATGTAAGCATTAAGATC 3660  
Db 3601 GTTGTCTCTTACAGAGCAGCACTGCGAGCATTAATCTATATGTAAGCATTAAGATC 3660  
QY 3661 GACCAATCAAGAGCAGCACTGCGAGCATTAATCTATATGTAAGCATTAAGATC 3720  
Db 3661 GACCAATCAAGAGCAGCACTGCGAGCATTAATCTATATGTAAGCATTAAGATC 3720  
QY 3721 GCGAGCGCAGCAGAGGATTAAGTCTGACAGAGACTGAGCAGAGAGGCGCAATGCG 3780  
Db 3721 GCGAGCGCAGCAGAGGATTAAGTCTGACAGAGACTGAGCAGAGAGGCGCAATGCG 3780  
QY 3781 AGAGGCGCGCTGACGCTGATTAATTAATGTCACAGCAGAGATTAATCTGATG 3840  
Db 3781 AGAGGCGCGCTGACGCTGATTAATTAATGTCACAGCAGAGATTAATCTGATG 3840  
QY 3841 AATATCAAGCTGATTTGCTGCGCGATTCGATTAAGAAATTTCCGATCTTACCGGCTG 3900  
Db 3841 AATATCAAGCTGATTTGCTGCGCGATTCGATTAAGAAATTTCCGATCTTACCGGCTG 3900  
QY 3901 ACAGTACTGCGGCTTCTGCGAAGATGAGGCAATTAAGCACTGAAACTTTCAATTA 3960  
Db 3901 ACAGTACTGCGGCTTCTGCGAAGATGAGGCAATTAAGCACTGAAACTTTCAATTA 3960  
QY 3961 TTTGAAATTAATTTTGAACAGCTGATTAATCACTATGATTTTAATGATGACTTACCTT 4020  
Db 3961 TTTGAAATTAATTTTGAACAGCTGATTAATCACTATGATTTTAATGATGACTTACCTT 4020  
QY 4021 TGGATTTAAGAGATGATCATCTGCGAAGAGCCCATACAGAGATTTTAATCACTTA 4080  
Db 4021 TGGATTTAAGAGATGATCATCTGCGAAGAGCCCATACAGAGATTTTAATCACTTA 4080  
QY 4081 TGGAGCAATTAATTAAGCTAATATTTCTTGGAAATGTTAATCAAGTGTGCGCTG 4140  
Db 4081 TGGAGCAATTAATTAAGCTAATATTTCTTGGAAATGTTAATCAAGTGTGCGCTG 4140  
QY 4141 GCTTCAAGTGTGATCTTCAACCAAGCGGTGATGCTGATTTGATGATGAT 4200  
Db 4141 GCTTCAAGTGTGATCTTCAACCAAGCGGTGATGCTGATTTGATGATGAT 4200  
QY 4201 CGCTTATCAACTTGTGCTTCACTTGTGAGAGTGTGATTTCAAGCTTCAAGCTA 4260  
Db 4201 CGCTTATCAACTTGTGCTTCACTTGTGAGAGTGTGATTTCAAGCTTCAAGCTA 4260  
QY 4261 TGGCAAGTAAAGAGCAGTGAACCACTAGCTGATGCGGATGAGGCGATGAGG 4320  
Db 4261 TGGCAAGTAAAGAGCAGTGAACCACTAGCTGATGCGGATGAGGCGATGAGG 4320  
QY 4321 TCGTCTTAATGCGCTGATCAAGCTATACGCTTCAATGTCATTTGCTGCTG 4380  
Db 4321 TCGTCTTAATGCGCTGATCAAGCTATACGCTTCAATGTCATTTGCTGCTG 4380  
QY 4381 TAAATTTTGGCTAATTTTGGCAATATGCTGATGAGCTTTTGTGCAAAATATTTTA 4440  
Db 4381 TAAATTTTGGCTAATTTTGGCAATATGCTGATGAGCTTTTGTGCAAAATATTTTA 4440  
QY 4441 AGTGGAGGACATGAATGAGCAGAGCTGAGGCGAGCATTAACCAATGCGAATGCT 4500  
Db 4441 AGTGGAGGACATGAATGAGCAGAGCTGAGGCGAGCATTAACCAATGCGAATGCT 4500  
QY 4501 GCGAGAGCGAGAACTACAGCTGAGTGAATCAGCAATGAATTTGATGATGATG 4560  
Db 4501 GCGAGAGCGAGAACTACAGCTGAGTGAATCAGCAATGAATTTGATGATGATG 4560  
QY 4561 CGTATCTGCTTTTCAAGTGGCACTTCAAGGCTGATTAATTAATGATGATG 4620  
Db 4561 CGTATCTGCTTTTCAAGTGGCACTTCAAGGCTGATTAATTAATGATGATG 4620  
QY 4621 CTATGATTCAGAGAGGTGAGCAGCAATCTGTTGAAAGCAATCTATGATG 4680



**ORIGIN**

Query Match	100.0%	Score 6513;	DB 6;	Length 6513;	ti: 1;
Best Local Similarity	100.0%	Pred. No. 0;			
Matches 6513; Conservative	0;	Mismatches	0;	Indels	0;

QY	1	TC	TG	AG	CG	TG	GG	CC	CG	CA	TG	CA	TG	CA	GA	GA	GA	AT	TC	CG	CA	TG	CA	TG	CA	GA	GA	AG	AC	60	
Db	1	TC	TG	AG	CG	TG	GG	CC	CG	CA	TG	CA	TG	CA	GA	GA	GA	AT	TC	CG	CA	TG	CA	TG	CA	GA	GA	AG	AC	60	
QY	61	GC	AG	TT	GT	TC	CG	TC	CC	TT	T	A	C	C	G	G	A	T	C	C	G	G	A	T	C	C	G	G	A	T	120
Db	61	GC	AG	TT	GT	TC	CG	TC	CC	TT	T	A	C	C	G	G	A	T	C	C	G	G	A	T	C	C	G	G	A	T	120
QY	121	CT	GA	AA	CA	TG	AA	AA	CA	GA	AG	AG	CT	CG	GA	AA	AA	GA	AG	CC	GA	GG	GA	GA	GG	AG	GG	TC	CG	CA	180
Db	121	CT	GA	AA	CA	TG	AA	AA	CA	GA	AG	AG	CT	CG	GA	AA	AA	GA	AG	CC	GA	GG	GA	GA	GG	AG	GG	TC	CG	CA	180
QY	181	AT	GT	TC	CG	CA	GA	AA	AA	AA	AA	AA	AA	AT	TC	CG	AT	GA	TG	CA	GA	GA	CA	GA	GA	TG	AA	AG	TC	240	
Db	181	AT	GT	TC	CG	CA	GA	AA	AA	AA	AA	AA	AA	AT	TC	CG	AT	GA	TG	CA	GA	GA	CA	GA	GA	TG	AA	AG	TC	240	
QY	241	C	A	C	A	A	C	C	G	G	A	T	C	T	A	C	T	T	G	A	C	A	G	G	T	G	C	C	A	T	300
Db	241	C	A	C	A	A	C	C	G	G	A	T	C	T	A	C	T	T	G	A	C	A	G	G	T	G	C	C	A	T	300
QY	301	T	C	C	G	C	C	G	G	A	T	T	G	C	C	T	C	T	C	T	C	G	A	G	A	T	T	G	A	T	360
Db	301	T	C	C	G	C	C	G	G	A	T	T	G	C	C	T	C	T	C	T	C	G	A	G	A	T	T	G	A	T	360
QY	361	T	G	A	C	A	T	T	T	C	C	T	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	420
Db	361	T	G	A	C	A	T	T	T	C	C	T	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	420
QY	421	T	G	T	G	A	G	T	G	C	T	C	A	T	T	C	A	T	T	C	A	T	T	C	A	T	T	C	A	T	480
Db	421	T	G	T	G	A	G	T	G	C	T	C	A	T	T	C	A	T	T	C	A	T	T	C	A	T	T	C	A	T	480
QY	481	C	A	T	A	T	T	T	T	C	C	T	A	T	C	A	T	C	A	C	A	A	T	T	C	T	C	T	C	A	540
Db	481	C	A	T	A	T	T	T	T	C	C	T	A	T	C	A	T	C	A	C	A	A	T	T	C	T	C	T	C	A	540
QY	541	C	G	A	C	A	A	C	G	C	C	A	C	G	T	T	G	A	G	T	G	A	T	T	C	A	C	C	G	A	600
Db	541	C	G	A	C	A	A	C	G	C	C	A	C	G	T	T	G	A	G	T	G	A	T	T	C	A	C	C	G	A	600
QY	601	C	A	G	C	T	G	T	T	A	A	G	T	A	T	G	G	A	G	T	T	A	T	T	A	T	T	A	T	T	660
Db	601	C	A	G	C	T	G	T	T	A	A	G	T	A	T	G	G	A	G	T	T	A	T	T	A	T	T	A	T	T	660
QY	661	C	A	T	G	A	A	T	T	G	C	T	G	A	T	T	A	T	A	G											

Qy	1021	ACGAGGGCATCTCATTTTCCGTTATGCGGCAATATATCCGCTGCGGGCAAGGCAACGACG	1087
Db	1021	ACGAGGGCATCTCATTTTCCGTTATGCGGCAATATATCCGCTGCGGGCAAGGCAACGACG	1087
Qy	1081	ATTATCGTGTGCTTCGACGAGGGTTTGTGTCCGAATCCGAATTATGTGCTACACAGCTTCGATT	1140
Db	1081	ATTATCGTGTGCTTCGACGAGGGTTTGTGTCCGAATCCGAATTATGTGCTACACAGCTTCGATT	1140
Qy	1141	CGTTCCGATGGGGCTTTCTCTGTCCGCTTCCGGCTGATGACACAGACTTCCTTGAGGAGATC	1200
Db	1141	CGTTCCGATGGGGCTTTCTCTGTCCGCTTCCGGCTGATGACACAGACTTCCTTGAGGAGATC	1200
Qy	1201	TGTACCAAGCTGATGTGTCGCGCGCGCCGACCATGSCACATGCTGTTCTTTATAGTCATCA	1266
Db	1201	TGTACCAAGCTGATGTGTCGCGCGCGCCGACCATGSCACATGCTGTTCTTTATAGTCATCA	1266
Qy	1261	TCTTCTCTAAGGTTCACTTCTATCTTGTGAATTGATTTTGTGGCATTGTTGGCCATGTTCGATG	1320
Db	1261	TCTTCTCTAAGGTTCACTTCTATCTTGTGAATTGATTTTGTGGCATTGTTGGCCATGTTCGATG	1320
Qy	1321	ACGAATTGCAAAAGGAAGGCGGAGAAAGAGAGGCTGCGCAAGAGAGAGGCGGATACGTAAG	1386
Db	1321	ACGAATTGCAAAAGGAAGGCGGAGAAAGAGAGGCTGCGCAAGAGAGAGGCGGATACGTAAG	1386
Qy	1381	CGAAGAAAGCTGCCCGCCGCAAAAGCGGCCAAAGCTGAGAGAGCGGGCCATGCGACGCTC	1440
Db	1381	CGAAGAAAGCTGCCCGCCGCAAAAGCGGCCAAAGCTGAGAGAGCGGGCCATGCGACGCTC	1440
Qy	1441	AGGAGAGAGCGGATATGCGCGCTGCCGCGCAAGAGGTGACCTGCAATCCGGAATATGCGCAAG	1500
Db	1441	AGGAGAGAGCGGATATGCGCGCTGCCGCGCAAGAGGTGACCTGCAATCCGGAATATGCGCAAG	1500
Qy	1501	GTCGACGATATTCTTGATCAGCTATAGCTATTGTTGTGGCGGAGAGGGCAACGATG	1566
Db	1501	GTCGACGATATTCTTGATCAGCTATAGCTATTGTTGTGGCGGAGAGGGCAACGATG	1566
Qy	1561	ACAAACAACAAAGAGAGATGTCATTTCGAGACGTTCGAGGTGTGAAGTCGAGTCCGTTAGCG	1620
Db	1561	ACAAACAACAAAGAGAGATGTCATTTCGAGACGTTCGAGGTGTGAAGTCGAGTCCGTTAGCG	1620
Qy	1621	TTATATCAAAAGACAAACGACCTTACACAGACACACCAAGCTTACCAAAAGTTCTTAAATGA	1686
Db	1621	TTATATCAAAAGACAAACGACCTTACACAGACACACCAAGCTTACCAAAAGTTCTTAAATGA	1686
Qy	1681	GCAAGACATCCTTATCTTATCTGTACCTGTTCACCGTTTAAATACATACGAGGGGATTCACGTAGTT	1740
Db	1681	GCAAGACATCCTTATCTTATCTGTACCTGTTCACCGTTTAAATACATACGAGGGGATTCACGTAGTT	1740
Qy	1741	CTCACAAAGTACAGATACGGAAGGAGTGTGGCGCTTTGGTATATCCCGGTATAGCATATGTA	1800
Db	1741	CTCACAAAGTACAGATACGGAAGGAGTGTGGCGCTTTGGTATATCCCGGTATAGCATATGTA	1800
Qy	1801	AGGCATTTGATTTGTCAACATATCAGAGATCCGACAGCACTTGCCCTTATGCGACGACT	1866
Db	1801	AGGCATTTGATTTGTCAACATATCAGAGATCCGACAGCACTTGCCCTTATGCGACGACT	1866
Qy	1861	CGAATGCGTACCCCGCATGTCCGAAAGAAATGGGGCATCATATGTGCCCGGTATCTATG	1920
Db	1861	CGAATGCGTACCCCGCATGTCCGAAAGAAATGGGGCATCATATGTGCCCGGTATCTATG	1920
Qy	1921	GCAATCTAAGGCTCCCGACATCATATCGATATCTTGATCTTGATCAAGTCCCGAATTCGTATACCT	1986
Db	1921	GCAATCTAAGGCTCCCGACATCATATCGATATCTTGATCTTGATCAAGTCCCGAATTCGTATACCT	1986
Qy	1981	CACATGGCGATCTTACTTCGCGGGCATGGCGGTCAATGGGCGTCACACATGACCAAGGAGA	2040
Db	1981	CACATGGCGATCTTACTTCGCGGGCATGGCGGTCAATGGGCGTCACACATGACCAAGGAGA	2040
Qy	2041	GCAAAATTGGCAACCGGACACACAGCAATCAATATGATGGGGCGCCACCAATGGCGGACCA	2100
Db	2041	GCAAAATTGGCAACCGGACACACAGCAATCAATATGATGGGGCGCCACCAATGGCGGACCA	2100

QY	2101	CCGTCTCTGGA	CCAAATCA	CAAGCTCGAT	CAATGCGCA	CTACAGAAATTTGGCTGAGTGA	2160
Db	2101	CCGTCTGGA	CCAAATCA	CAAGCTCGAT	CAATGCGCA	CTACAGAAATTTGGCTGAGTGA	2160
QY	2161	CGA	CGAAGCTGG	CAACATTTAA	CAATCATG	CAATCCCTTTATCGAGCCGTC	CAAC
Db	2161	CGA	CGAAGCTGG	CAACATTTAA	CAATCATG	CAATCCCTTTATCGAGCCGTC	CAAC
QY	2221	AAACGGTGTG	ATATGAAA	AGTATGAT	GTCCGAT	ATGATCATCATGAA	CAGCGCGCTG
Db	2221	AAACGGTGTG	ATATGAAA	AGTATGAT	GTCCGAT	ATGATCATCATGAA	CAGCGCGCTG
QY	2281	GTGCGCA	CAGT	CGGGCAAG	CGATGCGAGT	GTCTCCGTTTACTATTTCCAA	CAGAGACG
Db	2281	GTGCGCA	CAGT	CGGGCAAG	CGATGCGAGT	GTCTCCGTTTACTATTTCCAA	CAGAGACG
QY	2341	ATGA	CGAGATGGG	CCGACTTTCAA	AGACAGG	CAAGCTTCGAAAGG	CACTG
Db	2341	ATGA	CGAGATGGG	CCGACTTTCAA	AGACAGG	CAAGCTTCGAAAGG	CACTG
QY	2401	ATGATGTTTGTG	ATGGGAC	CTGTCGGGTTTGAT	TGATTTCA	GAGTGTGAT	CGC
Db	2401	ATGATGTTTGTG	ATGGGAC	CTGTCGGGTTTGAT	TGATTTCA	GAGTGTGAT	CGC
QY	2461	TCAT	CGTCTTCGAT	CCCTTCGTG	CAAGCTCTT	CATCAGCTGTG	CATTGTG
Db	2461	TCAT	CGTCTTCGAT	CCCTTCGTG	CAAGCTCTT	CATCAGCTGTG	CATTGTG
QY	2521	TGTT	CATGAGCA	ATGATACCA	CGATATGAC	CAAGAGATG	GAACGGGTG
Db	2521	TGTT	CATGAGCA	ATGATACCA	CGATATGAC	CAAGAGATG	GAACGGGTG
QY	2581	GCA	CTATATTTCTT	CA	CCGCA	CCCTTTG	CCCATCGA
Db	2581	GCA	CTATATTTCTT	CA	CCGCA	CCCTTTG	CCCATCGA
QY	2641	GCCCCA	GACTATTTT	CCAGAGAGG	GCTGGAA	CACTTCGAT	CAATATG
Db	2641	GCCCCA	GACTATTTT	CCAGAGAGG	GCTGGAA	CACTTCGAT	CAATATG
QY	2641	GCCCCA	GACTATTTT	CCAGAGAGG	GCTGGAA	CACTTCGAT	CAATATG
Db	2641	GCCCCA	GACTATTTT	CCAGAGAGG	GCTGGAA	CACTTCGAT	CAATATG
QY	2701	CGCTA	TTTGA	ACTGGG	ACTCGAGG	GCTGTCCG	TATGCGT
Db	2701	CGCTA	TTTGA	ACTGGG	ACTCGAGG	GCTGTCCG	TATGCGT
QY	2761	TGCT	CGCTG	TATTCAA	ATGCGCA	AGTCTTG	GGCCCA
Db	2761	TGCT	CGCTG	TATTCAA	ATGCGCA	AGTCTTG	GGCCCA
QY	2821	TGGG	CGACCA	TGGGCGCTTT	TGGGATCT	GACATTTG	ATGACTT
Db	2821	TGGG	CGACCA	TGGGCGCTTT	TGGGATCT	GACATTTG	ATGACTT
QY	2881	TCCTT	TCGCTG	ATGGA	ATGCA	CTGTT	CGAAGAA
Db	2881	TCCTT	TCGCTG	ATGGA	ATGCA	CTGTT	CGAAGAA
QY	2941	TTTC	CGGATGGG	AGCTGCGCGG	CTGGAA	CTTCA	CCGACTTTAT
Db	2941	TTTC	CGGATGGG	AGCTGCGCGG	CTGGAA	CTTCA	CCGACTTTAT
QY	3001	TGTT	TCGCGG	TGCTCT	TCGAGAA	TGATCGA	GTGAGT
Db	3001	TGTT	TCGCGG	TGCTCT	TCGAGAA	TGATCGA	GTGAGT
QY	3061	ATGT	CTCGTGA	TTCCCTT	CTTCTTGG	CA	CGCTTGA
Db	3061	ATGT	CTCGTGA	TTCCCTT	CTTCTTGG	CA	CGCTTGA
QY	3121	ACCT	TTTCTT	AGCCTT	TTTGTG	CCAAATTT	TGGCTCAT
Db	3121	ACCT	TTTCTT	AGCCTT	TTTGTG	CCAAATTT	TGGCTCAT
QY	3181	CCGAT	TA	CGATAT	GAATAT	ATAGCC	AGCCTT
Db	3181	CCGAT	TA	CGATAT	GAATAT	ATAGCC	AGCCTT

Db	3181	CCGATTAACGATACGATTAATAATATGCGGAGCCCTTCAATCGAATTGGCCCATTTAAAAGTT	3240
Qy	3241	GGGTTAAGCGCTAAATATTTGCTGATTTGTTTCAAATTAAATACGTAAACAATTTGACAAATTCMAA	3300
Db	3241	GGGTTAAGCGCTAAATATTTGCTGATTTGTTTCAAATTAAATACGTAAACAATTTGACAAATTCMAA	3300
Qy	3301	TAACTGATCAACAATCAAGGTGAAGAGACCAACAGATACAGTTGATTTTGGAGCGAAGAGC	3360
Db	3301	TAACTGATCAACAATCAAGGTGAAGAGACCAACAGATACAGTTGATTTTGGAGCGAAGAGC	3360
Qy	3361	ATGTGTCAACAAAGACTGGAGCTTGGGCCACGACGAGATCTTGGCCAGCGCTCATACAGA	3420
Db	3361	ATGTGTCAACAAAGACTGGAGCTTGGGCCACGACGAGATCTTGGCCAGCGCTCATACAGA	3420
Qy	3421	AGGGGATTCAGAGACGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAAATTCACGA	3480
Db	3421	AGGGGATTCAGAGACGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAAATTCACGA	3480
Qy	3481	TACACGGCGCATGTAAAGAACAAAGCCGAAAGAAATCCAATATCTTAATATACGCAACGA	3540
Db	3481	TACACGGCGCATGTAAAGAACAAAGCCGAAAGAAATCCAATATCTTAATATACGCAACGA	3540
Qy	3541	TGATTTGCGAACTCAATTTAACCAACCAAGACAAATGACTTGGAAACAGACTTAAACCTATAGAG	3600
Db	3541	TGATTTGCGAACTCAATTTAACCAACCAAGACAAATGACTTGGAAACAGACTTAAACCTATAGAG	3600
Qy	3601	GTTTGTGCTTACAGAGACGACCACTGCGACATTTACTATATGTGATAGCATTAAGATC	3660
Db	3601	GTTTGTGCTTACAGAGACGACCACTGCGACATTTACTATATGTGATAGCATTAAGATC	3660
Qy	3661	GACCAATTCAAGAGACGAGGCCACAAAGGGCAGCGCCGAGACGATGAGGGCGAGAGAACG	3720
Db	3661	GACCAATTCAAGAGAGAGAGGCCACAAAGGGCAGCGCCGAGAGACGATGAGGGCGAGAGAACG	3720
Qy	3721	GGCAGCGCAGAAAGAGAGATTTTAGGTCTCGACGAGAACTTGGACGAGAGCGGAATGCG	3780
Db	3721	GGCAGCGCAGAAAGAGAGATTTTAGGTCTCGACGAGAACTTGGAGAGAGAGCGGAATGCG	3780
Qy	3781	AGGAGGGCGCGCTCGACCGGTATATCATTTATTCATGCAACGACGAGATATACTGATG	3840
Db	3781	AGGAGGGCGCGCTCGACCGGTATATCATTTATTCATGCAACGACGAGATATATCTCATG	3840
Qy	3841	AATATCCAGCTGATTTGCTGCCCGCAATCGATCTAATAAGAAATTTCCGATCTTACCGGTG	3900
Db	3841	AATATCCAGCTGATTTGCTGCCCGCAATCGATCTAATAAGAAATTTCCGATCTTACCGGTG	3900
Qy	3901	ACGATGACTCGCGCTTCTGGCAGAGATGGGGCAATTTACGACTGAAAATTTCATATTA	3960
Db	3901	ACGATGACTCGCGCTTCTGGCAGAGATGGGGCAATTTACGACTGAAAATTTCATATTA	3960
Qy	3961	TTGAAATTAATATTTTGAACACGCTGTATCACTAATGATTTTAATAGATGCTTACTT	4020
Db	3961	TTGAAATTAATATTTTGAACACGCTGTATCACTAATGATTTTAATAGATGCTTACTT	4020
Qy	4021	TGGCATTTGAAGATGTACATCTGGCACAAGAACCCATATGCGAGATATTTTATACTATA	4080
Db	4021	TGGCATTTGAAGATGTACATCTGGCACAAGAACCCATATGCGAGATATTTTATACTATA	4080
Qy	4081	TGAGACAGATATTTACGGTTATATTTCTTTTGGAAATGTTATCAATGATGTTGGCGCTCG	4140
Db	4081	TGAGACAGATATTTTACGGTTATATTTCTTTTGGAAATGTTATCAATGATGTTGGCGCTCG	4140
Qy	4141	GCTTCAAGTGTACTTCAACCAAGCGGTGTGGTGGCTGATTTGCTGATTTGTCAAGTAT	4200
Db	4141	GCTTCAAGTGTACTTCAACCAAGCGGTGTGGTGGCTGATTTGCTGATTTGTCAAGTAT	4200
Qy	4201	CGCTTATCAACTTGGTTGCTTCACTGTGTGAGCTGGGTATTCAGAGCTTCAAGACTA	4260
Db	4201	CGCTTATCAACTTGGTTGCTTCACTGTGTGAGCTGGGTATTCAGAGCTTCAAGACTA	4260
Qy	4261	TGCGAAGCTTAAAGACATGAGACCACTAAGTGCATGTCCCGATATGAGGGCGATGAGGG	4320

Dh 4261 TGCGAAGCTTAAGACACTGAGACCACTACGTGCGCATGTCCTGTATGAGGCGATGAGG 4320  
Qy 4321 TCGGTGTAATGCGGTGTAACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380  
Db 4321 TCGGTGTAATGCGGTGTAACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380  
Qy 4381 TAAATTTTGGCTAATTTTGGCATATGAGGTGTACAGCTTTTCTGGAAAAATATTTTA 4440  
Db 4381 TAAATTTTGGCTAATTTTGGCATATGAGGTGTACAGCTTTTCTGGAAAAATATTTTA 4440  
Qy 4441 AGTGGAGGACATGATGGAAGCTCAGCCACGAGATCATACCAATCCGAATGCT 4500  
Db 4441 AGTGGAGGACATGATGGAAGCTCAGCCACGAGATCATACCAATCCGAATGCT 4500  
Qy 4501 GCGAGAGGAGACATACACGTGGGTGAATTGACGATGAAATTTGCAATGTAGGTAAAG 4560  
Db 4501 GCGAGAGGAGACATACACGTGGGTGAATTGACGATGAAATTTGCAATGTAGGTAAAG 4560  
Qy 4561 CGTATCTGCTTTTCAAGTGGCCACCTTCAAGGCTGATACAAATCATGAACGATG 4620  
Db 4561 CGTATCTGCTTTTCAAGTGGCCACCTTCAAGGCTGATACAAATCATGAACGATG 4620  
Qy 4621 CTATGATTCACGAGAGGTGGAACAAGCAATTCGTGAAGGAACATCTACATGTAAT 4680  
Db 4621 CTATGATTCACGAGAGGTGGAACAAGCAATTCGTGAAGGAACATCTACATGTAAT 4680  
Qy 4681 TATATTTGCTATCTTCAATCATATTTGATCTTTTCACTCATCTGTTCATTTGGTG 4740  
Db 4681 TATATTTGCTATCTTCAATCATATTTGATCTTTTCACTCATCTGTTCATTTGGTG 4740  
Qy 4741 TTATCATGATTAATTTTATGAGCAAAAGAAAAAGAGGTGATCATAGAAATGTTCA 4800  
Db 4741 TTATCATGATTAATTTTATGAGCAAAAGAAAAAGAGGTGATCATAGAAATGTTCA 4800  
Qy 4801 TGACAGAAAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTCTAAAAACAT 4860  
Db 4801 TGACAGAAAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTCTAAAAACAT 4860  
Qy 4861 TAAAGGCAATTCAGAGACCAAGGTGGCGACACAGCAATAGTCTTTGAAATAGTAACG 4920  
Db 4861 TAAAGGCAATTCAGAGACCAAGGTGGCGACACAGCAATAGTCTTTGAAATAGTAACG 4920  
Qy 4921 AATAAGAAATGCGATTAATCATATTAATGTTATTCATGCTGAACATGTTCAACGATGACC 4980  
Db 4921 AATAAGAAATGCGATTAATCATATTAATGTTATTCATGCTGAACATGTTCAACGATGACC 4980  
Qy 4981 TCGATCGTTACGATGCGTGGGACAGTAAACGGGCTCTGAGACTATCTCAATGCGATAT 5040  
Db 4981 TCGATCGTTACGATGCGTGGGACAGTAAACGGGCTCTGAGACTATCTCAATGCGATAT 5040  
Qy 5041 TCGTATGTTATTTTCAAGTCTCGAATGTCTAATTAATAATTTGGCTTTACGATATCAAT 5100  
Db 5041 TCGTATGTTATTTTCAAGTCTCGAATGTCTAATTAATAATTTGGCTTTACGATATCAAT 5100  
Qy 5101 TTAATGAGCCATGGAATTTATTTGATGATAGTATGATTTTATTCATCTTAGGCTTGG 5160  
Db 5101 TTAATGAGCCATGGAATTTATTTGATGATAGTATGATTTTATTCATCTTAGGCTTGG 5160  
Qy 5161 TACTTAAAGGATATTAATGAGAAATCTTCTGTGCGGACCCCTGCTCCGAGTGGTGG 5220  
Db 5161 TACTTAAAGGATATTAATGAGAAATCTTCTGTGCGGACCCCTGCTCCGAGTGGTGG 5220  
Qy 5221 TGGGGAAGTGGGCGGTCTCTTGGATGAGTGAAGGAGCCAGGCGATTGGGACATGCG 5280  
Db 5221 TGGGGAAGTGGGCGGTCTCTTGGATGAGTGAAGGAGCCAGGCGATTGGGACATGCG 5280  
Qy 5281 TCTTCGCGTGGCCATGTCGCTGCGGCGCTGTTCAATCTGCTGCTGCTGCTGCTGCG 5340  
Db 5281 TCTTCGCGTGGCCATGTCGCTGCGGCGCTGTTCAATCTGCTGCTGCTGCTGCTGCG 5340  
Qy 5341 TCAATGTCATCTTTGCGATTTTTCGCGATGTCGTTCTTCAATGCACTGGAAGGAAGACG 5400  
Db 5341 TCAATGTCATCTTTGCGATTTTTCGCGATGTCGTTCTTCAATGCACTGGAAGGAAGACG 5400

Qy 5401 GCATTAAGAGCTCTACAACTTCAAGACCTTTGGCCAGAGATGATCTCTGCTTTTCA 5460  
Db 5401 GCATTAAGAGCTCTACAACTTCAAGACCTTTGGCCAGAGATGATCTCTGCTTTTCA 5460  
Qy 5461 TGTGACGCTCAGCGGTGGGATGGTGTATGAGAGCCGATTAATCAATAGGAAGCATGCG 5520  
Db 5461 TGTGACGCTCAGCGGTGGGATGGTGTATGAGAGCCGATTAATCAATAGGAAGCATGCG 5520  
Qy 5521 ATCCACCCGACAGCACAAGGCTATCCGGGCAATTTGTTACGACGACCGTTGAATTA 5580  
Db 5521 ATCCACCCGACAGCACAAGGCTATCCGGGCAATTTGTTACGACGACCGTTGAATTA 5580  
Qy 5581 CGTTCTCTCTGCAATCTTACTATTAATGATTTTGAATGATTAATTAATGATTTGCTG 5640  
Db 5581 CGTTCTCTCTGCAATCTTACTATTAATGATTTTGAATGATTAATTAATGATTTGCTG 5640  
Qy 5641 TCATCTCGAAGACTATATGTCAGGCAACCGAGAGAGTCAAGAGGCTTAACCGACGAG 5700  
Db 5641 TCATCTCGAAGACTATATGTCAGGCAACCGAGAGAGTCAAGAGGCTTAACCGACGAG 5700  
Qy 5701 ACTACGACATGTAATGATCTGGGACCAATTCGATCCGAGGCGACCAAGTACATAC 5760  
Db 5701 ACTACGACATGTAATGATCTGGGACCAATTCGATCCGAGGCGACCAAGTACATAC 5760  
Qy 5761 GCTATGATCAGCTGTCGAAATTCCTGAGACGTAAGTGAAGGCTCCGCTGAGATCCCAAC 5820  
Db 5761 GCTATGATCAGCTGTCGAAATTCCTGAGACGTAAGTGAAGGCTCCGCTGAGATCCCAAC 5820  
Qy 5821 CGAACAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880  
Db 5821 CGAACAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880  
Qy 5881 GCGTGCATCTCGACGCGCTTACGAAAGACTTTTGGCGGAAAGGCAATCCGATAG 5940  
Db 5881 GCGTGCATCTCGACGCGCTTACGAAAGACTTTTGGCGGAAAGGCAATCCGATAG 5940  
Qy 5941 AGGAGACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6000  
Db 5941 AGGAGACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6000  
Qy 6001 TCTATCAACGCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6060  
Db 6001 TCTATCAACGCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6060  
Qy 6061 GCGGAAAGCACAAGGCGCGCGGAGAGGTGGGCTTTTGAAGCCGATACGATCATG 6120  
Db 6061 GCGGAAAGCACAAGGCGCGCGGAGAGGTGGGCTTTTGAAGCCGATACGATCATG 6120  
Qy 6121 GCGATGCGGTGATTCGAGATCCCGGAGACCCGCGGCGCGATGAGCAACGAGCGGATG 6180  
Db 6121 GCGATGCGGTGATTCGAGATCCCGGAGACCCGCGGCGCGATGAGCAACGAGCGGATG 6180  
Qy 6181 CGCCCGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6240  
Db 6181 CGCCCGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6240  
Qy 6241 AGAGTAATGTAATAGTCCGAGTGAAGTGAAGCGGCGCGGCGGACAGCAGCAGCAG 6300  
Db 6241 AGAGTAATGTAATAGTCCGAGTGAAGTGAAGCGGCGCGGCGGACAGCAGCAGCAG 6300  
Qy 6301 CCGGCGGCGGCGGAGACGAGCGGCGGAGATCCCGGAGCGGATGAGCGGCGGCGGAG 6360  
Db 6301 CCGGCGGCGGCGGAGACGAGCGGCGGAGATCCCGGAGCGGATGAGCGGCGGCGGAG 6360  
Qy 6361 CCGCGGCTTCTGAGAGAGCGAGCGGCTTCTGTAAGAAAGCGGCGCAAGAGTGGTCA 6420  
Db 6361 CCGCGGCTTCTGAGAGAGCGAGCGGCTTCTGTAAGAAAGCGGCGCAAGAGTGGTCA 6420  
Qy 6421 ACTGCGATGCGCGAGCATCACTGCGCGACGCGGATGTCTGAGCCAGGCTTGGCCCC 6480  
Db 6421 ACTGCGATGCGCGAGCATCACTGCGCGACGCGGATGTCTGAGCCAGGCTTGGCCCC 6480

RESULT 3  
LOCUS 174672  
DEFINITION Sequence 7 from patent US 5688917.  
ACCESSION 174672  
VERSION 174672.1 GI:3010813  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 6513)  
AUTHORS Arena, J.P., Peng, G., Hall, L.M., Liu, K., Van Der Ploeg, L.H.T.,  
Wang, P. and Warneke, J.W.  
TITLE Process for functional expression of the para cation channel  
JOURNAL Patent: US 5688917-A 7 18-NOV-1997;  
FEATURES  
source Location/Qualifiers  
1..6513  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 6513; DB 6; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6481 CCCTCCAGATGACGCGAGTATTAGCTTACA 6513  
Db 6481 CCCTCCAGATGACGCGAGTATTAGCTTACA 6513

QY 661 CATGGAATTGGCTGGAATTCTGTAATAGCTTTAGTTATGTGACCAATGGGTATAGATT 720  
Db 661 CATGGAATTGGCTGGAATTCTGTAATAGCTTTAGTTATGTGACCAATGGGTATAGATT 720  
QY 721 TAGGTATCTTACACCCCTGCGAAGCTTAAAGGGTGTGCGAGCGCTTAAACCGTAGCCA 780  
Db 721 TAGGTATCTTACACCCCTGCGAAGCTTAAAGGGTGTGCGAGCGCTTAAACCGTAGCCA 780  
QY 781 TTGTGCGAGGCTTGAAGACCATGTCGCGCGCGTCAATGAAATCGGTAAAGAACTTGGCGG 840  
Db 781 TTGTGCGAGGCTTGAAGACCATGTCGCGCGCGTCAATGAAATCGGTAAAGAACTTGGCGG 840  
QY 841 ATGTGATTAATCTGACCAATGTTCTCCCTGTGCGGTGTGCGGTGTAATGGGCTACAGATCT 900  
Db 841 ATGTGATTAATCTGACCAATGTTCTCCCTGTGCGGTGTGCGGTGTAATGGGCTACAGATCT 900  
QY 901 ATATGGGCGGTCTACCCGGAAGTGCATCAAGAAAGTTCCCGTGAACGGTTCTTGCGGCA 960  
Db 901 ATATGGGCGGTCTACCCGGAAGTGCATCAAGAAAGTTCCCGTGAACGGTTCTTGCGGCA 960  
QY 961 ATCTGACCGACGAGAACTGGGACTATCAATTCGCAATAGCTTCATATGGTATTCGAGG 1020  
Db 961 ATCTGACCGACGAGAACTGGGACTATCAATTCGCAATAGCTTCATATGGTATTCGAGG 1020  
QY 1021 ACGAGGCAATCTCATTTCCGTTATGCGGCAATATACCGGTGCGGGCAATGCGACGACG 1080  
Db 1021 ACGAGGCAATCTCATTTCCGTTATGCGGCAATATACCGGTGCGGGCAATGCGACGACG 1080  
QY 1081 ATTACGTGTGCTGACGAGGGGTTGATCCGAATTCGAATTAATGAGCTTACACCACTTCGATT 1140  
Db 1081 ATTACGTGTGCTGACGAGGGGTTGATCCGAATTCGAATTAATGAGCTTACACCACTTCGATT 1140  
QY 1141 CGTTCCGATGGGCTTCTCTGTCTGCGCTTCGCGTGAATGACAGAGCTTCTGAGGAGATC 1200  
Db 1141 CGTTCCGATGGGCTTCTCTGTCTGCGCTTCGCGTGAATGACAGAGCTTCTGAGGAGATC 1200  
QY 1201 TGTACCAAGCTGTGTTGCGCGCGCGGACCAATGACATGCTGTTCTTTAATAGTCATCA 1260  
Db 1201 TGTACCAAGCTGTGTTGCGCGCGCGGACCAATGACATGCTGTTCTTTAATAGTCATCA 1260  
QY 1261 TCTTCTAGGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTTGCCATGTCTATG 1320  
Db 1261 TCTTCTAGGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTTGCCATGTCTATG 1320  
QY 1321 ACGAATTGCAAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
Db 1321 ACGAATTGCAAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 CCGAAGAGCTGCGCGCGCGGCAAGGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
Db 1381 CCGAAGAGCTGCGCGCGCGGCAAGGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
QY 1441 AGGCAAGCGGATGCGGCTGCGCGCGGCAAGGCTGCACTGCAATCGGGAATGCGCAAG 1500  
Db 1441 AGGCAAGCGGATGCGGCTGCGCGCGGCAAGGCTGCACTGCAATCGGGAATGCGCAAG 1500  
QY 1501 GTCCGAGTATCTTGTGATGAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAAGATG 1560  
Db 1501 GTCCGAGTATCTTGTGATGAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAAGATG 1560  
QY 1561 ACAACAAAGAGAGAGATGCTCATTTGGAGCGTGGAGGTGGAGTGGAGTGGAGTGGAGCG 1620  
Db 1561 ACAACAAAGAGAGAGATGCTCATTTGGAGCGTGGAGGTGGAGTGGAGTGGAGTGGAGCG 1620  
QY 1621 TTATACAAAGACAAACGAGACCTACACAGACACCAAGCTACCAAGTTCTGTAAGTGA 1680  
Db 1621 TTATACAAAGACAAACGAGACCTACACAGACACCAAGCTACCAAGTTCTGTAAGTGA 1680  
QY 1681 GCAAGCATCTTATCTTACCTGTTACCGTTTACCGTTTAAATACGAGGGGATCACTGATGTT 1740  
Db 1681 GCAAGCATCTTATCTTACCTGTTACCGTTTACCGTTTAAATACGAGGGGATCACTGATGTT 1740

Qy 1741 CTCACAGTACGATACGAGACGCGCTTTGTATACCCGGTAGCGAT 1800  
Db 1741 CTCACAGTACGATACGAGACGCGCTTTGTATACCCGGTAGCGAT 1800  
Qy 1801 AGCCATTGGTATTTGCAACATATCAGAGTCCGACGACCTTGGCTTATGCGGAGCT 1860  
Db 1801 AGCCATTGGTATTTGCAACATATCAGAGTCCGACGACCTTGGCTTATGCGGAGCT 1860  
Qy 1861 GGAATGCGGTACCGCGGATGTCGAGAGAGATGGGCGCATATATGCGCGGTATG 1920  
Db 1861 GGAATGCGGTACCGCGGATGTCGAGAGAGATGGGCGCATATATGCGCGGTATG 1920  
Qy 1921 GCAATCTAGGCTCCGCACTCATCTATACCTCGCATCAGTCCGGAATATGATACCT 1980  
Db 1921 GCAATCTAGGCTCCGCACTCATCTATACCTCGCATCAGTCCGGAATATGATACCT 1980  
Qy 1981 CACATGGCGATCTACTCGGCGGATGCGCGTATGCGGCGTACAGCAATGACCAAGAGA 2040  
Db 1981 CACATGGCGATCTACTCGGCGGATGCGCGTATGCGGCGTACAGCAATGACCAAGAGA 2040  
Qy 2041 GCAATTTGCGGACCGGACACACGCGATCATATGATGGGCGCCCAATGCGGACCA 2100  
Db 2041 GCAATTTGCGGACCGGACACACGCGATCATATGATGGGCGCCCAATGCGGACCA 2100  
Qy 2101 CCTGTCTGACACCAATCACAAGCTCATCATCGGCACTAGCAAAATTTGGCTGAGTCA 2160  
Db 2101 CCTGTCTGACACCAATCACAAGCTCATCATCGGCACTAGCAAAATTTGGCTGAGTCA 2160  
Qy 2161 CGAGCAGAGCTGGCAGATTAACATCATGACATCTTTATCGAGCCGCTCGACAC 2220  
Db 2161 CGAGCAGAGCTGGCAGATTAACATCATGACATCTTTATCGAGCCGCTCGACAC 2220  
Qy 2221 AAAAGGTGTGATATGAAAGATGATGTCCTGAAATGACATCATGAAAGGCGGTG 2280  
Db 2221 AAAAGGTGTGATATGAAAGATGATGTCCTGAAATGACATCATGAAAGGCGGTG 2280  
Qy 2281 GTCCGACAGTCCGCGGACAGCATCGCGGTGTCTCCGTTTATCTATTTCCCAAGAGAG 2340  
Db 2281 GTCCGACAGTCCGCGGACAGCATCGCGGTGTCTCCGTTTATCTATTTCCCAAGAGAG 2340  
Qy 2341 ATGACAGAGATGGGCGGACGTTCAAGACAGGCACTGAAATGATCTCAAGGAGATG 2400  
Db 2341 ATGACAGAGATGGGCGGACGTTCAAGACAGGCACTGAAATGATCTCAAGGAGATG 2400  
Qy 2401 ATGATTTTGTGTGGGACCTGTGCTGGGTTTGTGAAATTTCAAGAGTGGATGCG 2460  
Db 2401 ATGATTTTGTGTGGGACCTGTGCTGGGTTTGTGAAATTTCAAGAGTGGATGCG 2460  
Qy 2461 TCATGCTTGTGATCCCTTGTGCGAGCTTTCATCAGCTGTGATGTTGGTCAACAGA 2520  
Db 2461 TCATGCTTGTGATCCCTTGTGCGAGCTTTCATCAGCTGTGATGTTGGTCAACAGA 2520  
Qy 2521 TGTTCATGCAATGATACCAACATATGAAAGAGAGATGGAAGCGCTGTCAAGAGTG 2580  
Db 2521 TGTTCATGCAATGATACCAACATATGAAAGAGAGATGGAAGCGCTGTCAAGAGTG 2580  
Qy 2581 GCAACTATTTTCTTCAACGCGCACTTTGCGATGAGGCGCAACATGAAAGTATGCGCATGA 2640  
Db 2581 GCAACTATTTTCTTCAACGCGCACTTTGCGATGAGGCGCAACATGAAAGTATGCGCATGA 2640  
Qy 2641 GCGCCAGTACTATTTTCAGAGAGGCGTGAACATCTTGAATCTTATGCGGCGCAT 2700  
Db 2641 GCGCCAGTACTATTTTCAGAGAGGCGTGAACATCTTGAATCTTATGCGGCGCAT 2700  
Qy 2701 CGCTATTGGAACGCGGACCTCGAGGGTGTCAAGGGTCTGTCCGATATGCGTTCTTTGAT 2760  
Db 2701 CGCTATTGGAACGCGGACCTCGAGGGTGTCAAGGGTCTGTCCGATATGCGTTCTTTGAT 2760  
Qy 2761 TGTCTGCGTATTTCAAACTGGCCAGATCTTGGCCCACTTAATTTATCTCATTTGATTA 2820  
Db 2761 TGTCTGCGTATTTCAAACTGGCCAGATCTTGGCCCACTTAATTTATCTCATTTGATTA 2820  
Qy 2821 TGGAGCGACATGCGGCGCTTTGGGTAATGACATTTGTACTTGTGATATCATCTTCA 2880

Db 2821 TGGAGCGACATGCGGCGCTTTGGGTAATGACATTTGTACTTGTGATATCATCTTCA 2880  
Qy 2881 TCTTTGCGGTATGGAATGCAACTGTTCCGAAAAGATTAATCATGATCAAGAGCCCT 2940  
Db 2881 TCTTTGCGGTATGGAATGCAACTGTTCCGAAAAGATTAATCATGATCAAGAGCCCT 2940  
Qy 2941 TTTCCGATGCGGACCTGCGCGGCTGGAACCTCACGCACTTATGACAGCTTCATGATCG 3000  
Db 2941 TTTCCGATGCGGACCTGCGCGGCTGGAACCTCACGCACTTATGACAGCTTCATGATCG 3000  
Qy 3001 TGTTCGCGGTGCTGTGCGGAAATGATGAGTCCATGATGAGGACTGATGACGCGGCG 3060  
Db 3001 TGTTCGCGGTGCTGTGCGGAAATGATGAGTCCATGATGAGGACTGATGACGCGGCG 3060  
Qy 3061 ATGTCTGCTGATTCCTTCTTTGCGGACCGTTTGCATGCGCATTTGTGTGATCTTA 3120  
Db 3061 ATGTCTGCTGATTCCTTCTTTGCGGACCGTTTGCATGCGCATTTGTGTGATCTTA 3120  
Qy 3121 ACCTTTCTTACCGTGTCTTTGTGCAATTTGGCTCATCTAGCTTACAGCGCGGACCTG 3180  
Db 3121 ACCTTTCTTACCGTGTCTTTGTGCAATTTGGCTCATCTAGCTTACAGCGCGGACCTG 3180  
Qy 3181 CCGATTAACGATACGAATTAATAACCGGAGCTTCAATCGAATTTGCCGATTTAAAGTT 3240  
Db 3181 CCGATTAACGATACGAATTAATAACCGGAGCTTCAATCGAATTTGCCGATTTAAAGTT 3240  
Qy 3241 GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATCGTAACAAATTTGACAAATCAA 3300  
Db 3241 GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATCGTAACAAATTTGACAAATCAA 3300  
Qy 3301 TAAATGATCAACCAATGAGTGAAGAGCAACCGAGATGATGATTTGAGCGGAGAGC 3360  
Db 3301 TAAATGATCAACCAATGAGTGAAGAGCAACCGAGATGATGATTTGAGCGGAGAGC 3360  
Qy 3361 ATGTGACCAAGAACTGAGCTGGGCGACGAGAGATCTTCCGCGACGCGCTCATCAAGA 3420  
Db 3361 ATGTGACCAAGAACTGAGCTGGGCGACGAGAGATCTTCCGCGACGCGCTCATCAAGA 3420  
Qy 3421 AGGGATCAAGAGACAGCACTGAGGAGTGGCCATCGGGAGATCGAATGGAATTCACGA 3480  
Db 3421 AGGGATCAAGAGACAGCACTGAGGAGTGGCCATCGGGAGATCGAATGGAATTCACGA 3480  
Qy 3481 TACACGGGATGATGAAGAACAAAGCGGAATCAATCTAATCTAATGAACGAAGA 3540  
Db 3481 TACACGGGATGATGAAGAACAAAGCGGAATCAATCTAATCTAATGAACGAAGA 3540  
Qy 3541 TGAATGCACTCAATTAACCAACGAATGAGCTGGAACAGAGCTAAACCTAGAG 3600  
Db 3541 TGAATGCACTCAATTAACCAACGAATGAGCTGGAACAGAGCTAAACCTAGAG 3600  
Qy 3601 GTTTGTCTTACAGAGACGACACTGCGACATTAATCTATATGATGATGAAGATC 3660  
Db 3601 GTTTGTCTTACAGAGACGACACTGCGACATTAATCTATATGATGATGAAGATC 3660  
Qy 3661 GACCATTTCAAGAGAGAGGCAAGGCGGCGGAGCATGAGGCGCAAGAGGCAAGG 3720  
Db 3661 GACCATTTCAAGAGAGAGGCAAGGCGGCGGAGCATGAGGCGCAAGAGGCAAGG 3720  
Qy 3721 GCGAGCGGACGAGAGAGATTTAGGTCTGACAGAGAACTGGAAGAGGCGCAATGCG 3780  
Db 3721 GCGAGCGGACGAGAGAGATTTAGGTCTGACAGAGAACTGGAAGAGGCGCAATGCG 3780  
Qy 3781 AGAGAGGCGCGCTGACGCGGTATATCATTTATGACAGAGAGATTAATCTGATG 3840  
Db 3781 AGAGAGGCGCGCTGACGCGGTATATCATTTATGACAGAGAGATTAATCTGATG 3840  
Qy 3841 AATATCAAGTGAATTTGCTGCGCGGATTCGTAATTAAGAAATTTCCATCTTACCGGTG 3900  
Db 3841 AATATCAAGTGAATTTGCTGCGCGGATTCGTAATTAAGAAATTTCCATCTTACCGGTG 3900  
Qy 3901 ACGATGACTGCGCGCTTGTGCAAGATGCGCAATTTACGACTGAAATCTTTCAATTA 3960

Db 3901 AGCATGATCGCCGCTTGGCGAAGATGGGGCAATTTAGCATGAAAACTTTTCATTTA 3960  
Qy 3961 TTGAAAAATAATTTTGAAGAGCTGTATATCATATGATTTTATGAGTAGCTTAGCTT 4020  
Db 3961 TTGAAAAATAATTTTGAAGAGCTGTATATCATATGATTTTATGAGTAGCTTAGCTT 4020  
Qy 4021 TGGCATTTAGAGATGATCATCTGCGCAAAAGACCCATCTGCGAGATTTTATCATATA 4080  
Db 4021 TGGCATTTAGAGATGATCATCTGCGCAAAAGACCCATCTGCGAGATTTTATCATATA 4080  
Qy 4081 TGGACGAATATTTTACGGTATATCTTCTTGGAAATGTTATCATAGTGGTGGCGCTCG 4140  
Db 4081 TGGACGAATATTTTACGGTATATCTTCTTGGAAATGTTATCATAGTGGTGGCGCTCG 4140  
Qy 4141 GCTTCAAAGTATCTTCCACCAACGCGTGTGTGCTGATTTGCTGATTTGCTGAT 4200  
Db 4141 GCTTCAAAGTATCTTCCACCAACGCGTGTGTGCTGATTTGCTGATTTGCTGAT 4200  
Qy 4201 CGCTTATCACTTCTGCTTCTTCACTTGTGTGAGTGTGTATTTCAAGCTTCAAGCTA 4260  
Db 4201 CGCTTATCACTTCTGCTTCTTCACTTGTGTGAGTGTGTATTTCAAGCTTCAAGCTA 4260  
Qy 4261 TGGCAAGCTTAAAGCACTGAGACCACTTATGCTGATCTCCGTTATGCAAGGCAATAGGG 4320  
Db 4261 TGGCAAGCTTAAAGCACTGAGACCACTTATGCTGATCTCCGTTATGCAAGGCAATAGGG 4320  
Qy 4321 TCGTCTGTTAATGCGCTGTGTAACAAGTATCCGTCATCTTCAATGTGCTATGCTGTGTC 4380  
Db 4321 TCGTCTGTTAATGCGCTGTGTAACAAGTATCCGTCATCTTCAATGTGCTATGCTGTGTC 4380  
Qy 4381 TAAATTTTGGCTAATTTTGGCAATAATGAGTATGAGCTTTTGGCTGAGAAATATTTTA 4440  
Db 4381 TAAATTTTGGCTAATTTTGGCAATAATGAGTATGAGCTTTTGGCTGAGAAATATTTTA 4440  
Qy 4441 AGTGGAGGACATGATGAGACGAGAGCTCAGCCAGATCATATCCAAATCGCATGCTCT 4500  
Db 4441 AGTGGAGGACATGATGAGACGAGAGCTCAGCCAGATCATATCCAAATCGCATGCTCT 4500  
Qy 4501 GCGAGAGCGGAACTACAGCTGGGTGAATTCAGCAATGAAATTTGATGATGATGATGATG 4560  
Db 4501 GCGAGAGCGGAACTACAGCTGGGTGAATTCAGCAATGAAATTTGATGATGATGATGATG 4560  
Qy 4561 CGTATCTGCTTTTCAAGTGGCCACCTTCAAAAGGCTGATTCATATCATGAAACGATG 4620  
Db 4561 CGTATCTGCTTTTCAAGTGGCCACCTTCAAAAGGCTGATTCATATCATGAAACGATG 4620  
Qy 4621 CTATGATTCAGAGAGTGGAGCAAGCAACCAATTCGTGAACGACATCTAATGATTT 4680  
Db 4621 CTATGATTCAGAGAGTGGAGCAAGCAACCAATTCGTGAACGACATCTAATGATTT 4680  
Qy 4681 TATATTTGATTTCTTATCATATTTGATCTTTTTCACATCTGCTCATTTGGTG 4740  
Db 4681 TATATTTGATTTCTTATCATATTTGATCTTTTTCACATCTGCTCATTTGGTG 4740  
Qy 4741 TTTATCATTTGATTTTAAATGAGCAAAAGAGAGGAGTGTGATTTGAAATGTTCA 4800  
Db 4741 TTTATCATTTGATTTTAAATGAGCAAAAGAGAGGAGTGTGATTTGAAATGTTCA 4800  
Qy 4801 TGAAGAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTTAAAAACAT 4860  
Db 4801 TGAAGAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTTAAAAACAT 4860  
Qy 4861 TAAAGGCAATTCAGAACCAAGGTGGGAGCAACAAGCAATAGTCTTGAATATGTAACG 4920  
Db 4861 TAAAGGCAATTCAGAACCAAGGTGGGAGCAACAAGCAATAGTCTTGAATATGTAACG 4920  
Qy 4921 AATAAGAAATTCGATATATATATATGTTATTCATTTGCTGAACATGTCACATGACCC 4980  
Db 4921 AATAAGAAATTCGATATATATATATGTTATTCATTTGCTGAACATGTCACATGACCC 4980  
Qy 4981 TCGATCTGTTAGATGCTGCGAGACGATATAACGCGGCTCTAGATATCTCATGCGATAT 5040  
Db 4981 TCGATCTGTTAGATGCTGCGAGACGATATAACGCGGCTCTAGATATCTCATGCGATAT 5040

Qy 5041 TGGTATGTTATTTTCAGTTTCCGATGCTATTAATAATTTGCTTACGATATCACTATT 5100  
Db 5041 TGGTATGTTATTTTCAGTTTCCGATGCTATTAATAATTTGCTTACGATATCACTATT 5100  
Qy 5101 TTAATGAGCCATGAAATTTATTTGATGATGATGATGATGATGATGATGATGATGATG 5160  
Db 5101 TTAATGAGCCATGAAATTTATTTGATGATGATGATGATGATGATGATGATGATGATG 5160  
Qy 5161 TACTTAGCAATATTAATGAGAAAGTACTTGTGTGCGGACCTGCTCCGAGTGTGCTG 5220  
Db 5161 TACTTAGCAATATTAATGAGAAAGTACTTGTGTGCGGACCTGCTCCGAGTGTGCTG 5220  
Qy 5221 TGGCAAAAGTGGGCGGCTGCTTCCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280  
Db 5221 TGGCAAAAGTGGGCGGCTGCTTCCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280  
Qy 5281 TCTTCCGCTTGGCGATGCTGCTGCGGCGCTGCTCAACATGCTGCTGCTGCTGCTG 5340  
Db 5281 TCTTCCGCTTGGCGATGCTGCTGCGGCGCTGCTCAACATGCTGCTGCTGCTGCTG 5340  
Qy 5341 TCAATGTTCAATTTTGGCAATTTTGGCAATGCTGCTTCAATGCAAGTGAAGAGAGAGG 5400  
Db 5341 TCAATGTTCAATTTTGGCAATTTTGGCAATGCTGCTTCAATGCAAGTGAAGAGAGG 5400  
Qy 5401 GCAATTAACAGAGCTTCAACTTCAAGACCTTTGGGAGGAGGAGGAGGAGGAGGAGGAG 5460  
Db 5401 GCAATTAACAGAGCTTCAACTTCAAGACCTTTGGGAGGAGGAGGAGGAGGAGGAGGAG 5460  
Qy 5461 TGTGAGAGTGCAGCGGCTGGAGTGTGTAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5520  
Db 5461 TGTGAGAGTGCAGCGGCTGGAGTGTGTAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5520  
Qy 5521 ATCCACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5580  
Db 5521 ATCCACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5580  
Qy 5581 CGTTTCTCTCTATACCTATGATTAAGCTTTTGAATGATTAATGATGATGATGATG 5640  
Db 5581 CGTTTCTCTCTATACCTATGATTAAGCTTTTGAATGATTAATGATGATGATGATG 5640  
Qy 5641 TCAATTCAGAACTATAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700  
Db 5641 TCAATTCAGAACTATAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700  
Qy 5701 ACTACGACATGATCTATGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5760  
Db 5701 ACTACGACATGATCTATGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5760  
Qy 5761 GCTATGATCAGCTGTGCGAAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5820  
Db 5761 GCTATGATCAGCTGTGCGAAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5820  
Qy 5821 CGAACAAGTACAGATCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5880  
Db 5821 CGAACAAGTACAGATCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5880  
Qy 5881 GCGTCCAGATCTCTGAGGCGCTTACGAAAGACTTTTGGCGGAGGAGGAGGAGGAGGAG 5940  
Db 5881 GCGTCCAGATCTCTGAGGCGCTTACGAAAGACTTTTGGCGGAGGAGGAGGAGGAGGAG 5940  
Qy 5941 AGGAGAGCGGAGTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6000  
Db 5941 AGGAGAGCGGAGTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6000  
Qy 6001 TCTCATCAACGCTGTGAGCTGACGCTGAGAGGAGTATGCGCGGCTTATTCAGACAGGCT 6060  
Db 6001 TCTCATCAACGCTGTGAGCTGACGCTGAGAGGAGTATGCGCGGCTTATTCAGACAGGCT 6060  
Qy 6061 GGGGAAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6120  
Db 6061 GGGGAAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6120

QY	6121	GGAGATGGGGGATATCCGGATGCCCCGGGACCCGGCGCCCCGATGAAACAAACGACGGCCGATG	6180
Db	6121	GCGATGGCGGATATCCGGATGCCCCGGGACCCGGCGCCCCGATGAAACAAACGACGGCCGATG	6180
QY	6181	CGCCCGCTGATGAGATGATGATGTTAAACGATACGACGAAGGAGACTCCGATGCCGATG	6240
Db	6181	CGCCCGCTGATGAGATGATGATGTTAAACGATACGACGAAGGAGACTCCGATGCCGATG	6240
QY	6241	AGATGATATGTAAATATGTCGGGATGAGATGCAACGGCGCGGACAGACGACGACGACG	6300
Db	6241	AGATGATATGTAAATATGTCGGGATGAGATGCAACGGCGCGGACAGACGACGACGACG	6300
QY	6301	CGGCGGCGGGCGGACGACGACGCGGGGAAAGTCCCGGAGCGGGTATGCCGCCGGCGACAGA	6360
Db	6301	CGGCGGCGGGCGGACGACGACGCGGGGAAAGTCCCGGAGCGGGTATGCCGCCGGCGACAGA	6360
QY	6361	CGCGCGTTCGTGTGAGAGACGACGGGTTTCGTGACCAAGAACGACCAAGATGATCATCC	6420
Db	6361	CGCGCGTTCGTGTGAGAGACGACGGGTTTCGTGACCAAGAACGACCAAGATGATCATCC	6420
QY	6421	ACTGCGCATCGCCGACGATCAAGTTCGCGACCGCGGATGTCGAGCCAGGCGCTCGCCCC	6480
Db	6421	ACTGCGCATCGCCGACGATCAAGTTCGCGACCGCGGATGTCGAGCCAGGCGCTCGCCCC	6480
QY	6481	CCCTCCAGATGACGACGAGTATTAAGTCTTGA	6513
Db	6481	CCCTCCAGATGACGACGAGTATTAAGTCTTGA	6513

#### RESULT 4 DROSODCHA

DEFINITION	Drosophila melanogaster sodium channel alpha subunit (para) gene, complete cds, alternatively spliced.
ACCESSION	M32078 M24285 M32079 M32080
VERSION	M32078.1 GI:403441

KEYWORDS  
SOURCE  
Drosophila melanogaster (fruit fly)

ORGANISM	REFERENCE
<i>Drosophila melanogaster</i>	1 (bases 1 to 6883)
Eukaryota; Metazoa; Archipoda; Insecta; Preyigota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridroidea; Drosophilidae; Drosophila.	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1 (bases 1 to 6883)  
Loughney K., Kreber R. and Ganetzky B.  
Molecular analysts of the para locus, a sodium channel gene in  
Drosophila  
Cell 58 (6), 1143-1154 (1989)

JOURNAL Cell 58 (6), 1143-1154 (1989)  
 MEDLINE 89376565  
 PUBMED 2550145  
 REFERENCE 2 (sites)  
 AUTHORS Ramaswami, M. and Tanouye, M.A.  
 TITLE Two sodium-channel genes in *Drosophila*: implications for channel

REFERENCE AUTHORS TITLE	
2 (sites) Ramawami, M. and Tanouye, M.A. Two sodium-channel genes in <i>Drosophila</i> : implications for channel diversity Proc. Natl. Acad. Sci. U.S.A. 86 (6), 2079-2082 (1989)	
JOURNAL MEDLINE PUBMED	89184571 2538830
REFERENCE	3 (sites)

REFERENCE	3 (sites)
AUTHORS	Thackeray, J.R. and Ganetzky, B.
TITLE	Developmentally regulated alternative splicing generates a complex array of <i>Drosophila</i> para sodium channel isoforms
JOURNAL	unpublished (1993)
COMMENT	On or before Apr 5, 2002 this sequence version replaced gi:158476.

JOURNAL COMMENT  
Unpublished (1993)  
On or before Apr 5, 2002 this sequence version replaced gi:158476, gi:158478, gi:158474.  
Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky, 25-APR-1989.

```

FEATURES
Source
    location/Qualifiers
    1..6883
    /organism="Drosophila melanogaster"
    /mol_type="genomic DNA"
    /strain="para-hd2"
    /db_xref="taxon:7227"
    /clone="ZS10.3"

```

gene

repeat\_region

**mRNA**

**mRNA**

mRNA

**mRNA**

mRNA

mRNA

CDS

[illegible]

CDS

AAAAAAAAAGTTAGSPGASAGROTAVALVESDGFVTKNGHKVVIHSRSPSITSRTADV"  
join(272..3606,3637..6667)  
/gene="para"  
/note="alternative exon f for optional inclusion in mRNA.  
this alternative exon exists in two forms (f30) presented  
here and (f24) see variation"  
/citation=[3]  
/codon\_start=1  
/product="sodium channel alpha subunit"  
/protein\_id="AAB59194.1"  
/db\_xref="GI:403446"

CDS

/db\_xref="FLYBASE:FBgn0003036"  
/translation="WTEBDSISSEBSLPRPTRESLVOIEORIAEHKOKELERK  
RAEGEVRGRKKKQKIRYDEDEDEGPDPTLEQGVIPRLQSGSPPELSTPL  
EDIDPYSNVLTVVVSCKGDIIPRSASAKAMMLDEPNIRVAIYLHPLESLFI  
TTLVNCILIMPTPTVSTEVIFGTIYFESAVKMARGLICFPTFLRAMMLND  
FVIALAVYTMGIDIGNALARTFVRILAKTVAIYVGLKTIYAGVIESKRLVDYI  
LNPISLAVFMKLOITMGVLTREKIKKPLDGSNGNLDENMDYHNRNSNMVSEDE  
GISPLCGNISGAGCCDDVYCLQGFENPNYCTSPDSFGNAFLSAPFLMODPEED  
LYOLVRAAGPWHMLPFIYIIFLSFYLVNLLAIYAMVSGDELQRAEESBAEBAI  
REAEBAALAAKALEERANAQAADAAAEALHPKASPTVSCISYELFVGE  
KQNDNNKEMKISRYVESSESVIQRQAPPTAAQATKRVKSTTSLPSSPNI  
RGRSRSHKVTINGRGRFGI PGSDRKPILSTYDAAOQHLPYADSNVATPMSENG  
AIVPYVYGNLSGRHSYTSRSHOSRISYTSBGDILGGMAVWGVSTMTKESLRYNRTRN  
QSVATNGTTCCTDTHNKLDRHYEIGLCTDEAGKIKHNDNFIPYOTQVYVMDK  
VMVNDIIEQAAHRSASDRGVSYIFPEDDEDEGPTFKDALEYILKGDIVFCW  
DCWVWLKPEWVSLIVFDPVBLFTLCVNTMFMADHDMKEMEKVLSGVF  
FATPALEATMKLAMSPTKYFOEGWNIIPFIIVALSLELGEVQGLSVLSFPL  
RVFRLAKSWPTLNLILISIMGTMGALNLTFFVLCIIFVAVMGOLFQYVHIDHR  
PPGDDIPRNMPTFMSFMTVPRVLCGEMWDCVDCYCEPFLATYVIGLV  
VLNIFALLISNRSGLSAPYADNNTKIAEAPNGRKSVMKNIADCEPLINK  
LTVQISQPSGERTNQISWISRGHGNELIEGHDELADGLIKGIKETQLEVAIG  
DMEFTIHGMKNNKPKSKYLNNAATDDNLSINSYSHNRPKDSHSGASATMG  
EERKDAKEDLGDDEIDEBEGCEGLDIDIIIHADEDIIDEPADCCPDYKXP  
PILAGDDSPMGGMNLRKTPFLIEDKFEYATIMMISLALAEVNDHLPORPI  
LODLYMDRIFTYIFLEMLIKWLAGFYVLNACMIDPIYVWVSLNPFASIVG  
AGGIAQKTRTIRALRPLRAMSMOGRVAVNAVOAISFNVLVCLIPWILFPI  
MGVOLFAGKTFKEDMNGTLSHEIIPNRACSEBNTWNSMNPNGNAYLCLFO  
VATPKWIOIMNDALDSREVDKOPRETNTYMLYIFPFIIFGSPFLNPIVLIIDN  
FNEOKKAGSGLMEWMTEDOKYYSANKKSGKPLAIPRRPAPVIAFVITDCK  
FDIILMFIGLMFTMLIDRYDASDTYNAVLADYNAIFVIFSECKLIPALRYKAT  
LEPNLNVVVVLSILGLVSDIIEKYFVSPPLIRVAVAKVRVLRVAKGART  
LIFLMSLPALENICLLFLWMTFPAIFGSPFMHYKESGINDVYFIPQCSMLI  
LFQMSISAGMDGVDAIINEACDPDNDGSPGNCGATVGTIFLSYVIFSLYI  
NMVTAILENTSQTEDYVBSLTDYDMYETIWOCPDPTQVIRPDQISEPLDYE  
PPIQIHKNKIKITISMDIPICRGLMTLIDMLTODFARKKPNIEEGGEIGETIA  
RPDTEGYPVSTILMRQREYCARLIQHAKRKARBGSGSPEDTDHGDGPBGD  
DPADDEATGDAPAGDGSVNGTAEAGADNDESNNSPGBDAAAIAAAAAAAAAAGTT  
TAGSPGASAGROTAVALVESDGFVTKNGHKVVIHSRSPSITSRTADV"  
join(272..3606,3637..6667)  
/gene="para"  
/codon\_start=1  
/product="sodium channel alpha subunit"  
/protein\_id="AAB59193.1"  
/db\_xref="GI:403445"  
/db\_xref="FLYBASE:FBgn0003036"  
/translation="WTEBDSISSEBSLPRPTRESLVOIEORIAEHKOKELERK  
RAEGEVRGRKKKQKIRYDEDEDEGPDPTLEQGVIPRLQSGSPPELSTPL  
EDIDPYSNVLTVVVSCKGDIIPRSASAKAMMLDEPNIRVAIYLHPLESLFI  
TTLVNCILIMPTPTVSTEVIFGTIYFESAVKMARGLICFPTFLRAMMLND  
FVIALAVYTMGIDIGNALARTFVRILAKTVAIYVGLKTIYAGVIESKRLVDYI  
LNPISLAVFMKLOITMGVLTREKIKKPLDGSNGNLDENMDYHNRNSNMVSEDE  
GISPLCGNISGAGCCDDVYCLQGFENPNYCTSPDSFGNAFLSAPFLMODPEED  
LYOLVRAAGPWHMLPFIYIIFLSFYLVNLLAIYAMVSGDELQRAEESBAEBAI  
REAEBAALAAKALEERANAQAADAAAEALHPKASPTVSCISYELFVGE  
KQNDNNKEMKISRYVESSESVIQRQAPPTAAQATKRVKSTTSLPSSPNI  
RGRSRSHKVTINGRGRFGI PGSDRKPILSTYDAAOQHLPYADSNVATPMSENG  
AIVPYVYGNLSGRHSYTSRSHOSRISYTSBGDILGGMAVWGVSTMTKESLRYNRTRN  
QSVATNGTTCCTDTHNKLDRHYEIGLCTDEAGKIKHNDNFIPYOTQVYVMDK  
VMVNDIIEQAAHRSASDRGVSYIFPEDDEDEGPTFKDALEYILKGDIVFCW  
DCWVWLKPEWVSLIVFDPVBLFTLCVNTMFMADHDMKEMEKVLSGVF  
FATPALEATMKLAMSPTKYFOEGWNIIPFIIVALSLELGEVQGLSVLSFPL  
RVFRLAKSWPTLNLILISIMGTMGALNLTFFVLCIIFVAVMGOLFQYVHIDHR  
PPGDDIPRNMPTFMSFMTVPRVLCGEMWDCVDCYCEPFLATYVIGLV  
VLNIFALLISNRSGLSAPYADNNTKIAEAPNGRKSVMKNIADCEPLINK  
LTVQISQPSGERTNQISWISRGHGNELIEGHDELADGLIKGIKETQLEVAIG  
DMEFTIHGMKNNKPKSKYLNNAATDDNLSINSYSHNRPKDSHSGASATMG  
EERKDAKEDLGDDEIDEBEGCEGLDIDIIIHADEDIIDEPADCCPDYKXP  
PILAGDDSPMGGMNLRKTPFLIEDKFEYATIMMISLALAEVNDHLPORPI  
LODLYMDRIFTYIFLEMLIKWLAGFYVLNACMIDPIYVWVSLNPFASIVG  
AGGIAQKTRTIRALRPLRAMSMOGRVAVNAVOAISFNVLVCLIPWILFPI  
MGVOLFAGKTFKEDMNGTLSHEIIPNRACSEBNTWNSMNPNGNAYLCLFO  
VATPKWIOIMNDALDSREVDKOPRETNTYMLYIFPFIIFGSPFLNPIVLIIDN  
FNEOKKAGSGLMEWMTEDOKYYSANKKSGKPLAIPRRPAPVIAFVITDCK  
FDIILMFIGLMFTMLIDRYDASDTYNAVLADYNAIFVIFSECKLIPALRYKAT  
LEPNLNVVVVLSILGLVSDIIEKYFVSPPLIRVAVAKVRVLRVAKGART  
LIFLMSLPALENICLLFLWMTFPAIFGSPFMHYKESGINDVYFIPQCSMLI  
LFQMSISAGMDGVDAIINEACDPDNDGSPGNCGATVGTIFLSYVIFSLYI  
NMVTAILENTSQTEDYVBSLTDYDMYETIWOCPDPTQVIRPDQISEPLDYE  
PPIQIHKNKIKITISMDIPICRGLMTLIDMLTODFARKKPNIEEGGEIGETIA  
RPDTEGYPVSTILMRQREYCARLIQHAKRKARBGSGSPEDTDHGDGPBGD  
DPADDEATGDAPAGDGSVNGTAEAGADNDESNNSPGBDAAAIAAAAAAAAAAGTT  
TAGSPGASAGROTAVALVESDGFVTKNGHKVVIHSRSPSITSRTADV"

Query Match	96.5%	Score 6288	DB 3	Length 6883
Best Local Similarity	98.2%	Pred. No. 0	Mismatches 15	Indels 105
Matches 6422	Conservative	0		Gaps 2
1	TCTAGACGTTGGCCCGCATGACATGACAGAAAGATTCGACTCGATATCTGAGAGAAGAC	60		
249	TCTCATCGTTGGCCCGCATGACATGACAGAAAGATTCGACTCGATATCTGAGAGAAGAC	308		
61	GGAATTTGTTCCGTCCTTTACCCCGCAATCTTTGTCGAATTCGACAAAGCATTTGCCG	120		
309	GGAATTTGTTCCGTCCTTTACCCCGCAATCTTTGTCGAATTCGACAAAGCATTTGCCG	368		
121	CTGAACATGAAAAGCAGAAAGAGCTGAAAAGAAAGAGCCGAGGAGAGGTCGCCGAT	180		
369	CTGAACATGAAAAGCAGAAAGAGCTGAAAAGAAAGAGCCGAGGAGAGGTCGCCGAT	428		
181	ATGTTGCAAGAAAAGAAAAGAAAATTCGATGATGATGACAGAGACGAGATGAAGGTC	240		
429	ATGTTGCAAGAAAAGAAAAGAAAATTCGATGATGATGACAGAGACGAGATGAAGGTC	488		
241	CAGAACCGGATCTCACTGTAACAGGGGTCGCAATCTGTCGATTCGAGGAGAGCT	300		
489	CAGAACCGGATCTCACTGTAACAGGGGTCGCAATCTGTCGATTCGAGGAGAGCT	548		
301	TCCGCGCGGAATTTGGCTCCACTCTCTGAGAGATATCGATCCCTACTACAGCAATGTC	360		
549	TCCGCGCGGAATTTGGCTCCACTCTCTGAGAGATATCGATCCCTACTACAGCAATGTC	608		
361	TGACATTTGATGTTGTAAGCAAGAAAGAAATTTTGGCTTTCTGATCAAAAGCAA	420		
609	TGACATTTGATGTTGTAAGCAAGAAAGAAATTTTGGCTTTCTGATCAAAAGCAA	668		
421	TGAGATGTCGATTCATTCATCCGATCGATCGTGTGTCGCAATTTACATTTAGTGCATC	480		
669	TGAGATGTCGATTCATTCATCCGATCGATCGTGTGTCGCAATTTAGTGCATC	728		
481	CATTATTTTCCATTATCATCATCAACAATTTCTGTCATCTGCATCTGATGATATGC	540		
729	CATTATTTTCCATTATCATCATCAACAATTTCTGTCATCTGCATCTGATGATATGC	788		
541	CAGCAAGCCCAAGGTTGAGTCCAGTGAAGTATATTCACCCGGAATCTACATTTGAAT	600		
789	CAGCAAGCCCAAGGTTGAGTCCAGTGAAGTATATTCACCCGGAATCTACATTTGAAT	848		
601	CAGCTGTTAAGTGAAGGCAAGAGTTTCAATTTATGCCCCGTTTACGATCTTGAAGATG	660		
849	CAGCTGTTAAGTGAAGGCAAGAGTTTCAATTTATGCCCCGTTTACGATCTTGAAGATG	908		
661	CATGAATTTGCTGAGCTTGTGATGATATAGCTTTAGCTTATGACATGAGGATATGATT	720		
909	CATGAATTTGCTGAGCTTGTGATGATATAGCTTTAGCTTATGACATGAGGATATGATT	968		
721	TAGGATATCTAGACAGCCCTCGAAACGTTTGGGGGCTGGAGAGGCTTAAACGCTAGCCA	780		
969	TAGGATATCTAGACAGCCCTCGAAACGTTTGGGGGCTGGAGAGGCTTAAACGCTAGCCA	1028		
781	TTTGCCAGGCTTGAAGACCATCGTCGGCCGCTCATCGATCGGTGAAGAAATCTGCGCG	840		
1029	TTTGCCAGGCTTGAAGACCATCGTCGGCCGCTCATCGATCGGTGAAGAAATCTGCGCG	1088		

QY	841	ATGTGATTATCTCTGCACCAATGTTCTTCCTCTGTGGGTTCGCGTTGATGAGCCCTACAGATCT	900
Db	1089	ATGTGATTATCTCTGCACCAATGTTCTTCCTCTGTGGGTTCGCGTTGATGAGCCCTACAGATCT	1148
QY	901	ATTATGGGGGTGTCTCAACGAGAAATGTCATCAAGAAGTTCGCGTGGACGGTTCCTGGGGCA	960
Db	1149	ATTATGGGGGTGTCTCAACGAGAAATGTCATCAAGAAGTTCGCGTGGACGGTTCCTGGGGCA	1208
QY	961	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCCAATTGGTATTTCCGAGG	1020
Db	1209	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCCAATTGGTATTTCCGAGG	1266
QY	1021	ACGAGGGCACTCATTTCCGTTATGCGGCAATATATCCGATGCGGGCAATGCGACGACG	1086
Db	1269	ACGAGGGCACTCATTTCCGTTATGCGGCAATATATCCGATGCGGGCAATGCGACGACG	1328
QY	1081	ATTACGATGCTGTGACGGGGTTTGGTTCGGAATTCGGAATTATAGGCTACACAGCTCCGATT	1144
Db	1329	ATTACGATGCTGTGACGGGGTTTGGTTCGGAATTCGGAATTATAGGCTACACAGCTCCGATT	1388
QY	1141	CGTTTCGATGAGCTTTCCCTGTCCGCTTCGCGCTGATGACACAGGACTTCTGGAGAGATC	1200
Db	1389	CGTTTCGATGAGCTTTCCCTGTCCGCTTCGCGCTGATGACACAGGACTTCTGGAGAGATC	1446
QY	1201	TGTACACAGCTGGTGTGTGGCGCGCCGCGACCAATGCGACATGCTGTTCTTTATATGATCA	1266
Db	1449	TGTACACAGCTGGTGTGTGGCGCGCCGCGACCAATGCGACATGCTGTTCTTTATATGATCA	1508
QY	1261	TCTTCCTTAGTTCATTTCTATCTGTGAAATTTGATTTTGGCCATTGTTGCCATGTCGTATG	1322
Db	1509	TCTTCCTTAGTTCATTTCTATCTGTGAAATTTGATTTTGGCCATTGTTGCCATGTCGTATG	1566
QY	1321	ACGAATTTCCAAAGAGAGCCCGAAGAAAGAGAGGCTGCGAAGAGAGAGGCGATACSTGTAG	1386
Db	1569	ACGAATTTCCAAAGAGAGCCCGAAGAAAGAGAGGCTGCGAAGAGAGAGGCGATACSTGTAG	1622
QY	1381	CGAAGAAAGCTGCCCGCCGACCAAGCGGCGCAAGCTGAGAGAGCGGGCCATGCGCAGGCTC	1440
Db	1629	CGAAGAAAGCTGCCCGCCGACCAAGCGGCGCAAGCTGAGAGAGCGGGCCATGCGCAGGCTC	1688
QY	1441	AGCGACGACCGGATATCCGGCTGTCCGCGCAAGAGGCTGCACTGATCCCGGAAATATGCGACAGA	1500
Db	1669	AGCGACGACCGGATATCCGGCTGTCCGCGCAAGAGGCTGCACTGATCCCGGAAATATGCGACAGA	1748
QY	1501	GTCCGACGTATTTCTTGATCAGCTATGAGCTATTTTGTGGCGCGCGAGAAAGGCGCAACGATG	1566
Db	1749	GTCCGACGTATTTCTTGATCAGCTATGAGCTATTTTGTGGCGCGCGAGAAAGGCGCAACGATG	1806
QY	1561	ACAAACAAACAAAGAGAAATGTCATTGCGAGGCTGAGAGTGGAGTCCGAGTCCGATGAGCG	1620
Db	1809	ACAAACAAACAAAGAGAAATGTCATTGCGAGGCTGAGAGTGGAGTCCGAGTCCGATGAGCG	1866
QY	1621	TTTATCAAAAGACACACAGACCTTACCAACAGCACACCAAGCTTACCAAAGTTGCTAAAGTGA	1688
Db	1869	TTTATCAAAAGACACACAGACCTTACCAACAGCACACCAAGCTTACCAAAGTTGCTAAAGTGA	1928
QY	1681	GAAGACATCCTTATCTTACTCTGATCAGCGTTTAAATACAGCAGGGGATACAGCTAGTT	1740
Db	1929	GAAGACATCCTTATCTTACTCTGATCAGCGTTTAAATACAGCAGGGGATACAGCTAGTT	1988
QY	1741	CTCACAAAGTACAGATACGGAACGGAACGTGCGCGCTTTGTATACCCGATAGCATCTGTA	1800
Db	1989	CTCACAAAGTACAGATACGGAACGGAACGTGCGCGCTTTGTATACCCGATAGCATCTGTA	2048
QY	1801	AGCCATTGGTATTTGTCAACATATCAGATATGCCACAGACATTTGCCCTTATATGCCACGACT	1866
Db	2049	AGCCATTGGTATTTGTCAACATATCAGATATGCCACAGACATTTGCCCTTATATGCCACGACT	2108
QY	1861	CGAATAGCCGTCAACCCGATATGTCGGAAGAGATGGGGCCATCATATAGTCCCGTATCTATG	1922
Db	2109	CGAATAGCCGTCAACCCGATATGTCGGAAGAGATGGGGCCATCATATAGTCCCGTATCTATG	2166
QY	1921	GCAATCTTAGGCTCCGACACTCATATGATTAACCTGCGATCAGTCCGAAATATGTAACCT	1980

Db	2169	GCATCTAAGGCTCCCGACACTCATCTGTAACCTTGCATCAAGTCTCCGAAATCTGTAATCTT	2228
QY	1981	CACATGGCGATCTCTACTGGCGCGGCATGGCCGTCATGGCGGCTCAGACCAATGACCAAGAGA	2049
Db	2229	CACATGGCGATCTTACTGGCGCGCATGGCCGCTCAATGGCGTCAACATGATCAAGAGA	2288
QY	2041	GCAAAATGGCGAACCGCAACACGCGCAATCAATGATGGCGCCCAATGGCGGACCA	2100
Db	2289	GCAAAATGGCGAACCGCAACACGCGCAATCAATGATGGCGCCCAATGGCGGACCA	2348
QY	2101	CCTGCTTGGACACCAATCAACAAGCTCCATTCATCCCGACTAAGAAATGGCGCTTGAAGTCA	2166
Db	2349	CCTGCTTGGACACCAATCAACAAGCTCCATTCATCCCGACTAAGAAATGGCGCTTGAAGTCA	2408
QY	2161	CGGACGAAGCTGGCGAAGATTAACATCATCATGACAAATCCCTTATCGAGCCGCTCAGACAC	2220
Db	2409	CGGACGAAGCTGGCGAAGATTAACATCATCATGACAAATCCCTTATCGAGCCGCTCAGACAC	2468
QY	2221	AAACGGTGGTGAATATGAAGATGTATGTCTCTGAATGACATCATCAACAGCCGCTG	2280
Db	2469	AAACGGTGGTGAATATGAAGATGTATGTCTCTGAATGACATCATCAACAGCCGCTG	2528
QY	2281	GTCGGCACATGTCGGGCAAGGCAATGGCGGTGTCTCCGTTACTATTTTCCCAACAGAGACG	2344
Db	2529	GTCGGCACATGTCGGGCAAGGCAATGGCGGTGTCTCCGTTACTATTTTCCCAACAGAGACG	2588
QY	2341	ATGACAGAGATGGGCGGACGTTCAAAGACAGGCACTGCAAGTATCTCTCAAAGGACATCG	2400
Db	2589	ATGACAGAGATGGGCGGACGTTCAAAGACAGGCACTGCAAGTATCTCTCAAAGGACATCG	2644
QY	2401	ATGATGTTTGTGTGTGGGACTGTGCTGGTGTGGTAAATTTCAAGAGTGGGTATGC	2466
Db	2649	ATGATGTTTGTGTGTGGGACTGTGCTGGTGTGGTAAATTTCAAGAGTGGGTATGC	2708
QY	2461	TCATGCTCTTCGATCCCTTGGTGGAGCTCTTCATCAACGCTGTGCATTTGTGTCAACAGCA	2522
Db	2709	TCATGCTCTTCGATCCCTTGGTGGAGCTCTTCATCAACGCTGTGCATTTGTGTCAACAGCA	2766
QY	2521	TGTTTCATGGCAATGGATACCAACGATATGAACAGAGAGATGAAACGCGTGTCAAAGATG	2580
Db	2769	TGTTTCATGGCAATGGATACCAACGATATGAACAGAGAGATGAAACGCGTGTCAAAGATG	2822
QY	2581	GCAACTATATTTCTTACCGCGCACTTTTGGCATCGAGGCCACATGAAAGCTAATGGCCATGA	2640
Db	2829	GCAACTATATTTCTTACCGCGCACTTTTGGCATCGAGGCCACATGAAAGCTAATGGCCATGA	2888
QY	2641	GCCCCAAGTACTATTTCCAGAGAGGCTTGGCAATCTTGCATTTATGTGGCCCTAT	2700
Db	2889	GCCCCAAGTACTATTTCCAGAGAGGCTTGGCAATCTTGCATTTATGTGGCCCTAT	2948
QY	2701	CGCTATTGGAACTGGGAACTGAGGGGTGTCCAGGGTCTGTCCGTAATGGGTCCTTTGCAT	2766
Db	2949	CGCTATTGGAACTGGGAACTGAGGGGTGTCCAGGGTCTGTCCGTAATGGGTCCTTTGCAT	3008
QY	2761	TGCTGCGGTATTTGAAACTTGCCCAAGTCTTGGCCCACTTAATTTACTCATTTTGCATTA	2820
Db	3009	TGCTGCGGTATTTGAAACTTGCCCAAGTCTTGGCCCACTTAATTTACTCATTTTGCATTA	3066
QY	2821	TGGAGCGCACTATGGGCGCTTTGGGTATCTGACATTTGTAATCTTGCATTAATCATCTTCA	2888
Db	3069	TGGAGCGCACTATGGGCGCTTTGGGTATCTGACATTTGTAATCTTGCATTAATCATCTTCA	3128
QY	2881	TCTTTTGGCGGTATGGGAAATGCAATCTTGGGAAAGAAATTAATCATGATCAACAGGACCGCT	2944
Db	3129	TCTTTTGGCGGTATGGGAAATGCAATCTTGGGAAAGAAATTAATCATGATCAACAGGACCGCT	3188
QY	2941	TTCCGGAATGGGAACTGCGCGCTGGAATTTCAACGCACTTTATGACAGCTTCAATGATCG	3000
Db	3189	TTCCGGAATGGGAACTGCGCGCTGGAATTTCAACGCACTTTATGACAGCTTCAATGATCG	3248
QY	3001	TGTTTCGGGTGCTCTGCGGAGATGATCGAGTCCATGTGGGACTGATGTAGCTGGCG	3066

Db 3249 TGTTCGGGTGCTCTGGGAGAAATGATCGATGCTGAGCTGATGTCGTCG 3308  
QY 3061 ATGTCGTGTCATCCCTCTCTCTGCGCCACGTTGTCATCGGCAATCTGTGTA 3120  
Db 3309 ATGTCTGTCATCTCTCTCTCTGCGCCACGTTGTCATCGGCAATCTGTGTA 3368  
QY 3121 ACCTTTTCTTACGCTTGTCTTGTCTGCAATTTTGCTTCATCTGATTCACGCGCACTG 3180  
Db 3369 ACCTTTTCTTACGCTTGTCTTGTCTGCAATTTTGCTTCATCTGATTCACGCGCACTG 3428  
QY 3181 CCGATACGATTAAGAAATTAAGCGAGGCTTCATGGAATTTGGCCGTTTAAAGTT 3240  
Db 3429 CCGATACGATTAAGAAATTAAGCGAGGCTTCATGGAATTTGGCCGTTTAAAGTT 3488  
QY 3241 GGGTAAAGCTAAATATGCTGATTTGTTTCAAGTTAATCGTAACTAAATGACAAATCAAA 3300  
Db 3489 GGGTAAAGCTAAATATGCTGATTTGTTTCAAGTTAATCGTAACTAAATGACAAATCAAA 3548  
QY 3301 TAAAGTCAACCATCAAGTGAAGACCAACGATCACTGATTTGGAAGCGA----- 3355  
Db 3549 TAAAGTCAACCATCAAGTGAAGACCAACGATCACTGATTTGGAAGCGA----- 3608  
QY 3356 -----AGAGCATGGTGAACAAGACTGGAAGCTGGGCGACG 3390  
Db 3609 AAGGCGTTTGTCTGTATATCTGCAAGCATGTTGCAACGAACTGGAGCTGGGCGACG 3668  
QY 3391 ACGAGATCTCTGCGCGACGCTCTCAAGAAAGGGATCAAGAGCAGACGCAACTGGAGG 3450  
Db 3669 ACGAGATCTCTGCGCGACGCTCTCAAGAAAGGGATCAAGAGCAGACGCAACTGGAGG 3728  
QY 3451 TGGCGATCGGGAGTCGATGGAATTCACGATCAACGCGGCACTGAAGAACAAGAGCGA 3510  
Db 3729 TGGCGATCGGGAGTCGATGGAATTCACGATCAACGCGGCACTGAAGAACAAGAGCGA 3788  
QY 3511 AGAATCAAAATATCTAAATTAAGCAACGATGATTGGCACTCAATTAAACCAACAGCA 3570  
Db 3789 AGAATCAAAATATCTAAATTAAGCAAC----- 3816  
QY 3571 ATAGCTGGAACACAGACTAAACCATAGAGTTTGTCTTACAGACGACGACCTGCCA 3630  
Db 3817 -----GAGACGACGACCTGCCA 3833  
QY 3631 GCATTAATCTCATATGTCATAGCATTAAGATCGAACATTCAGAGAGAGGACCAAGAGGCA 3690  
Db 3834 GCATTAATCTCATATGTCATAGCATTAAGATCGAACATTCAGAGAGAGGACCAAGAGGCA 3893  
QY 3691 GCGCGGAGACGATGAGGCGAGAGGAAGCGCGACGCGCAGCAAGAGAGATTTAGGTCG 3750  
Db 3894 GCGCGGAGACGATGAGGCGAGAGGAAGCGCGACGCGCAGCAAGAGAGATTTAGGTCG 3953  
QY 3751 ACGAGGAATGAGAGAGAGGCGCAATGCGAGAGGCGCGCTGCAACGCTGATTCATTTA 3810  
Db 3954 ACGAGGAATGAGAGAGGCGCAATGCGAGAGGCGCGCTGCAACGCTGATTCATTTA 4013  
QY 3811 TTTCAGCACAGAGAGATATCTCGATGAATTCAGCTGATTTGCTGCCCATTCGT 3870  
Db 4014 TTTCAGCACAGAGAGATATCTCGATGAATTCAGCTGATTTGCTGCCCATTCGT 4073  
QY 3871 ACTATAAGAAATTTCCGATCTTACGCGGTGAACGATGCTGCGCTTGGCAAGATGG 3930  
Db 4074 ACTATAAGAAATTTCCGATCTTACGCGGTGAACGATGCTGCGCTTGGCAAGATGG 4133  
QY 3931 GCAATTTTACGCTGAAAATCTTTCAATTAATTTGAATAATTTTGAACAGCTGTA 3990  
Db 4134 GCAATTTTACGCTGAAAATCTTTCAATTAATTTGAATAATTTTGAACAGCTGTA 4193  
QY 3991 TCACATATATTTAATGAGTACGTTGCGCATTAAGAGATGATCATCTGCACAAA 4050  
Db 4194 TCACATATATTTAATGAGTACGTTGCGCATTAAGAGATGATCATCTGCACAAA 4253  
QY 4051 GACCCATATCTGAGAGATATTTTATATCTATATGACAGAAATTTTACGGTTATATTTCT 4110  
Db 4254 GACCCATATCTGAGAGATATTTTATATCTATATGACAGAAATTTTACGGTTATATTTCT 4313

QY 4111 TGGAAATGTTAATCAAGTGTGGGCTTCGCTTCAAGTGTACTTCAACAGGCTGT 4170  
Db 4314 TGGAAATGTTAATCAAGTGTGGGCTTCGCTTCAAGTGTACTTCAACAGGCTGT 4373  
QY 4171 GTTGGCTGATTTGCGATATGTCATGATTCGCTTATCAACTGCTTGTCTTGTG 4230  
Db 4374 GTTGGCTGATTTGCGATATGTCATGATTCGCTTATCAACTGCTTGTCTTGTG 4433  
QY 4231 GAGCTGTGTTATCAAGCTTCAAGACTATGCGAAGCTTAAAGACATGAGACATTAAC 4290  
Db 4434 GAGCTGTGTTATCAAGCTTCAAGACTATGCGAAGCTTAAAGACATGAGACATTAAC 4493  
QY 4291 GTGCGATGCTGATTCAGGCGCATGAGGCTGTGTTAATGCGCTGTTCAAGCTATAC 4350  
Db 4494 GTGCGATGCTGATTCAGGCGCATGAGGCTGTGTTAATGCGCTGTTCAAGCTATAC 4553  
QY 4351 CGTCCATCTTCAATGCTATTTGTGTCTAATATTTTGGCTAAATTTTGGCATATGG 4410  
Db 4554 CGTCCATCTTCAATGCTATTTGTGTCTAATATTTTGGCTAAATTTTGGCATATGG 4613  
QY 4411 GTGTACAGCTTTTGTGTGAAAATTTTAAAGTGGAGACATGAAATGGCAAGGCTCA 4470  
Db 4614 GTGTACAGCTTTTGTGTGAAAATTTTAAAGTGGAGACATGAAATGGCAAGGCTCA 4673  
QY 4471 GCGACGAGATCAATCAATTCGAATGCTGCGAGAGCAGAACTACAGTGGTGAAT 4530  
Db 4674 GCGACGAGATCAATCAATTCGAATGCTGCGAGAGCAGAACTACAGTGGTGAAT 4733  
QY 4531 CAGCAATGAATTCATCATATGATGATACGCGATATGCTTTTCAAGTGGCACT 4590  
Db 4734 CAGCAATGAATTCATCATATGATGATACGCGATATGCTTTTCAAGTGGCACT 4793  
QY 4591 TCAAAGCTGATTCAAATCAATGAAAGATGATTCAGAGAGTGGCAAGCAAC 4650  
Db 4794 TCAAAGCTGATTCAAATCAATGAAAGATGATTCAGAGAGTGGCAAGCAAC 4853  
QY 4651 CAATTCGTGAAAGCAATCTACATGATTTAATTTCTATTTCTTCAATATTTGGAT 4710  
Db 4854 CAATTCGTGAAAGCAATCTACATGATTTAATTTCTATTTCTTCAATATTTGGAT 4913  
QY 4711 CCTTTTCAACATCTGATCTGTTGTTATTCATGATTAATTTTAAAGCAAAAG 4770  
Db 4914 CATTTTCAACATCTGATCTGTTGTTATTCATGATTAATTTTAAAGCAAAAG 4973  
QY 4771 AAAAAGAGTGTGATCATTAAGAAATGTCATGACAGAAAGTCAAGAAAGTACTATATG 4830  
Db 4974 AAAAAGAGTGTGATCATTAAGAAATGTCATGACAGAAAGTCAAGAAAGTACTATATG 5033  
QY 4831 CTATGAAAAAGATGGCTCTTAAAAAACAATTAAGCAATTCGAAGACCAAGGTGGCAG 4890  
Db 5034 CTATGAAAAAGATGGCTCTTAAAAAACAATTAAGCAATTCGAAGACCAAGGTGGCAG 5093  
QY 4891 CACAGCAATATGCTTTGAAATGTAACGATTAAGAAATTCGATTAATCATTAATGTTAT 4950  
Db 5094 CACAGCAATATGCTTTGAAATGTAACGATTAAGAAATTCGATTAATCATTAATGTTAT 5153  
QY 4951 TCATTTGCTGAAACATGTTTCAACCATGACCTCGATGTTACGATGGCTGCGACATATA 5010  
Db 5154 TCATTTGCTGAAACATGTTTCAACCATGACCTCGATGTTACGATGGCTGCGACATATA 5213  
QY 5011 ACGGCTCTTACGATATCTCAATGCAATATGTAATTTTCAAGTTCCGAATGCTAT 5070  
Db 5214 ACGGCTCTTACGATATCTCAATGCAATATGTAATTTTCAAGTTCCGAATGCTAT 5273  
QY 5071 TAAAAATATTTGCTTTACGATATCACTATTTTATGAGCCATGAAATTTATTTGAGTAG 5130  
Db 5274 TAAAAATATTTGCTTTACGATATCACTATTTTATGAGCCATGAAATTTATTTGAGTAG 5333  
QY 5131 TAGTTGCTATTTATCATCTTAAAGTCTTGTATCTTACGATATTTATGAGAAAGTACTTG 5190  
Db 5334 TAGTTGCTATTTATCATCTTAAAGTCTTGTATCTTACGATATTTATGAGAAAGTACTTG 5393



QY 361 TGACATTCGATGTTGTAAGCAAGAAAGATATTTTCGCTTTCTGCATCAAAAGCA 420  
| | | | |  
Db 469 TGCATTCGATGTTGTAAGCAAGAAAGATATTTTCGCTTTCTGCATCAAAAGCA 528  
| | | | |  
QY 421 TGTGATGCTGCATTCATTCATCCGATACGTGTGTGGCCATTTCATTAGTCATC 480  
| | | | |  
Db 529 TGTGATGCTGCATTCATTCATCCGATACGTGTGTGGCCATTTCATTAGTCATC 588  
| | | | |  
QY 481 CATTAATTTCCGATTCATCATCAACCAATTCCTGCTCACTGATGATATATC 540  
| | | | |  
Db 589 CATTAATTTCCGATTCATCATCAACCAATTCCTGCTCACTGATGATATATC 648  
| | | | |  
QY 541 CGACAAAGCCCAAGCTTGAAGTCACTGAGGTATATTCACCGAATCTACATTTGAAT 600  
| | | | |  
Db 649 CGACAAAGCCCAAGCTTGAAGTCACTGAGGTATATTCACCGAATCTACATTTGAAT 708  
| | | | |  
QY 601 CAGCTGTAAAGTGAAGGCAAGAGTTTCATTTTACCCGTTAGGTATCTAGAGATG 660  
| | | | |  
Db 709 CAGCTGTAAAGTGAAGGCAAGAGTTTCATTTTACCCGTTAGGTATCTAGAGATG 768  
| | | | |  
QY 661 CAGGAAATGCTGATCTGATGATATAGCTTTAGCTTATGTACCATGGTATAGAT 720  
| | | | |  
Db 769 CAGGAAATGCTGATCTGATGATATAGCTTTAGCTTATGTACCATGGTATAGAT 828  
| | | | |  
QY 721 TAGGTAATCTAGCAAGCCCTGCGAAGCTTTAGGCTGCGAGGCTTAAACCGTAGCA 780  
| | | | |  
Db 829 TAGGTAATCTAGCAAGCCCTGCGAAGCTTTAGGCTGCGAGGCTTAAACCGTAGCA 888  
| | | | |  
QY 781 TTGGGCAAGGCTTGAAGACCATGTCGGGCGCCGTCATGATCGGTGAAGATCTGCGCG 840  
| | | | |  
Db 889 TTGGGCAAGGCTTGAAGACCATGTCGGGCGCCGTCATGATCGGTGAAGATCTGCGCG 948  
| | | | |  
QY 841 ATGTGATTAATCTGACCAATGTTCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
| | | | |  
Db 949 ATGTGATTAATCTGACCAATGTTCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008  
| | | | |  
QY 901 ATATGAGGCGTGTCTACCGGAAAGTGCATCAAGAAATCCCGCTGGAAGGTTCCGAGGCA 960  
| | | | |  
Db 1009 ATATGAGGCGTGTCTACCGGAAAGTGCATCAAGAAATCCCGCTGGAAGGTTCCGAGGCA 1068  
| | | | |  
QY 961 ATTCGACGACGAGAACTGGGACTATGACAAATCGCAATAGCTCCAAATGTGTATCCGAGG 1020  
| | | | |  
Db 1069 ATTCGACGACGAGAACTGGGACTATGACAAATCGCAATAGCTCCAAATGTGTATCCGAGG 1128  
| | | | |  
QY 1021 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATATCCGCTGCGGCGCAATGCGACACG 1080  
| | | | |  
Db 1129 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATATCCGCTGCGGCGCAATGCGACACG 1188  
| | | | |  
QY 1081 ATTAAGTGTGCTGACGAGGCTTGTGCGGAATCGGAATTAAGCTACACAGCTTCGAT 1140  
| | | | |  
Db 1189 ATTAAGTGTGCTGACGAGGCTTGTGCGGAATCGGAATTAAGCTACACAGCTTCGAT 1248  
| | | | |  
QY 1141 CGTTCGAGTGGGCTTTCCTGTCCGCTTCGCGCTGATGACACAGAGCTTCGAGGAGATC 1200  
| | | | |  
Db 1249 CGTTCGAGTGGGCTTTCCTGTCCGCTTCGCGCTGATGACACAGAGCTTCGAGGAGATC 1308  
| | | | |  
QY 1201 TGTACCAAGCTGTGTGTGCGCGCCGCGGACATGCGACATGCTGTCTTTATATCTATCA 1260  
| | | | |  
Db 1309 TGTACCAAGCTGTGTGTGCGCGCCGCGGACATGCGACATGCTGTCTTTATATCTATCA 1368  
| | | | |  
QY 1261 TCTTCCTAGGTTCAATCTATCTGTGAATTTGATTTTGGCCATTTGTGCAATGTCTATG 1320  
| | | | |  
Db 1369 TCTTCCTAGGTTCAATCTATCTGTGAATTTGATTTTGGCCATTTGTGCAATGTCTATG 1428  
| | | | |  
QY 1321 ACGAATTCGAAAGAGGCGGAGAAAGAGAGGCTGCGGAGAGAGAGGCGATACGTGAG 1380  
| | | | |  
Db 1429 ACGAATTCGAAAGAGGCGGAGAAAGAGAGGCTGCGGAGAGAGAGGCGATACGTGAG 1488  
| | | | |  
QY 1381 CGGAAGAGCTGCGCGCGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGGCTC 1440  
| | | | |  
Db 1489 CGGAAGAGCTGCGCGCGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGGCTC 1548  
| | | | |  
QY 1441 AGGACGACGAGATCGGCTGCGCGCGGAGAGGAGGCTGACCTGATCCGGAATGCGCAAGA 1500  
| | | | |

Db 1549 AGGACGACGAGATCGGCTGCGCGGAGAGGCTGACCTGATCCGGAATGCGCAAGA 1608  
| | | | |  
QY 1501 GTCCGACGTAATCTTCATCAGCTATGAGCTATTTGTGGCGCGAGAGGCGCAACGATG 1560  
| | | | |  
Db 1609 GTCCGACGTAATCTTCATCAGCTATGAGCTATTTGTGGCGCGAGAGGCGCAACGATG 1668  
| | | | |  
QY 1561 ACAACAAAGAGAGAGATGTTCATTTGCGAGGCTGAGGTGAGTGGAGTCCGAGCG 1620  
| | | | |  
Db 1669 ACAACAAAGAGAGAGATGTTCATTTGCGAGGCTGAGGTGAGTGGAGTCCGAGCG 1728  
| | | | |  
QY 1621 TTATCAAGAGCAACAGACCTACACAGACACACAACTACAAAGTTGTAAGTGA 1680  
| | | | |  
Db 1729 TTATCAAGAGCAACAGACCTACACAGACACACAAAGTTGTAAGTGA 1788  
| | | | |  
QY 1681 GCACGACATCTTATCTTACCTGCTTACCGTTTACATACGACGAGGATACGATG 1740  
| | | | |  
Db 1789 GCACGACATCTTATCTTACCTGCTTACCGTTTACATACGACGAGGATACGATG 1848  
| | | | |  
QY 1741 CTCACAGTACAGATACGGAACGGAAGTGGCGGCTTGTATACCGGATAGCATGTA 1800  
| | | | |  
Db 1849 CTCACAGTACAGATACGGAACGGAAGTGGCGGCTTGTATACCGGATAGCATGTA 1908  
| | | | |  
QY 1801 AGCCATGCTATTTGCAACATATCAGATGCCCACAGACCTTGCCCTATGCGACGAT 1860  
| | | | |  
Db 1909 AGCCATGCTATTTGCAACATATCAGATGCCCACAGACCTTGCCCTATGCGACGAT 1968  
| | | | |  
QY 1861 CGAATGCGCTACCCCGATGTCCGAGAGAGATGGGGCCATCTATGCCCCGTTACTATG 1920  
| | | | |  
Db 1969 CGAATGCGCTACCCCGATGTCCGAGAGAGATGGGGCCATCTATGCCCCGTTACTATG 2028  
| | | | |  
QY 1921 GCAATGAGCTCCGACACCTCATGATACCTGCAATGATCCGAAATATGATATCT 1980  
| | | | |  
Db 2029 GCAATGAGCTCCGACACCTCATGATACCTGCAATGATCCGAAATATGATATCT 2088  
| | | | |  
QY 1981 CACATGCGATCTACTGCGGCGATGCGGTATGAGGCGTACGCAATGACAAAGAGA 2040  
| | | | |  
Db 2089 CACATGCGATCTACTGCGGCGATGCGGTATGAGGCGTACGCAATGACAAAGAGA 2148  
| | | | |  
QY 2041 GCAAATTTGGGCAACCGGCAACACGCAATCAATCGATGGGCGCCCAATGCGGCA 2100  
| | | | |  
Db 2149 GCAAATTTGGGCAACCGGCAACACGCAATCAATCGATGGGCGCCCAATGCGGCA 2208  
| | | | |  
QY 2101 CCTGTGACACCAATCAACAGCTGATCATGCGACTACGCAATTTGGCTGTGATGCA 2160  
| | | | |  
Db 2209 CCTGTGACACCAATCAACAGCTGATCATGCGACTACGCAATTTGGCTGTGATGCA 2268  
| | | | |  
QY 2161 CGGACGAGCTGCGCAAGATTTAAATCATGACATCTTTTATCGAGCCGCTCCAGAC 2220  
| | | | |  
Db 2269 CGGACGAGCTGCGCAAGATTTAAATCATGACATCTTTTATCGAGCCGCTCCAGAC 2328  
| | | | |  
QY 2221 AAACGCTGTGTAATGAAGAGTGTATGCTGCTGAATGACATCATGCAAGGCGCTG 2280  
| | | | |  
Db 2329 AAACGCTGTGTAATGAAGAGTGTATGCTGCTGAATGACATCATGCAAGGCGCTG 2388  
| | | | |  
QY 2281 GTGCGACAGTCCGGCAAGGATGCGGTGTCTCCGTTACTATTTCCCAACAGAGAG 2340  
| | | | |  
Db 2389 GTGCGACAGTCCGGCAAGGATGCGGTGTCTCCGTTACTATTTCCCAACAGAGAG 2448  
| | | | |  
QY 2341 ATGACGAGATGGGCGGAGCTTCAAGACAGGACATCGAAGGATCTCAAGAGGATG 2400  
| | | | |  
Db 2449 ATGACGAGATGGGCGGAGCTTCAAGACAGGACATCGAAGGATCTCAAGAGGATG 2508  
| | | | |  
QY 2401 ATGAGTTTGTGTGAGGACTGTGCTGGGTTGTGTAATTTCAAGAGTGGGATTCG 2460  
| | | | |  
Db 2509 ATGAGTTTGTGTGAGGACTGTGCTGGGTTGTGTAATTTCAAGAGTGGGATTCG 2568  
| | | | |  
QY 2461 TCAATGCTTCAATCCCTTGTGAGCTTTCATACGCTGTGATTTGTGTCAACGA 2520  
| | | | |  
Db 2569 TCAATGCTTCAATCCCTTGTGAGCTTTCATACGCTGTGATTTGTGTCAACGA 2628  
| | | | |  
QY 2521 TGTTCATGCAATGATACCAAGATATGAACAAAGAGATGGAACGCGTCTCAAGATG 2580  
| | | | |

Db 2629 TGTTCATGCGAATGATGACCAACGATATGAAACAAGAGATGGAACGGTGTCAAGATG 2688  
 Qy 2581 GCAACTATTTCTTCCCGCCACCTTTGCCATCGAGGCCAACAATGAAGCTAATGGCCATGA 2640  
 Db 2689 GCAACTATTTCTTCCCGCCACCTTTGCCATCGAGGCCAACAATGAAGCTAATGGCCATGA 2748  
 Qy 2641 GCCCAAGTACTGATTTCCAGAGGGGCTGGAACATCTTGACCTTCAATTCATTCGAGGCCAT 2700  
 Db 2749 GCCCAAGTACTGATTTCCAGAGGGGCTGGAACATCTTGACCTTCAATTCATTCGAGGCCAT 2808  
 Qy 2701 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGTCTGTCCGATATTCGCTTCTTCCAT 2760  
 Db 2809 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGTCTGTCCGATATTCGCTTCTTCCAT 2868  
 Qy 2761 TGTCTGCTGTATTCAACTGGCCAAAGTCTTGCCCAACTTAATTACTCATTTGATTA 2820  
 Db 2869 TGTCTGCTGTATTCAACTGGCCAAAGTCTTGCCCAACTTAATTACTCATTTGATTA 2928  
 Qy 2821 TGGGACGACACATGGGGGCTTTGGGTATCTGACATTTGTACTTGTGCAATTATCATCTTCA 2880  
 Db 2929 TGGGACGACACATGGGGGCTTTGGGTATCTGACATTTGTACTTGTGCAATTATCATCTTCA 2988  
 Qy 2881 TCTTTGCGGTATGAGGAATGCACTGTTCGAAAGAAATTAATCATGATCAAGAAGCCGT 2940  
 Db 2989 TCTTTGCGGTATGAGGAATGCACTGTTCGAAAGAAATTAATCATGATCAAGAAGCCGT 3048  
 Qy 2941 TTCCGAGATGCGACCTGCGCGCTGGAACTTCAACGACTTATGCAAGCTTCATGATCG 3000  
 Db 3049 TTCCGAGATGCGACCTGCGCGCTGGAACTTCAACGACTTATGCAAGCTTCATGATCG 3108  
 Qy 3001 TGTTCGCGGGTCTCGCGGAGAAATGAGTCGATCGATGGGACGTCATGACGTGAGGCG 3060  
 Db 3109 TGTTCGCGGGTCTCGCGGAGAAATGAGTCGATCGATGGGACGTCATGACGTGAGGCG 3168  
 Qy 3061 ATGTCTCGTGAATCCCTTCTTCTTGCCACCGTGTGATCGGCAATCTTGTGACTTA 3120  
 Db 3169 ATGTCTCGTGAATCCCTTCTTCTTGCCACCGTGTGATCGGCAATCTTGTGACTTA 3228  
 Qy 3121 ACCTTTCTTAGCCTGCTTGTTCGAATTTGGCTCATCTAGCTTATCAGGCGCATG 3180  
 Db 3229 ACCTTTCTTAGCCTGCTTGTTCGAATTTGGCTCATCTAGCTTATCAGGCGCATG 3288  
 Qy 3181 CCGATTAACGATACGAATAAATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAGTT 3240  
 Db 3289 CCGATTAACGATACGAATAAATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAGTT 3348  
 Qy 3241 GGGTTAAGCGTAAATTTGCTGATTTTCAAGTTAATCGTAACAATTTGAACAATCAA 3300  
 Db 3349 GGGTTAAGCGTAAATTTGCTGATTTTCAAGTTAATCGTAACAATTTGAACAATCAA 3408  
 Qy 3301 TAAAGTATCAACATCAGGTGAGAGCAACACGATCAGTTGATTTGAGCCGA---- 3355  
 Db 3409 TAAAGTATCAACATCAGGTGAGAGCAACACGATCAGTTGATTTGAGCCGA 3468  
 Qy 3356 -----AGAGCATGTGACAAGCAACTGGAGCTGGGCCAG 3390  
 Db 3469 AAGGCGTTTGTCTGTATATCTGCAAGCAATGTGACAACGAACTGGAGCTGGGCCAG 3528  
 Qy 3391 ACGAGATCTGCGCAGCGGCTCATCAAGAAAGGGATCAAGAGAGCAAGCACTGGAGG 3450  
 Db 3529 ACGAGATCTGCGCAGCGGCTCATCAAGAAAGGGATCAAGAGAGCAAGCACTGGAGG 3588  
 Qy 3451 TGGCCATGCGGAGATCGATGGAATTCAGGATACAGCGGCAATGAAGAAACAAGCCGA 3510  
 Db 3589 TGGCCATGCGGAGATCGATGGAATTCAGGATACAGCGGCAATGAAGAAACAAGCCGA 3648  
 Qy 3511 AGAATTCGAATATCTAATAAGCAAGATGTTGCACTCAATTAAACCAACAAGCA 3570  
 Db 3649 AGAATTCGAATATCTAATAAGCAAC----- 3676  
 Qy 3571 ATAGACTGGAACACGAGCTAAACCATAGAGTTGTCTTACAGGACGACGACTGCGCA 3630  
 Db 3677 -----GGACGACGCACTGCGCA 3693

Qy 3631 GCATTAATCTATATGTAAGCAATGCAACCATTCAGAGACGAGCCACAAGGCA 3690  
 Db 3694 GCATTAATCTATATGTAAGCAATGCAACCATTCAGAGACGAGCCACAAGGCA 3753  
 Qy 3691 GCGCGAGACGATGAGGCGGAGAGAAAGCCGACGCAAGCAAGAGATTAGGCTCG 3750  
 Db 3754 GCGCGAGACGATGAGGCGGAGAGAAAGCCGACGCAAGCAAGAGATTAGGCTCG 3813  
 Qy 3751 ACGAGAACTGGAACGAGAGGCGAATGCGAGAGGCGCGCTGACCGGTATATCATTA 3810  
 Db 3814 ACGAGAACTGGAACGAGAGGCGAATGCGAGAGGCGCGCTGACCGGTATATCATTA 3873  
 Qy 3811 TTCAATGCAACGAGAGATATATCTCATGAAATATCCAGCTGATTTGCTGCCCATTCGT 3870  
 Db 3874 TTCAATGCAACGAGAGATATATCTCATGAAATATCCAGCTGATTTGCTGCCCATTCGT 3933  
 Qy 3871 ACTATAAGAAATTTCCGATCTTACCGGTCAGATGACTCGCCGTTCTGGCAAGATGG 3930  
 Db 3934 ACTATAAGAAATTTCCGATCTTACCGGTCAGATGACTCGCCGTTCTGGCAAGATGG 3993  
 Qy 3931 GCAATTTACGACTGAAAATTTTCAATTAATGAAAAATTAATTTGAAAACAGCTGTTA 3990  
 Db 3994 GCAATTTACGACTGAAAATTTTCAATTAATGAAAAATTAATTTGAAAACAGCTGTTA 4053  
 Qy 3991 TCATATGATTTTATAGATAGTACCTTACCTTGGCATTTGAAGATGTACTGCAACAA 4050  
 Db 4054 TCATATGATTTTATAGATAGTACCTTACCTTGGCATTTGAAGATGTACTGCAACAA 4113  
 Qy 4051 GACCATATGACGAGATATTTATTAATATATGACAGAAATTTACGGTTATATCTCT 4110  
 Db 4114 GACCATATGACGAGATATTTTATTAATATATGACAGAAATTTACGGTTATATCTCT 4173  
 Qy 4111 TGAATATGTTAATCAAGTGTGCGCTCGGCTTCAAGTGTACTTCAACACGCTGT 4170  
 Db 4174 TGAATATGTTAATCAAGTGTGCGCTCGGCTTCAAGTGTACTTCAACACGCTGT 4233  
 Qy 4171 GTTGCTCGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4230  
 Db 4234 GTTGCTCGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4293  
 Qy 4231 GAGCTGTGTATTAAGGCTTCAAGACTATGCAACGTTAAGAGACTGAGACCACTAC 4290  
 Db 4294 GAGCTGTGTATTAAGGCTTCAAGACTATGCAACGTTAAGAGACTGAGACCACTAC 4353  
 Qy 4291 GTGCTATGTCCGTAATGAGGCAATGAGGCTGTGTTAATGCGCTGTATCAAGCTATAC 4350  
 Db 4354 GTGCTATGTCCGTAATGAGGCAATGAGGCTGTGTTAATGCGCTGTATCAAGCTATAC 4413  
 Qy 4351 GGTTCATCTTAATGTGCTATGTTGTGTCTAATATTTTGGCTAATTTTGGCTAATATG 4410  
 Db 4414 GGTTCATCTTAATGTGCTATGTTGTGTCTAATATTTTGGCTAATTTTGGCTAATATG 4473  
 Qy 4411 GTGTACAGCTTTTGTGTAATAATTTTAAAGTCAAGAGCATGATATGACAGAGCTCA 4470  
 Db 4474 GTGTACAGCTTTTGTGTAATAATTTTAAAGTCAAGAGCATGATATGACAGAGCTCA 4533  
 Qy 4471 GCGACGAGATCATCAAAATGCAATGCTGCGAGAGGAGAACTACACGTTGAGATTT 4530  
 Db 4534 GCGACGAGATCATCAAAATGCAATGCTGCGAGAGGAGAACTACACGTTGAGATTT 4593  
 Qy 4531 CAGCAATGAATTTGATCATGATAGTAAACGGTATCTGTGCTTTTCCAAATGGCCACT 4590  
 Db 4594 CAGCAATGAATTTGATCATGATAGTAAACGGTATCTGTGCTTTTCCAAATGGCCACT 4653  
 Qy 4591 TCAAGGCTGATCAATATCAATGAAAGATGCTATGATTCAGAGAGGTGCAAGCAAC 4650  
 Db 4654 TCAAGGCTGATCAATATCAATGAAAGATGCTATGATTCAGAGAGGTGCAAGCAAC 4713  
 Qy 4651 CAATTCGTGAACGAAATCTAATGATTAATTTTGTATTTCTTCAATATTTGAT 4710  
 Db 4714 CAATTCGTGAACGAAATCTAATGATTAATTTTGTATTTCTTCAATATTTGAT 4773

OY	4711	CCCTTTTCAACCTCAATCTGTCATTGGTGCTCATCTGTGAATAATTTTTAAAGACAAGA	4770
Db	4774	CATTTTTCACACCAACTGTTCAATGGTGTTATCATTGTAATTTAATGAAGAAAAGA	4833
OY	4771	AAAAAGCAGGTGCATCTTAGAAATGTTCTCATGACAGAAATCGAAAAAGTACTAATATG	4830
Db	4834	AAAAAGCAGGTGCATCTTAGAAATGTTCTCATGACAGAAATCGAAAAAGTACTAATATG	4893
OY	4831	CTATGAAAAAGATGGGCTCTTAAAAAACCTTTAAAGCATTCCAAAGCAAAGTGCGAC	4890
Db	4894	CTATGAAAAAGATGGGCTCTTAAAAAACCTTTAAAGCATTCCAAAGCAAAGTGCGAC	4953
OY	4891	CACAAGCAATAGTCTTGAATAGTAACCGATAGAAGAAATTCGATATATCATTTATGTAT	4950
Db	4954	CACAGCAATAGTCTTGAATAGTAACCGATAGAAGAAATTCGATATATCATTTATGTAT	5013
OY	4951	TCAATGGTCTGAACATGTCCACATGACCCTCGATCGTTACGATGGTGCGACAGTATA	5010
Db	5014	TCATTTGGTCTGAACATGTCCACATGACCCTCGATCGTTACGATGGTGCGACAGTATA	5073
OY	5011	AACGGGCTCCTAGACTATCTCAATGGGATATTGAGTAAATTTTCAGTTCCGAATGTAT	5070
Db	5074	AACGGGCTCCTAGACTATCTCAATGGGATATTGAGTAAATTTTCAGTTCCGAATGTAT	5133
OY	5071	TAAAAATATTCGCTTTACGATATCACTAATTTATGACCATGGAAATTTATTTGATGTAG	5130
Db	5134	TAAAAATATTCGCTTTACGATATCACTAATTTATGACCATGGAAATTTATTTGATGTAG	5193
OY	5131	TAGTTGTCAATTTTATCCATCTTAGTCTTGACTTACCTACGATATATGAGAAAGTACTCG	5190
Db	5194	TAGTTGTCAATTTTATCCATCTTAGTCTTGACTTACCTACGATATATGAGAAAGTACTCG	5253
OY	5191	TGTGCGCGACCCCTGCTCGAGTGTGTGGTGATGAGGAAAGTGAGGCCGTGTCTTGACTCG	5250
Db	5254	TGTGCGCGACCCCTGCTCGAGTGTGTGGTGATGAGGAAAGTGAGGCCGTGTCTTGACTCG	5313
OY	5251	TGAAGGAGGCCAAGGGCATTTGGACAATGTCCTTCGGTTGGCCATGTGCTGCGCGCCC	5310
Db	5314	TGAAGGAGGCCAAGGGCATTTGGACAATGTCCTTCGGTTGGCCATGTGCTGCGCGCCC	5373
OY	5311	TGTTCAACATCTGCTGCTGCTGTCTGCTTCGTCATAGTTTCATCTTTTGCCATTTTGGCAGT	5370
Db	5374	TGTTCAACATCTGCTGCTGCTGTCTGCTTCGTCATAGTTTCATCTTTTGCCATTTTGGCAGT	5433
OY	5371	CGTTCTTCATCAAGTGAAGGAGAAAGCGGCCTTAAAGACGTCTAACACTTCAAAGCCT	5430
Db	5434	CGTTCTTCATCAAGTGAAGGAGAAAGCGGCCTTAAAGACGTCTAACACTTCAAAGCCT	5493
OY	5431	TTGGCCAGAGCATGATCTGCTCTTTCAGATGTGCAAGCTCAGCCGGTTGGATGGTGTAC	5490
Db	5494	TTGGCCAGAGCATGATCTGCTCTTTCAGATGTGCAAGCTCAGCCGGTTGGATGGTGTAC	5553
OY	5491	TGAGCGCCATTATCAATGAGGAAGCATGCATCCAACCCGACAGGACAAAGGCTATCCGG	5550
Db	5554	TGAGCGCCATTATCAATGAGGAAGCATGCATCCAACCCGACAGGACAAAGGCTATCCGG	5613
OY	5551	GCAATTTGGTTCACGCGACCGTTGGAAATAAGTTTTCTCTCAATACCTTAGTTAATAGCT	5610
Db	5614	GCAATTTGGTTCACGCGACCGTTGGAAATAAGTTTTCTCTCAATACCTTAGTTAATAGCT	5673
OY	5611	TTTTGATAGTTATTTATATATGTATCATTTGCTGTCTATTCTGAGAACTATAGCAGCACCG	5670
Db	5674	TTTTGATAGTTATTTATATATGTATCATTTGCTGTCTATTCTGAGAACTATAGTACAGCACCG	5733
OY	5671	AGGACGTGCAAGAGGCTCTAACCCAGACGACTACGATGATGATACATAGATCTGGCAGC	5730
Db	5734	AGGACGTGCAAGAGGCTCTAACCCAGACGACTACGATGATGATGATACATAGATCTGGCAGC	5793
OY	5731	AATTCGATCCGGAAGGCAACCCAGTACATACGCTATGATCAGGTGTCCAAATTCCTCGACG	5790
Db	5794	AATTCGATCCGGAAGGCAACCCAGTACATACGCTATGATCAGGTGTCCAAATTCCTCGACG	5853
OY	5791	TACTGAGCCCCGCTGCGAGATCCACAAACCGAACAGTACAAATCATATTCAGTACACA	5850

Db	5854	TACTGAGGCCCGCTGCGATGATCAAAACGAAAGTACAAAGTACATTCATCGATGACA	5913
QY	5851	TACCCATCTGTCCGCGGTGACCTCATGTACTGCTGACATCTTCGACGCCCTTACGAAAG	5910
Db	5914	TACCCATCTGTCCGCGGTGACCTCATGTACTGCTGACATCTTCGACGCCCTTACGAAAG	5913
QY	5911	ACTTCTTTTGGCGGAAAGGGCAATCCCATGTAGAGAGACGGGTGAGATTGTGAAATAGCGG	5970
Db	5974	ACTTCTTTTGGCGGAAAGGGCAATCCCATGTAGAGAGACGGGTGAGATTGTGAAATAGCGG	6033
QY	5971	CCGCGCCCGGATAGGAGAGGGCTTAGAGCCGCTTCATCAACGCTGTGGCGCTCAACGTGAGG	6030
Db	6034	CCGCGCCCGGATAGGAGAGGGCTTAGAGCCGCTTCATCAACGCTGTGGCGCTCAACGTGAGG	6093
QY	6031	AGTACTGCGCCCGGCTTAATCAGACAAGCTGTGGGAAAGCAAGCGCGCGCGAGGGAG	6090
Db	6094	AGTACTGCGCCCGGCTTAATCAGACAAGCTGTGGGAAAGCAAGCGCGCGCGAGGGAG	6153
QY	6091	GTGGGTCTTTTAGACCAGATACGATATATGGCGATGGCGGTGATTCGGATAGCCGGGGAC	6150
Db	6154	GTGGGTCTTTTAGACCAGATACGATATATGGCGATGGCGGTGATTCGGATAGCCGGGGAC	6213
QY	6151	CGGCGCCCGGATGGAAGCAACGGAACGGCGATCGCCCGCTGTGGTAGATGTAGTGTAAAC	6210
Db	6214	CGGCGCCCGGATGGAAGCAACGGAACGGCGATTCGCCCTGTGGTAGATGTAGTGTAAAC	6273
QY	6211	GTACTGCAAGAGAGACTGCCGATGCCGATGAGATATGTAAATATGTCGCGGTGAGATG	6270
Db	6274	GTACTGCAAGAGAGACTGCCGATGCCGATGAGATATGTAAATATGTCGCGGTGAGATG	6333
QY	6271	CAGCGCGCGCGCGACAGACAGACAGACAGCGCGCGCGGGGACAGACAGCGCGGGAA	6330
Db	6334	CAGCGCGCGCGCGACAGACAGACAGACAGCGCGCGGGGACAGACAGCGCGGGAA	6393
QY	6331	GTCCCGGAGCGGTAGCGCGCGCGGACAGACAGCCGCTTCTCTGTGAGAGCGACGGGTTCC	6390
Db	6394	GTCCCGGAGCGGTAGCGCGCGCGGACAGACAGCCGCTTCTCTGTGAGAGCGACGGGTTCC	6453
QY	6391	TGACGAAGAACCGGCAACAGGTGTATCCACTCTGCGATGCGCCGACGATCACTGTGCGGA	6450
Db	6454	TGACGAAGAACCGGCAACAGGTGTATCCACTCTGCGATGCGCCGACGATCACTGTGCGGA	6513
QY	6451	CGGCGGATGTCTGA 6464	
Db	6514	CGGCGGATGTCTGA 6527	
RESULT 6			
AR028545	LOCUS	AR028545	6519 bp DNA linear PAT 29-SEP-1999
AR028545	DEFINITION	Sequence 24 from patent US 5858713.	
AR028545	ACCESSION	AR028545	
AR028545.1	VERSION	AR028545.1	GI:5940518
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 6519)		
AUTHORS	Soderlund,D.M. and Ingles,P.J.		
TITLE	Calcium permeable insect sodium channels and use thereof		
JOURNAL	Patent: US 5858713-A 24 12-JUN-1999;		
FEATURES	Location/Qualifiers		
source	1..6519		
ORIGIN	/organism="unknown" /mol_type="unassigned DNA"		
QY	Query Match	94.6%;	Score 6163.8; DB 6; Length 6519;
	Best Local Similarity	97.7%;	Pred. No. 0;
	Matches 6339;	Conservative	0; Mismatches 12; Indels 138; Gaps 3
QY	24 ATGACGAAGATTCCGACTCGATATCTGAGGAAGAACGACAGTTTGTCCGTCCCTTACC	83	

Db	1	ATGACGAAAGATTTCCACTCGATATCTGAGGAAAGACGAGTTTGTTCCTCCCTTAC	60
Qy	84	CCCGAATCAATTTGGTGCMAATCCGAAACAACGATTTGCCGCTGAAACATGAAAAAGCAAGAG	143
Db	61	CCCGAATCAATTTGGTGCMAATCCGAAACAACGATTTGCCGCTGAAACATGAAAAAGCAAGAG	120
Qy	144	CTGGAAGAAGAAAGACCCGAGGGAGAGTGTCGCGCATATGGTGCAGAGAAAAACAATA	203
Db	121	CTGGAAGAAGAAAGACCCGAGGGAGAGTGTCGCGCATATGGTGCAGAGAAAAACAATA	180
Qy	204	GAAATTCGATATGATGACGAGGACGAGGATGAAGGTTCACAAACCGGATCCTACACTTGA	263
Db	181	GAAATTCGATATGATGACGAGGACGAGGATGAAGGTTCACAAACCGGATCCTACACTTGA	240
Qy	264	CAGGGGTGTCCAATACCTGTTGCAATTTGACAGGGCAGGCTCCCGCGGAATTTGGCTCCACT	323
Db	241	CAGGGGTGTCCAATACCTGTTGCAATTTGACAGGGCAGGCTCCCGCGGAATTTGGCTCCACT	300
Qy	324	CCTCTCGAGGATATCGATCCCTACCTACAGCAATGTATCTGACATTGTAAGTGTGAAGCAA	383
Db	301	CCTCTCGAGGATATCGATCCCTACCTACAGCAATGTATCTGACATTGTAAGTGTGAAGCAA	360
Qy	384	GGAAGAAGATTTTTTGGCTTTTCTGCATCAAAAGCATGTGGATGCTCCGATCCATTCAT	443
Db	361	GGAAGAAGATTTTTTGGCTTTTCTGCATCAAAAGCATGTGGATGCTCCGATCCATTCAT	420
Qy	444	CCGATACGTCGTGGCCATTTACATTTCTAGTGCATCCATTAATTTTTCCCTAATCATCATC	503
Db	421	CCGATACGTCGTGGCCATTTACATTTCTAGTGCATCCATTAATTTTTCCCTAATCATCATC	480
Qy	504	ACCACAATTCCTGTCACATCGATCCTGATGATATATCCGACAAACGCCCAACGGTTGAGTCC	563
Db	481	ACCACAATTCCTGTCACATCGATCCTGATGATATATCCGACAAACGCCCAACGGTTGAGTCC	540
Qy	564	ACTGAGGTGATATTTACCCGGAAATCTACACATTTGAATCAGCTGTAAAGTATGATGACAGA	623
Db	541	ACTGAGGTGATATTTACCCGGAAATCTACACATTTGAATCAGCTGTAAAGTATGATGACAGA	600
Qy	624	GGTTTCATTTTATGCCCGTTTACGTATCTTAAAGATGATGAAATTTGGCTGAGCTTCGTA	683
Db	601	GGTTTCATTTTATGCCCGTTTACGTATCTTAAAGATGATGAAATTTGGCTGAGCTTCGTA	660
Qy	684	GTAATAGCTTTAGCTTATGTGACCATGAGGTATAGATTTAGTATAGACAGCCCTGCGA	743
Db	661	GTAATAGCTTTAGCTTATGTGACCATGAGGTATAGATTTAGTATAGACAGCCCTGCGA	720
Qy	744	ACGTTTAAAGGTGCTGCGAGCGCTTAAACCGTACCGCATTTGTGCGAGGCTTGAAGACATC	803
Db	721	ACGTTTAAAGGTGCTGCGAGCGCTTAAACCGTACCGCATTTGTGCGAGGCTTGAAGACATC	780
Qy	804	GTCGGCGCGCTCATGGAATCCGCTGAAAGAAATCTGCGGATGTGATTAATCCTGACCATGTTT	863
Db	781	GTCGGCGCGCTCATGGAATCCGCTGAAAGAAATCTGCGGATGTGATTAATCCTGACCATGTTT	840
Qy	864	TCCCTGTGCTGTGGCGTTGATGAGGCTACAGATCTATATGAGGCGTGTCAACCGAAG	923
Db	841	TCCCTGTGCTGTGGCGTTGATGAGGCTACAGATCTATATGAGGCGTGTCAACCGAAG	900
Qy	924	TGCATCAGAAAGTTCCCGCTGACCGGTTCTTGGGGCAATCTGACCGACAGAACTTGGAGC	983
Db	901	TGCATCAGAAAGTTCCCGCTGACCGGTTCTTGGGGCAATCTGACCGACAGAACTTGGAGC	960
Qy	984	TATACCAATCCGAATAGCTCCAAATTTGTATATCCGAGAGAGAGGCAATCTCATTTCCGTTA	104
Db	961	TATACCAATCCGAATAGCTCCAAATTTGTATATCCGAGAGAGAGGCAATCTCATTTCCGTTA	102
Qy	1044	TGCGGCAATATATCCGCTGCGGGGCAATCGACGACATTAACGTGTGCTGACAGGGGTTT	110
Db	1021	TGCGGCAATATATCCGCTGCGGGGCAATCGACGACATTAACGTGTGCTGACAGGGGTTT	108
Qy	1104	GGTCCGAATCCGAATTAATGCTACACACAGCTTCGATTCGTTCCGATGGGCTTTTCTGTCTC	116

Db	1081	GGTCCGAATCCGAATTATG3CTAACAACAGCTTCGATTCGTTCCGATGG3GCTTTCCTGTCC	114C
Qy	1164	GCCTTCCGGCTGATGACACAGACACTTCGGAGAGATCTGATCCAGCTGGTGGCGGCC	122Z
Db	1141	GCTTTCGGCTGATGACACAGACCTTCGGAGAGATCTGATCCAGCTGGTGGCGGCC	1200
Qy	1224	GCCGACCATGGACATGCTGTTCTTTATGATCATCTTTCGAGTTCAATCTTATCTT	128B
Db	1201	GCCGACCATGGACATGCTGTTCTTTATGATCATCTTTCGAGTTCAATCTTATCTT	1260
Qy	1284	GTGAATTTGATTTTGGCCATTTGTTGCCATGTCTGATGACGAAATTGGCAAGAGAGCCGAA	1343
Db	1261	GTGAATTTGATTTTGGCCATTTGTTGCCATGTCTGATGACGAAATTGGCAAGAGAGCCGAA	1320
Qy	1344	GAAGAAGAGGCTGCCAAGAGAGAGGCGCATACGTGAAGGAGAAAGAGCTGCCGCCCAA	1403
Db	1321	GAAGAAGAGGCTGCCAAGAGAGAGGCGCATACGTGAAGGAGAAAGAGCTGCCGCCCAA	1380
Qy	1404	GCGGCGAAGCTGAGAGAGCGGGCCAAATGCGAGGCTCAGGAGCAGCGCGATGCGGCTGCC	1463
Db	1381	GCGGCGAAGCTGAGAGAGCGGGCCAAATGCGAGGCTCAGGAGCAGCGCGATGCGGCTGCC	1448
Qy	1484	GCCGAAGAAGGCTGACATCTGCATCCGGAAATGCGCAAGAGTCCGAGGTATTTCTTGACATCAGC	152Z
Db	1441	GCCGAAGAAGGCTGACATCTGCATCCGGAAATGCGCAAGAGTCCGAGGTATTTCTTGACATCAGC	1500
Qy	1524	TATGAGCTAATTTGTTGGCGCGAGAGAGGGCAACATGACAAACAAGAGAAAGATGCC	1583
Db	1501	TATGAGCTAATTTGTTGGCGCGAGAGAGGGCAACATGACAAACAAGAGAAAGATGCC	1566
Qy	1584	ATTGCGAGCGTTCGAGGTGGAGTTCGAGTCCGTTGACGCTTATACAAAGACAAACAAGACTT	1643
Db	1561	ATTGCGAGCGTTCGAGGTGGAGTTCGAGTCCGTTGACGCTTATACAAAGACAAACAAGACTT	1628
Qy	1644	ACCACAGACACCAAGCTACCAAACTTGTTAAAGTAGACACAGACATCTTATCTTACTT	1703
Db	1621	ACCACAGACACCAAGCTACCAAACTTGTTAAAGTAGACACAGACATCTTATCTTACTT	1680
Qy	1704	GATTCAACCGTTTAAATATACGAGAGGGAAATACAGTAGTTCTCAACAAGTACAGATACGGAAAC	1763
Db	1681	GATTCAACCGTTTAAATATACGAGAGGGAAATACAGTAGTTCTCAACAAGTACAGATACGGAAAC	1740
Qy	1764	GGAAGTGGCCGCTTTGGTATACCCCGTATAGCATCTGAAGCCATTTGTTATCTCAACATAT	1823
Db	1741	GGAAGTGGCCGCTTTGGTATACCCCGTATAGCATCTGAAGCCATTTGTTATCTCAACATAT	1800
Qy	1824	CAGAGATGCCACAGACACTTGTCCTTATGCGACGACTCGAATGCCGTCGACCCCGATGCC	1883
Db	1801	CAGAGATGCCACAGACACTTGTCCTTATGCGACGACTCGAATGCCGTCGACCCCGATGCC	1860
Qy	1884	GAAAGAAATGGGGGCATCATATAGTCCCGGTACTATAGGCAATCMAAGCTCCCGACATCTCA	1943
Db	1861	GAAAGAAATGGGGGCATCATATAGTCCCGGTACTATAGGCAATCMAAGCTCCCGACATCTCA	1920
Qy	1944	TGCTATACCTTGCAATCAGTCCCGAAATTCGTAATCTCAACATGGCGAATCTTACTGGCGGC	2003
Db	1921	TGCTATACCTTGCAATCAGTCCCGAAATTCGTAATCTCAACATGGCGAATCTTACTGGCGGC	1980
Qy	2004	ATGCGCCGTCAATGGCGCTGACGACAAATGACCAAGAGAGCAAAATTCGCGAATCCGCAACA	2063
Db	1981	ATGCGCCGTCAATGGCGCTGACGACAAATGACCAAGAGAGCAAAATTCGCGAATCCGCAACA	2040
Qy	2064	CGCAATCAATAGTGGGGCGCAACAATGGGGGCAACACTGTCTGGAGCAACAATCAACAAG	2123
Db	2041	CGCAATCAATAGTGGGGCGCAACAATGGGGGCAACACTGTCTGGAGCAACAATCAACAAG	2100
Qy	2124	CTCGATCATGCGCACTACGAAATTTGGCTGTGAGTGCACGACGAAAGCTGGCAAGATTAAA	2183
Db	2101	CTCGATCATGCGCACTACGAAATTTGGCTGTGAGTGCACGACGAAAGCTGGCAAGATTAAA	2160
Qy	2184	CATCATGACAAATCTTTTATGAGCCCGCTCCAGACAAACGGTGGTTGATATGAAGAT	2243
Db	2161	CATCATGACAAATCTTTTATGAGCCCGCTCCAGACAAACGGTGGTTGATATGAAGAT	2220

OY	2244	GTGATGCTCTGGAATGAATCATCATGGAACAGCCGCTGCTGTGGCAACATGTGGGGCAACGCAT	2303
Db	2221	GTGATGCTCTGGAATGAATCATCATGGAACAGCCGCTGCTGTGGCAACATGTGGGGCAACGCAT	2280
OY	2304	CGGAGTGTCTCCGTTTACTATTTTCCCAACAGAGACGATGACGAGATGGGCGGAGCTTC	2363
Db	2281	CGCGGT-----GAGGACATGACAGAGATGGGCGGAGCTTC	2316
OY	2364	AAAGACAAGGCACTTCGAAGTGATCTCTAAGGCAATGCATGTGTTTTGTGTGTGGACTGT	2423
Db	2317	AAAGACAAGGCACTTCGAAGTGATCTCTAAGGCAATGCATGTGTTTTGTGTGTGGACTGT	2376
OY	2424	TGCTGGGTTTGGTTGAATTTCAAGAGGGGTATCGCTACGCTCTGCATCCCTTCGTC	2483
Db	2377	TGCTGGGTTTGGTTGAATTTCAAGAGGGGTATCGCTACGCTCTGCATCCCTTCGTC	2436
OY	2484	GAGCTCTTCATCAGCGCTGTGCAATTTGTGTCAACGATGTTCATGTCGATGTGATCACAC	2543
Db	2437	GAGCTCTTCATCAGCGCTGTGCAATTTGTGTCAACGATGTTCATGTCGATGTGATCACAC	2496
OY	2544	GATATGAACAAAGAGATGGAACCGGTGTCAAGAGTGGCACTATTTCTTCAACGCGCAC	2603
Db	2497	GATATGAACAAAGAGATGGAACCGGTGTCAAGAGTGGCACTATTTCTTCAACGCGCAC	2556
OY	2604	TTTGCATCGAGGCCACCATGAGCTATGCGCATAGCCCCAAGTACTATTTCCAGAG	2663
Db	2557	TTTGCATCGAGGCCACCATGAGCTATGCGCATAGCCCCAAGTACTATTTCCAGAG	2616
OY	2664	GCGTGAACATCTTGCATCTTATTCGTGGCCCTATTCGCTATTTGGAACCTGGACTGAG	2723
Db	2617	GCGTGAACATCTTGCATCTTATTCGTGGCCCTATTCGCTATTTGGAACCTGGACTGAG	2676
OY	2724	GGTGTCCAGGGCTGTCCGTATGTGGTCCCTTGATGTGCTGCTGATTTCAACTGACC	2783
Db	2677	GGTGTCCAGGGCTGTCCGTATGTGGTCCCTTGATGTGCTGCTGATTTCAACTGACC	2736
OY	2784	AAGTCTTGGCCCACTTAATTTACTCATTTGATTAATGGAACGCAACCATGGCGCTTTG	2843
Db	2737	AAGTCTTGGCCCACTTAATTTACTCATTTGATTAATGGAACGCAACCATGGCGCTTTG	2796
OY	2844	GGTATCTGCACTTTTGACTTTGCTATTCATCTTATTCATCTTGGCGTATGGAGATGCA	2903
Db	2797	GGTATCTGCACTTTTGACTTTGCTATTCATCTTATTCATCTTGGCGTATGGAGATGCA	2856
OY	2904	CTGTTCGGAAGAATTTATCATGATCAAGAAGCCGCTTTCGGATGCGACTGCGCGC	2963
Db	2857	CTGTTCGGAAGAATTTATCATGATCAAGAAGCCGCTTTCGGATGCGACTGCGCGC	2916
OY	2964	TGGAATTTCAACGACTTTATGCAAGCTTCATGATCGTTCGCGGTCTCTGGGAGAGA	3023
Db	2917	TGGAATTTCAACGACTTTATGCAAGCTTCATGATCGTTCGCGGTCTCTGGGAGAGA	2976
OY	3024	TGGAATCGAGTCACTGAGGCACTGCAAGTACGTGGGCGATGTCTCTGTGATTCCTTCTC	3083
Db	2977	TGGAATCGAGTCACTGAGGCACTGCAAGTACGTGGGCGATGTCTGTGATTCCTTCTC	3036
OY	3084	TTGGCCACCGTTGTCAATCGGCAATCTTGTGTACTTAACTTTTCTTACGCTTGTGTTTG	3143
Db	3037	TTGGCCACCGTTGTCAATCGGCAATCTTGTGTACTTAACTTTTCTTACGCTTGTGTTTG	3096
OY	3144	TCCAAATTTTGGCTACTGATGCTTATGAGCGCGCATGCGCGATGACATACGAATTAATA	3203
Db	3097	TCCAAATTTTGGCTACTGATGCTTATGAGCGCGCATGCGCGATGACATACGAATTAATA	3156
OY	3204	GCCGAGCGCTTCATCGAATGAGCCGATTTAAAGTTGGGTTAAGCGTATATTTCTGAT	3263
Db	3157	GCCGAGCGCTTCATCGAATGAGCCGATTTAAAGTTGGGTTAAGCGTATATTTCTGAT	3216
OY	3264	TGTTTCAAGTTATACGTAAACAATTTGCAAAATCAAAATTAAGATCAACCAAGTGTG	3322
Db	3217	TGTTTCAAGTTATACGTAAACAATTTGCAAAATCAAAATTAAGATCAACCAAGTGTG	3266

[illegible]

Db	42.53	ATAATGGGTGTACAGCTTTTGTCTGGAAAATTTTAAAGTGGAGACATGAATGGCACG	43020
QY	4464	AAGCTCAGCCACGAGATCATACCAATGCGAATGCTCTGCGAGGCGAATCAACGCTG	45233
Db	4303	AAGCTCAGCCACGAGATCATACCAATGCGAATGCTCTGCGAGGCGAATCAACGCTG	43626
QY	4544	GTGAATTCAGCAATGAATTTTGATCATGTAGGTAAAGCGTATCTGTGCTTTCCAGTG	45833
Db	4363	GTGAATTCAGCAATGAATTTTGATCATGTAGGTAAAGCGTATCTGTGCTTTCCAGTG	44222
QY	4584	GCCACCTTCAAAGGCTGATACCAATCATGAAACGATGTATCGATCTACCGAGGCTGAC	46433
Db	4423	GCCACCTTCAAAGGCTGATACCAATCATGAAACGATGTATCGATCTACCGAGGCTGAC	44822
QY	4644	AAGCAACCAATTCGTGAACGAAACATCAACATGATATTAATTTTCATTCATCATTA	47033
Db	4483	AAGCAACCAATTCGTGAACGAAACATCAACATGATATTAATTTTCATTCATCATTA	45424
QY	4704	TTTGATTCCTTTTCACTCAATCTGTTCATTTGGTGTATCATGTATTAATTTAATGAG	47633
Db	4543	TTTGATTCCTTTTCACTCAATCTGTTCATTTGGTGTATCATGTATTAATTTAATGAG	46020
QY	4764	CAAAAGAAAAAAGCGAGGTGATCATTTAATAATGTTCAAGACAAAGATCAAAAAAGTAC	48233
Db	4603	CAAAAGAAAAAAGCGAGGTGATCATTTAATAATGTTCAAGACAAAGATCAAAAAAGTAC	46622
QY	4824	TATATATGCTATGAAAAAAGATGGGCTCTTAAAAACCAATTAAAAAGCAATCCAAAGCAAG	48833
Db	4663	TATATATGCTATGAAAAAAGATGGGCTCTTAAAAACCAATTAAAAAGCAATCCAAAGCAAG	47222
QY	4884	TGGCGACCAACGACATATGTCTTTGAAATAGTAACCGATTAAGAAATTCGATATATCATTT	49433
Db	4723	TGGCGACCAACGACATATGTCTTTGAAATAGTAACCGATTAAGAAATTCGATATATCATTT	47822
QY	4944	ATGTATTCATTTGGTCTGGAACATGTTCCATGACCCCTCGATTCGTACGATAGCGCTCGAC	50033
Db	4783	ATGTATTCATTTGGTCTGGAACATGTTCCATGACCCCTCGATTCGTACGATAGCGCTCGAC	48422
QY	5004	ACGATATAACGGGAGTCTTACGATCTCAATCGCATATTCGATATTAATTTTCAGTTCCGAA	50633
Db	4843	ACGATATAACGGGAGTCTTACGATCTCAATCGCATATTCGATATTAATTTTCAGTTCCGAA	49022
QY	5064	TGTCTATTTAAATAATTTGCTTACGATATCACTAATTTATTTGAGCCATGGAATTTATTT	51233
Db	4903	TGTCTATTTAAATAATTTGCTTACGATATCACTAATTTATTTGAGCCATGGAATTTATTT	49622
QY	5124	GATGTAGTATGTTGTTCATTTTATTCATCTTAGGCTCTTGATTAAGCATATTTATGAGAG	51833
Db	4963	GATGTAGTATGTTGTTCATTTTATTCATCTTAGGCTCTTGATTAAGCATATTTATGAGAG	50222
QY	5184	TACTTCGTGTGCGCGAACCCCTGCTCGAGATGGGTGGGTGGGAAAGTGGGCGGTGCTT	52433
Db	5023	TACTTCGTGTGCGCGAACCCCTGCTCGAGATGGGTGGGTGGGAAAGTGGGCGGTGCTT	50822
QY	5244	CGACTGTGTAAGGAGCCAAAGGACATTCGACACATGCTTCGCGTTGGGACATGCTGCTG	53033
Db	5083	CGACTGTGTAAGGAGCCAAAGGACATTCGACACATGCTTCGCGTTGGGACATGCTGCTG	51422
QY	5304	CCGGCCCTGTTCAACATCTGCTGCTGTGTTCCGTGTGATGTTCAATCTTTGCCATTTTC	53633
Db	5143	CCGGCCCTGTTCAACATCTGCTGCTGTGTTCCGTGTGATGTTCAATCTTTGCCATTTTC	52022
QY	5364	GGCAGTGTGCTTTCATGACGATGAAAGGAGAAAGCCGCAATTAAAGCATGTTAACAATTC	54233
Db	5203	GGCAGTGTGCTTTCATGACGATGAAAGGAGAAAGCCGCAATTAAAGCATGTTAACAATTC	52622
QY	5424	AAGACCTTTGGCCAGAGCATGATCTGCTCTTTAGATGTTGACGTCAGCCGCTTGGGAT	54833
Db	5263	AAGACCTTTGGCCAGAGCATGATCTGCTCTTTAGATGTTGACGTCAGCCGCTTGGGAT	53222
QY	5484	GGTGTACTGACGCGCATTTATCAATGAGAGCATGCGATCCACCCGACAGCGACAAAGGC	55433

Db	5323	GGTGTACTGACGCCATTATCAATAGBAGAAAGCATGCGATCCACCCGACAAGCAAAAGGC	5382
QY	5544	TATCCGGGCAATTGTGGTTGACGCCAGCTTGGAAATACGTTTCTCTCTCATACCTAAGTT	5603
Db	5383	TATCCGGGCAATTGTGGTTGACGCCAGCTTGGAAATACGTTTCTCTCTCATACCTAAGTT	5442
QY	5604	ATAAGCTTTTGAATAGTATTAAATATGTACATTGCTGTCAATTCTCGAAGAACTATAGTCAG	5663
Db	5443	ATAAGCTTTTGAATAGTATTAAATATGTACATTGCTGTCAATTCTCGAAGAACTATAGTCAG	5502
QY	5664	GCCACCGAGAGCGTGCAGAGGGGCTTAACCGAGAGCACTACAGCATGTACTATGATATC	5723
Db	5503	GCCACCGAGAGCGTGCAGAGGGGCTTAACCGAGAGCACTACAGCATGTACTATGATATC	5562
QY	5724	TGGCAGCAATTGCATCCGAGAGGGGCAACCAGTACATACGCTATGTATGACTGTCCGAATTC	5783
Db	5563	TGGCAGCAATTGCATCCGAGAGGGGCAACCAGTACATACGCTATGTATGACTGTCCGAATTC	5622
QY	5784	CTGGAAGTACTGGAAGCCCCCGCTGCAGATCCAAACCGAACAAATACAAATATATTCG	5843
Db	5623	CTGGAAGTACTGGAAGCCCCCGCTGCAGATCCAAACCGAACAAATATATATTCG	5682
QY	5844	ATGGAACATTAACCATCTGTGCGGGGCTACCTATGACTGCGTCCGACATCCCTGCAGGCCCTT	5903
Db	5683	ATGGAACATTAACCATCTGTGCGGGGCTACCTATGACTGCGTCCGACATCCCTGCAGGCCCTT	5742
QY	5904	ACGAAGAAGCTTCTTTGGCGCGGAAGGGCAATCCGATAGAGAGAAGGCTGAGATTGTGAG	5963
Db	5743	ACGAAGAAGCTTCTTTGGCGCGGAAGGGCAATCCGATAGAGAGAAGGCTGAGATTGTGAG	5802
QY	5964	ATAGCGGCGCGCCCCCGGATACGAGAGGGCTACGAGCCGCTTCATATCAACGCTGTGGCGTCAG	6023
Db	5803	ATAGCGGCGCGCCCCCGGATACGAGAGGGCTACGAGCCGCTTCATATCAACGCTGTGGCGTCAG	5862
QY	6024	CGTGAAGAGTACTGTGGCGCGCGCTTAATCCACACCGCTGGGGAAAGCAACAAGGCGCGGGCG	6083
Db	5863	CGTGAAGAGTACTGTGGCGCGCGCTTAATCCACACCGCTGGGGAAAGCAACAAGGCGCGGGCG	5922
QY	6084	GAGGAGAGGTGGGTCTCTTTGAGCCGAGTACCGGATATCATGGCATGAGCGGTGATCCGGAATGCC	6143
Db	5923	GAGGAGAGGTGGGTCTCTTTGAGCCGAGTACCGGATATCATGGCATGAGCGGTGATCCGGAATGCC	5982
QY	6144	GGGGACCCGGCGCCCGATGTAAGCAACGAGCGCGCATGCGCCGCTGGTGGAGATGTTAGT	6203
Db	5983	GGGGACCCGGCGCCCGATGTAAGCAACGAGCGCGCATGCGCCGCTGGTGGAGATGTTAGT	6042
QY	6204	GTTTAAACGGTACTGTGACAGAAAGAGCTGCGGATGCGGATGAGAGTAAATGTATGCTCCGGGT	6263
Db	6043	GTTTAAACGGTACTGTGACAGAAAGAGCTGCGGATGCGGATGAGAGTAAATGTATGCTCCGGGT	6102
QY	6264	GAGGATCGAGCGCGCGGCGGAGCAGCAGCAGCAGCAGCGGCGCGCGCGGAGCAGCAGCAGC	6323
Db	6103	GAGGATCGAGCGCGCGGCGGAGCAGCAGCAGCAGCAGCGGCGCGCGCGGAGCAGCAGCAGC	6162
QY	6324	GCGGGAAGTCCCGGAGCGGGTAAAGCGCGCGGCGCAGACAGCCGCTTCTCTGTGAGAGCGAC	6383
Db	6163	GCGGGAAGTCCCGGAGCGGGTAAAGCGCGCGGCGCAGACAGCCGCTTCTCTGTGAGAGCGAC	6222
QY	6384	GGGTTTCGTGACGAAGAACCGGCACACAGTGTGTATCCACTTCGGGATGCGCGAGCATACG	6443
Db	6223	GGGTTTCGTGACGAAGAACCGGCACACAGTGTGTATCCACTTCGGGATGCGCGAGCATACG	6282
QY	6444	TTCGGGCAACGGCGGATGTCTGAGCGCAGGCTCGGCCGCCCTCCAAAGATGACGCGAGTAT	6503
Db	6283	TTCGGGCAACGGCGGATGTCTGAGCGCAGGCTCGGCCGCCCTCCAAAGATGACGCGAGTAT	6342
QY	6504	TAGCTTGA 6512	
Db	6343	TAGCATGAG 6351	

## RESULT 7



Qy 911 GCTCCAGAGATGTCATCAAGAGTTCCCGCTGGACGGTTCCTGGGGCAATCTGACCGA 970  
Db 868 TCTAACACAAAATGTCATTTAAACGATTTCCCTGGACGGAGTTGGGGCAATCTAACCGA 927  
Qy 971 CGAGACTGGAGCTATCACAATCGCAATAGCTCCAAATGGTATTTCCGAGGACGAGGGCAT 1030  
Db 928 TGAATACTGGTTTCTACCAATAGCAACAGTTCCAAATGGTTTACGGAGAACGATGGCGA 987  
Qy 1031 CTCATTTCCGTTATGCGCAATATATCCGGTGGGGGCAATGGCGACGAGTAACTGTGTG 1090  
Db 988 GTCAATCCGGGTGGGGAATGTAATCCGGTGGGAGCAATGGCGAGAAATTAAGTCTGTG 1047  
Qy 1091 CCTGCAAGGGGTTTGGTCCGAATCCGAATTAATGGCTACACAGCTTCGATTCGTTGGAGT 1150  
Db 1048 CTTGAGAGGGCTTCGGGCCCAATCCCACTACGATTAACACAGTTTCGATTCATTTGGTTG 1107  
Qy 1151 GGCCTTCCTGTCCGCTTCCTGGCTGATGACAGAGACTTCTGGAGAGATCTGTACAGCT 1210  
Db 1108 GGCCTTCCTGTCCGCTTCCTGTATGACCAAGATTTCTGGAGAGATCTGTATCAGCA 1167  
Qy 1211 GGTGTGGCGCCCGCCGACCATGGCAATGCTGTTCTTTATAGTCATCTTCTTAGG 1270  
Db 1168 CGTGTGAGACGAGCTGAGACCTGGCAATGTTCTTTATAGTCATCTTCTTAGG 1227  
Qy 1271 TTCAATTCATCTTGTGAATTTGATTTTGCCCATTTGTTGCAATGCTGTAAGCAATTTGA 1330  
Db 1228 TTCAATTCATCTTGTGAATTTGATTTTGCCCATTTGTTGCAATGCTGTAAGCAATTTGA 1287  
Qy 1331 AAGAGAGCCGAGAGAGAGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1390  
Db 1288 AAGAGAGCCGAGAGAGAGAGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347  
Qy 1391 TGGCCGCGCCAAAGGCGCCAAAGCTGAGAGAGCGGGCCATGGCGAGCTCAGAGCAGAC 1450  
Db 1348 GCGCAGCAGCCAAAGGCGCCAAAGCTGAGAGAGCGGGCCATGAGCAGCTCAGAGCAGCTCA 1407  
Qy 1451 GGATGCGGCTGCGCGCGAGAGAGGCTGCACTGCAATCCGAAATGGCCAAAGTCCGAGCTA 1510  
Db 1408 GGATGCGGAGATGCGCGCTGCGGCGAGCTGTGATCCGAGATGGCAAGAGTCCGAGCTA 1467  
Qy 1511 TTCTTGCAATGAGCTATGAGCTATTTTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1570  
Db 1468 CTCTTGCAATGAGCTATGAGCTATTTTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1527  
Qy 1571 AGAAGAGATGTCATTTGCGAGAGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1630  
Db 1528 AGAAGAGATGTCATTTGCGAGAGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1587  
Qy 1631 ACAACAGCAGCTTACCAAGCAACCAAGCTACCAAGCTTGGTAAAGTGAAGAGAGAGAGATC 1690  
Db 1588 ACAACAGCAGCTTACCAAGCAACCC--GCTAATTAAGTCCGTAAAGTTAGAGAGAGCTTC 1644  
Qy 1691 CTATTCCTTACCTGCTTACCGCTTTTACATAACGAGGGAGTACAGTATCTTCAACAGTA 1750  
Db 1645 CTATTCCTTACCTGCTTACCGCTTTTACCTAAGCGGGAGTACAGTATCTTCAACAGTA 1704  
Qy 1751 CACGATAGGAG 1810  
Db 1705 CACATATGGAATGGGCTGAGAGAGTGGTATACAGAGTGGAGTGGAGTGGAGTGGAGTGG 1764  
Qy 1811 ATTGTCACATATGAGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1870  
Db 1765 ACTGCAACATATGAG 1824  
Qy 1871 CACCCGAGTGTCCGAG 1930  
Db 1825 AAGACCAATGTCCGAG 1884  
Qy 1931 CTCCGAG 1990  
Db 1885 TTCTAGAGATTTCTTATATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1944  
Qy 1991 TCTACTGGGAG 2050

Db 1945 TTTATTTGGGTGGCATGGGCGCCATGGGTGCCAGCAGTATGACCAAGAGAGAGAGAGAGAG 2004  
Qy 2051 CAACCGCAACACAGCAATCAATCAATGAGGCGCCACCAATGGCGGACCACTGTCTGTGA 2110  
Db 2005 CAGTGGCAACACAGCAATCAATCAATGAGGCGCCACCAATGGGTGGAGAGAGAGAGAGAG 2064  
Qy 2111 CACCAATCAAGAGTCCGAT-----CATGGGAGCTGAGAAATTTGGCTGTGA 2155  
Db 2065 CCGTGGGTGCTATCCAGATGGCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2124  
Qy 2156 GTGACAG 2215  
Db 2125 TTTATACATAG 2184  
Qy 2216 GACCAAAAG 2275  
Db 2185 AACTCAAAAG 2244  
Qy 2276 CGCTGTGGGAG 2335  
Db 2245 CGTGTGGAG 2280  
Qy 2336 GAGAGATGACAG 2395  
Db 2281 GAGAGATGACAG 2340  
Qy 2396 CATGAGATGTTTTGTGTGAG 2455  
Db 2341 CATGAGATGTTTTGTGTGAG 2400  
Qy 2456 ATGCTCATGCTTTTCCATTCCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2515  
Db 2401 GTCTTCATTTGTGTGAG 2460  
Qy 2516 CACGATGTCATGAG 2575  
Db 2461 TACATGTTTCAATGAG 2520  
Qy 2576 GAGTGGCAATATTTTCTTACCGGCACTTTTGCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2635  
Db 2521 AAGTGTGATATTTTCTTACCGGCACTTTTGCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Qy 2636 CATGAG 2695  
Db 2581 CATGAG 2640  
Qy 2696 CCTATGCTATTTGGAACCTGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2755  
Db 2641 CTGTCTCTGTGAG 2700  
Qy 2756 TCGATGCTGTGATTAATCAACTGGCCAGCTTTTGCATGAGAGAGAGAGAGAGAGAGAGAGAG 2815  
Db 2701 TCGTTTGTGCTGTGATTAATCAACTGGCCAGCTTTTGCATGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Qy 2816 GATTATGAG 2875  
Db 2761 GATTATGAG 2820  
Qy 2876 CTTCATCTTTTGGGAG 2935  
Db 2821 CTTCATCTTTTGGGAG 2880  
Qy 2936 CCGCTTTCCGAG 2995  
Db 2881 TCGCTTCAAG 2940  
Qy 2996 GATGCTGTTCCGAG 3055  
Db 2941 GATTGTGTGCGAG 3000  
Qy 3056 GGGGAGTGTCCGAG 3115

Db 3001 GGCGCATGTCAGCTGTATACCTCTCTTGCCACGCTCGATCGCAATCTGTGT 3060  
QY 3116 ACTTAACCTTTTCTTAGCCTTGCTTTTGTTCATTTTGGCTCATCTAGCTTATCAGCGCC 3175  
Db 3061 TCTTAACTTTTCTTAGCTTGTCTTTTGTTCACACTTGGTTCACTAGTTATCAGCCCC 3120  
QY 3176 GACTGCGATTAACGATACGATTAATAATAGCCGAGCTTCAATCGAATTTGGCGATTTAA 3235  
Db 3121 GACTGCGCAATAGATACCAATTAATAATAGCAGAGGCTTCAATCGAATTTGGCTTTTAA 3180  
QY 3236 AATTGGGTAAAGGTAATATGCTGATGTTTCAAGTTAATACGTAACTTAATGACAAA 3295  
Db 3181 GAATGGGTAAAGGTAATATGCTGATGTTTCAAGTTAATGCAATTAATGACAAA 3240  
QY 3296 TCAATTAAGTATCAACCATCAGGTGAGAGAACCAACAGATCAGTTGATTTGAGCGA 3355  
Db 3241 TCAATTAAGTATCAACCATC----- 3261  
QY 3356 AGAGCATGTGACACGACCTGAGCTGGGCGACGACGAGATCTCGCCGACGCGCTCAT 3415  
Db 3262 AGAATCATGGCGATATGACCTGGAGTTGGGTCAATGAGAAATCATGGGCGATGGCTTGAT 3321  
QY 3416 CAAGAAGGATCAAGAGGACGACGCAACTGAGGTGGCCATCGGGATCGCATGGAAT 3475  
Db 3322 CAATAAGGATCAAGAGGACGACGCAACTGAGGTGGCCATCGGGATCGCATGGAAT 3381  
QY 3476 CACGATACACGCGACATGAGAAACAAAGCCGAGAAATCCAAATATCTTAATAACGC 3535  
Db 3382 CAGATACATGGCGATATGAGAAACAAAGCCGAGAAATCCAAATATCTTAATAACGC 3441  
QY 3536 AAGCATATTTGGCACTCAATTAACCAAGCAATAGACTGGACACAGCGCTAAACCA 3595  
Db 3442 AACCATATTTGGAACTCAATTAACCAAGCAATAGACTGGAACTGAAGCTTAACCA 3501  
QY 3596 TAGAGTTTGTCTTAAGGACGACGACCTGCCAGATTAATCATATGTTAGCCATAA 3655  
Db 3502 TAGAGTTTGTCTTAAGGACGACGACCTGCCAGATTAATCATATGTTAGCCATAA 3561  
QY 3656 GAATGCACTTCAAGACGAGAGCCACAGGGGAGGCGGAGACGATGAGAGGCGGAGA 3715  
Db 3562 GAATGCACTTCAAGACGAGAGCCACAGGGGAGGCGGAGACGATGAGAGGCGGAGA 3621  
QY 3716 GAAAGGAGGCGGACGAGAGGATTTAGTCTGACGAGGAACTGACGAGAGGAGCGGA 3775  
Db 3622 GAAAGGAGGCGTACGAGAGAGGACCTGCGCTGACGAGGAACTGACGAGAGGCGGA 3681  
QY 3776 ATGCGAGAGGCGCGCTCGACGCTGATATTCATTTATTCATG---ACACGAGGATAT 3832  
Db 3682 GGGGAGTGAAGGCGGAGCTGATGGTGAATCATCATTCATGCGAATAACGACGAGAT 3741  
QY 3833 ACTGATGATATATCAGCTGATTTGCTGCCGATTTCCGATTAATAAGAAATTTCCGATCTT 3892  
Db 3742 AATGACACATATTCGCGCGACTGTTTCCGACCTCGATCAAGAAAGTTTCCGATCTT 3801  
QY 3893 AGCGGTGACGATGACTCGCGTCTGCGACAGATGAGGCAATTTACGATGAAACTTT 3952  
Db 3802 GCGCGGACACGAGACTCGCGTCTGCGACAGATGAGGCAATTTACGATGAAACTTT 3861  
QY 3953 TCAATTAATGAAATAAATATTTTGAACAGCTGTTATCATCTATGATTTTAATGAGTAG 4012  
Db 3862 TCAATTAATGAAATAAATATTTTGAACAGCTGTTATCATCTATGATTTTAATGAGTAG 3921  
QY 4013 CTTAGCTTTGGCATTTAGAAATGATCATCTGCAACAAAGCCCATCTGCGAGATATTT 4072  
Db 3922 CTTAGCTTTGGCATTTAGAAATGATCATCTGCAACAAAGCCCATCTGCGAGATATCT 3981  
QY 4073 ATACTATATGACAGAAATATTTACGTTATATTTCTTGTGAAATGTTAATCAAGTGTG 4132  
Db 3982 GTACTATATGACAGAAATATTTAAGGTATATTTCTTTTGGAGATGTTGATCAATGAGTT 4041  
QY 4133 GCGCTGTGCTTCAAGTGTATCTTACACAGCGGTGTGTGTGCTGCAATTTGCTGATGT 4192  
Db 4042 GCGCTGTGCTTCAAGTGTATCTTACCAATGCTGTGTGTGTGCTGCAATTTGCTGATGT 4101

QY 4193 CATGATATGCTTATCAACTTGTGCTTCACTTGTGAGGTGTGATTAACAACCTT 4252  
Db 4102 CATGCTATGCTTATTAATAATTTGTGTGCGTTTGTGCGGCTTAATATATATGCGGTGT 4161  
QY 4253 CAAGACTATGCGAAGCTTAAGAGCACTAGACCACTAGCTGCAATGTCCTGATCAGGG 4312  
Db 4162 TAGATCAATGCGCACACTGCGGCGCTTAAGGCAATGGGTGTGTCTCTAGATGGAGGG 4221  
QY 4313 CATGAGGTGTGCTTATGCGCTGTGTACAGCTATACCGTCCATCTCAATGTCTAT 4372  
Db 4222 TATGAAGTGTGTGAAATGCGCTGTGTCAACCTATACCGTCAATCTCAATGTCTAT 4281  
QY 4373 GGTGTGTCTAATATTTTGGCTAATTTTGGCCATTAATGAGGTGTACAGCTTTTGTGAAA 4432  
Db 4282 GGTGTGTCTAATATTTTGGCTAATTTTGGCCATTAATGAGGTGTACAGCTTTTGTGAAA 4341  
QY 4433 ATATTTTAAGTGCAGGACATGAAATGCGACGAAGCTCAGCCACGAGATCATACCAATCG 4492  
Db 4342 ATATTTTAAGTGTAAAGATGTATAGACATGTGCTGAGCCATGAAATCATACCGAATCG 4401  
QY 4493 CAATGCTTGCAGAGCGAGAACTACACGCTGGTGAATTCAGAAATGAATTTGATCATGT 4552  
Db 4402 TATGCTTGCAGAAAGTGAACCTACACCTGGGAAATTTGCGAATGAACCTTGATCATGT 4461  
QY 4553 AGGTAAAGGTATCTGTGCTTTTCCAAAGTGCACCTTCAAGGCTGTGATCAAAATCAT 4612  
Db 4462 AGGTAAAGGTATCTGTGCTTTTCCAAAGTGCACCTTCAAGGCTGTGATCAAAATCAT 4521  
QY 4613 GAAAGATGTATGATTCACGAGAGGTGACAAAGCAACAAATCTGTGAAACGACATCTA 4672  
Db 4522 GAACGATGCAATGATTCACGAGAGGTGACAAAGCGCGATCCGAGAAACCAATATCTA 4581  
QY 4673 CAGTATTAATATTTGATTTCTTCAATCATATTTGGAATCTTTTTCACCTCAATGTGT 4732  
Db 4582 CAGTATTAATATTTGATTTCTTCAATCATATTTGGAATCAITTTTTCACCTCAATGTGT 4641  
QY 4733 CATGTGTTATCATGATTAATTTTAATGACAAAAGAAAAGAGGTGATCAATTA 4792  
Db 4642 CATGTGTTATCATGATTAATTTTAATGACAAAAGAAAAGAGGTGATCAATTA 4701  
QY 4793 AATGTTATGACAGAAATGACAAAAGTATTAATGATGATGAAAGTGGGCTTAA 4852  
Db 4702 AATGTTATGACAGAAATGACAAAAGTATTAATGATGATGAAAGTGGGCTTAA 4761  
QY 4853 AAAACCATTAAGCCATTCAGAACCAAGGTGGCAGCAAGCAATATGCTTTGAAAT 4912  
Db 4762 AAAACCATTAAGCCATTCAGAACCGAGGTGGCAGCAAGCAATATGATGAAAT 4821  
QY 4913 AGTAAACGATTAAGAAATTCGATTAATCATTAATGATTTATGTTGTGAACATGTTAC 4972  
Db 4822 AGTAAACGATTAAGAAATTCGATTAATCATTAATGATTTATGTTGTGAACATGTTAC 4881  
QY 4973 CATGACCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5032  
Db 4882 CATGACCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4941  
QY 5033 TGGCATATTCGATTAATTTTCAAGTTCGATTAATTTTCAAGTTCGATTAATTTTCAAG 5092  
Db 4942 TGGCATATTCGATTAATTTTCAAGTTCGATTAATTTTCAAGTTCGATTAATTTTCAAG 5001  
QY 5093 TCACTATTTATTTAGGCAATGATTAATTTATGATGATGATGATGATGATGATGATGAT 5152  
Db 5002 TCACTATTTATTTAGGCAATGATTAATTTATGATGATGATGATGATGATGATGATGAT 5061  
QY 5153 AGGCTTGTATTTAGGCAATTTATTTAGGCAATTTATTTAGGCAATTTATTTAGGCAAT 5212  
Db 5062 AGGCTTGTATTTAGGCAATTTATTTAGGCAATTTATTTAGGCAATTTATTTAGGCAAT 5121  
QY 5213 GGTGCTGTGCGGAAAGTGGGCGGTGTCTTGCATCTGTGAGAGGAGCCAAAGGCAATGG 5272  
Db 5122 GGTGAGAGTGGCCAAAGTGGGCGGTGTCTGCGTTAGTCAAGGAGTCCAAAGGATATCG 5181

5273 GACACTGCTCTTCCGCTTGGCAATGTCGTCGCGCCGCTTCAACATCTGCTGCT 5332  
 5182 GACCTGCTGTTGCGGTAGCAGATGCTGCTGCTTATCAACATTTGCTGCT 5241  
 5333 GTTCTGTGATGTTTCACTCTTGGCAATTTGGCAATGCTGCTTCAACATGTAAGA 5392  
 5242 GTTCTGTGATGTTTCACTCTTGGCAATTTGGCAATGCTGCTTCAACATGTAAGA 5301  
 5393 GAAAGCGCGCATTAACAGAGCTTACACTTCAAGCTTTGGCCAGAGCATGATCTGCT 5452  
 5302 GAAAGCGCGCATTAACAGAGCTTACACTTCAAGCTTTGGCCAGAGCATGATCTGCT 5361  
 5453 CTTTCAGATGTCAGAGCTGAGCGGCTTGGAGTGTGTAACGCGCATTAATCAAGAGA 5512  
 5362 GTTTCAGATGTCAGAGCTGAGCGGCTTGGAGTGTGTAACGCGCATTAATCAAGAGA 5421  
 5513 AGCATGCGATCAACCCGACAGCGCAAGAGGCTATCCGGGCAATGTGTTGACGACCGT 5572  
 5422 AGATGCGATCAACCCGACAGCGCAAGAGGCTATCCGGGCAATGTGTTGACGACCGT 5481  
 5573 TGGAAATACGTTTCTCTCTCATACCTTATTAAGCTTTTGAATGTTATTAATGTA 5632  
 5482 TGGAAATACGTTTCTCTCTCATACCTTATTAAGCTTTTGAATGTTATTAATGTA 5541  
 5633 CATGCTGCTCATTTCTCGAAGACTATAGTCAGGCGCACGAGGACGTAAGGCTTAC 5692  
 5542 CATGCTGCTCATTTCTCGAAGACTATAGTCAGGCGCACGAGGACGTAAGGCTTAC 5601  
 5693 CGACGACGACTACGACATGTAATGATGATGTCGAGCAATTTGATCCGAGGCGACCA 5752  
 5602 CGACGACGACTATGATGTAATGATGTCGAGCAATTTGATCCGAGGCGACCA 5661  
 5753 GTACATACGCTATGATGTCGAGTGTCCGAATTTCTGAGCTGACGCGCCGCTGACAT 5812  
 5662 GTACATACGCTATGATGTCGAGTGTCCGAATTTCTGAGCTGACGCGCCGCTGACAT 5721  
 5813 CCACAAACCGAACAAGTACAGATGATGATGTCGAGCAATTTGATCCGAGGCGACCT 5872  
 5722 CCACAAACCGAACAAGTACAGATGATGATGTCGAGCAATTTGATCCGAGGCGACCT 5781  
 5873 CATGCTGCTCATTTCTCGAAGACTATAGTCAGGCGCACGAGGACGTAAGGCTTAC 5932  
 5782 GATGCTGCTCATTTCTCGAAGACTATAGTCAGGCGCACGAGGACGTAAGGCTTAC 5841  
 5933 TCCGATACGAGAGAGAGCGGTGATGTTGAGATGAGCGCGCCGCGGATACGAGGCTA 5992  
 5842 TCCGATACGAGAGAGAGCGGTGATGTTGAGATGAGCGCGCGCGGACGACCGAGGCTA 5901  
 5993 CGAGCGGCTGTCATCAACGCTGTCGAGCGGCGGAGAGAGTACGCGCGGCTTATGCA 6052  
 5902 TGAATCGGTCGTCGACACTGTGCGCGGAGCGGAGAGTACGCGCGGCTTATGCA 5961  
 6053 GCACGCGCTGCGAAGAGCAAGAGCGCGCGGAGAGAGTGTGCTTTTGAACGCGGATAC 6112  
 5962 GAATGCGGTGCGG-----GCGTTACAAGAAATGGCCCAACCCGAGAGGGGTGATGA 6009  
 6113 GGATCATGAGCAATGCGGTGATTCGAGTCCGAGGAGCCGCGCGCGTGAAGCAACGGA 6172  
 6010 GGGGAGAGCGCGCTGTCGAGAGAGTGTGCTGAAGCGCGTGAAGGCGGAGCGG 6069  
 6173 CGGCGATGCGCGCGCTGTCGAGAGTGTGAAGTGAAGCTGCTGCAAGAGAGGCTGCGGA 6232  
 6070 CGGCGCGCGCGCGCGGTGATGATGAT-----GCTCAAGAGAGAGAGCAACGCGC 6120  
 6233 TGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6292  
 6121 GCGCGCGCGCGGAGCAATCAACCTGATGATGAT-----GCGCGGAGAGAGC 6168  
 6293 AGCAGCAGCGCGCGCGCGCGCGAGAGCAAGCGCGGAGAGTCCCGAGCGGCTGAGCGCGG 6352  
 6169 AGATGCGTCCAGCGTCCG 6228  
 6353 GCGACAGACCGCGCGTCTCGTGAAGAGCGAGCGGCTGCGTGAAGAGAGCGCGCAAGAGT 6412

Db 6229 CCGCCAAACGCGCGTACTGCTGCGAAGAGAGTGTGTTTCAAAAAACGCTCATAGCT 6288  
 Qy 6413 GGTATCATCATCGCGATCGCGAGCATCATCGTCGCGAGCGGATGTTGAGCCAGGCC 6472  
 Db 6289 TGTATACACTCGAGATCGCGAGCATTAATCAAGAGCGGAGATGTTGAGCCAGGCC 6348  
 Qy 6473 TCGCCCCCCTCCCAAGATGACGCGAGTATTA 6505  
 Db 6349 TCGCCCCCCTCCCAAGATGACGCGAGACTTA 6381  
 RESULT 8  
 MDU38813  
 LOCUS 6318 bp mRNA linear INV 19-FEB-1997  
 DEFINITION Musca domestica insecticide-susceptible strain voltage-sensitive  
 sodium channel mRNA, complete cds.  
 ACCESSION U38813  
 VERSION U38813.1 GI:1783372  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Musca domestica (house fly)  
 Musca domestica  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Muscoidea; Muscidae; Musca.  
 REFERENCE  
 1 (bases 1 to 6318) Ingles, P.J., Adams, P.M., Knipple, D.C. and Soderlund, D.M.  
 Tight genetic linkage between the kdr insecticide resistance trait  
 and a voltage-sensitive sodium channel gene in the house fly  
 Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)  
 94195766  
 JOURNAL MEDLINE  
 PUBMED 8146143  
 2 (bases 1 to 6318) Ingles, P.J., Adams, P.M., Knipple, D.C. and Soderlund, D.M.  
 Characterization of voltage-sensitive sodium channel gene coding  
 sequences from insecticide-susceptible and knockdown-resistant  
 house fly strains  
 Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)  
 96245434  
 JOURNAL MEDLINE  
 PUBMED 8814780  
 3 (bases 1 to 6318) Ingles, P.J., Adams, P.M., Knipple, D.C. and Soderlund, D.M.  
 Direct Submission  
 Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York  
 State Agricultural Experiment Station, Cornell University, Castile  
 Street, Geneva, NY 14456, USA  
 4 (bases 1 to 6318) Ingles, P.J., Adams, P.M., Knipple, D.C. and Soderlund, D.M.  
 Direct Submission  
 Submitted (15-JUN-1997) Dave M. Soderlund, Entomology, New York  
 State Agricultural Experiment Station, Cornell University, Castile  
 Street, Geneva, NY 14456, USA  
 REMARK  
 COMMENT Nucleotide and protein update by submitter  
 On Jan 18, 1997 this sequence version replaced gi:1104398.  
 FEATURES  
 source  
 1..6318  
 /organism="Musca domestica"  
 /mol\_type="mRNA"  
 /strain="NAIDM"  
 /db\_xref="taxon:7370"  
 /chromosome="3"  
 /note="insecticide-susceptible reference strain"  
 1..6318  
 /codon\_start=1  
 /product="voltage-sensitive sodium channel"  
 /protein\_id="AAB47604.1"  
 /db\_xref="GI:1783373"  
 /translation="MTSDSDSISSEERSLPRPRRBSLDTGRIAEHOKELERK  
 AARERQIRYDDBDSDGPDPTBQGVPIPRMOSFPPELSTPLDPTFNSVL  
 TFWVTSKGDIFRFSASAKMWLDPNPRIVAIYLHPLFSLFITTLILNIML  
 MPTFVTSKEVEFTGIYTESAVKWAIRFALICPFIYLDANMWLDFVIALAYTM  
 GIDGNLAALRTFRVRLALKTVAIVPLKTIYGVIESVKNLSDVILITWESLSVFL  
 MGIDYNGVLTQKICRKPPLDGSNGNLTDENWFLHNSNSNMFBNDESEYPVCGNVS

[illegible]

ORIGIN						
Query Match	68.3%	Score 4447.8;	DB 3;	Length 6318;		
Best Local Similarity	82.0%;	Ped. No. 0;				
Matches 5298; Conservative	0;	Mismatches 1002;	Indels 15;	Gaps 9		

QY	24	TTGACAGAAAGTTCCGACCTCGATATCTGAGGAAAGACGAGTTGTCGGTCCCTTATCC	83
Db	1	ATGACAGAAAGATTCCGACTCGATATCTGAGGAAAGACGAGTTGTCGGTCCCTTATCC	60
QY	84	CGCGAATCATTTGGTGCMAATCGAACACGCAATTCGCCCTGAAACATGAAAAACGAAAGAG	143
Db	61	CGCGAATCATTTGTTCAAAATCGAACACGCAATTC---CGCTGAACATGAAAAACGAAAGAG	117
QY	144	CTGGAAGAAAGAGAGCGGAGGAGGAGCGCCGCGATATGTCGCAAGAAAAACAAAAA	203
Db	118	CTGGAAGAAAGAGAGCGCCCGCGAAGAGAGC-----	148
QY	204	GAAATCCGATATGATGACGAGGACGAGAGATGAAGTTCACAAACCGGATCTTACACTTGA	263
Db	149	-AGATACGATATGATGACGAGGACGAGAGATGAAGTTCACAGCGGATCCCACTTGA	207
QY	264	CAGGTTGGCCAAATCCCTGTCATGACGAGGACGCTTCCCGCGGAATTTGGCTCCACT	323
Db	208	CAGGTTGGCTTATCCTTTCGAAATGACGAGGAGCTTCCCGCGGAATTTGGCTCCACT	267
QY	324	CCTCTCGAGGATATCGATCCCTAATAAGCAATGTACTGACATTTGTAATTTGAACAAA	383
Db	268	CCTCTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTTGTAATTTGAATAAA	327
QY	384	GGAAGAAAGATTTTTCGCTTTCGATCGAAGAAAGCATGGAGTGCATCATTCAT	443
Db	328	GGAAGAAAGATTTTTCGTTTTTTCGCTCGAAGAAAGCATGGAGTGCATCATTCAT	387
QY	444	CGGATACGTCGTGTGCGCAATTAACATTTAGTGCATCCATTAATTTTCCATTATCATC	503
Db	388	CGGATACGTCGTGTAGCAATTAATTTAGTGCATCCCTGTGTTTCGTTATCATTAATC	447
QY	504	ACCAACAATTCGTCAACATCGCAATCCGATGATATAGCCGACAAAGGCCACAGTTGAGTCC	563
Db	448	ACCAACAATTCATTAATTAATGATTTTAATATATATAGCCGACAAAGGCCACAGTGCATCC	507

QY	564	ACTGAGGTGATATTCACCCGGAATCTCCACATTTGAATCAGCGTTTAAAGTATGGACACA	623
Db	508	ACAGAGGTGATATTCACCCGGAATCTCCACATTTGAATCAGCGTTTAAAGTATGGACACA	567
QY	624	GGATTCAATTTATGCGCGTTTACGTAATCTTAAAGATGATGGAATTTGGCTGACTTCGTA	683
Db	568	GGTTTCATTTTATGCGCGTTTACGTAATCTTAAAGATGATGGAATTTGGCTGACTTCGTA	627
QY	684	GTAATTAAGCTTAACTTAATGACACATGGGATATGATTTAGTATCTAGACAGCCCTGCA	743
Db	628	GTAATTAAGCTTAACTTAACTTAATGACACATGGGATATGATTTAGTATCTAGACAGCCCTGCA	687
QY	744	ACGTTTAAAGGTGTGCGAGCGCTTAAACCGTACGATGTGCGAGCTTTGAAGACCAATC	803
Db	688	ACATTTAAGGGTAACTGCGAGCTCTGAACACCGTACGATGTGCGAGCTTTGAAGACCAAT	747
QY	804	GTCGGCGCCGTCAATCGAAATGGGTGAAGAAATCTCGCGAGTGTATTTATCCGACCATGTC	863
Db	748	GTCGGCTCTGTCATTTGAATCTGTAAATAAATCTAGCGATGTGAATTTTGAACATGTTT	807
QY	864	TCCCTGTCCGGGTTCGAGTTGATGAGGCGCTACAGATCTAATAGGCGTGTCTACCGGAAG	923
Db	808	TCCCTGTCCGGGTTCGAGCTGATGAGGCGCTAACAATCTAATAGGCGTGTCTAACAACAAAG	867
QY	924	TGCATCAAGAAGTTCGCGCTGAGCGTTTCTGGGGCAATGTACCCACACAGAACTGGGAC	983
Db	868	TGCATTTAAACATTTCCCGCTGAGCGAGTGTGGGGCAATCTGACCGATGAAATCGGTTT	927
QY	984	TATCAACATGCGCAATAGCTCCAAATGGATTTCCGAGACAGGGCAATCTCATTTCCGTTA	1043
Db	928	CTACACAAATAGCAACAGTTTCCAAATTTGGTTTACGAGAACATAGCGCATATATCCGGTG	987
QY	1044	TGCGGCATATATCCGGTGCGGGGCAATGCGACGACGATTAAGTGTGCTGCGAGGGTTT	1103
Db	988	TGCGGAATGTATCCGGTGCGGGCAATGACGGCAGGATTAACGTTCTGCGAGGGCTTC	1047
QY	1104	GATCCGAATCCGAATTAAGGCTAACACAGCTCGATTGTTCCGATGAGGCTTTCCTGTCC	1163
Db	1048	GCCCCCAATCCCACTACGACTACACAGTTTCAATTCATTCCGTTGGGCTTTCCTGTCC	1107
QY	1164	GCGTTCCGGCTGATGACACAGAGCTTCTGGAGAGATCTGTACACGCTGTGTGGCGGCC	1223
Db	1108	GCGTTTCGTCATGACACCAAGATTTCTGGAGAGATCTGTATCAGCACGCTGTCCAAACA	1167
QY	1224	GCCGACCATGAGCACATCTGTTCTTTATATCATCATCTCCTAAGTTCAATTTATCTT	1283
Db	1168	GCTGACCCCTGGCACATGTGTCTTTATATCATCATCTTCTTAAGTTCAATTTATCTT	1227
QY	1284	GTTGAATTTGATTTTGGCATTGTGGCCATGTCTGATGACGAATTTGCAAAGGAGCGCGAA	1343
Db	1228	GTTGAATTTGATTTTGGCATTGTGGCCATGTCTGATGACGAATTTGCAAAGGAGCGCGAA	1287
QY	1344	GAAAGAGAGCTGCCGAAGAGAGGCGCATACGTGAAGCGGAAGAAAGCTGCCGCGCCAA	1403
Db	1288	GAAAGAGAGCTGCCGAAGAGAGGCGCATACGTGAAGAGAGGAGCGCGCACAG	1347
QY	1404	GCGGCCAAGCTGAGAGAGAGCGGCCCAATCGCAGAGCTCAGAGACGACCGATGCGGCTGC	1463
Db	1348	GCGGCCAATCTAGAGAGAGCGGCCCAATGTAGAGCTCAAGGGGCTCAGAGATGACGCGAT	1407
QY	1464	GCCGAAGAGCTGCACTGTCATCCGAAATAGCCAAAGATCCGACGTATTTCTTGCAATCAGC	1523
Db	1408	GCGCGTGGCGGACCTCTGCATCCGAGATGGCAAGAGATCCACCTACTCTTTCGATTTAGC	1467
QY	1524	TATGACTATTTTGTGTGGCGGCAGAAAGGCAACGATGACAAACAAAGAGAGATGTCC	1583
Db	1468	TATGACTTGTGTGTGGCGGCAGAAAGGCAACGATGACAAACAAAGAGAGATGTCC	1527
QY	1584	ATTTCGAGAGGTGAGAGTGCAGATGCAGATGCAGTGAATCAAAAGCAACACAGACTT	1643
Db	1528	ATTTCGAGAGGTGAGATGTGAATTCGAGTGTGATGAGGTTATCAAAAGCAACACAGACTT	1587
QY	1644	ACCAACGACACCAACGCTACAAATTTGCTAAATGTAGACGACATCTCTATCTTACTCT	1703

```

Db      1588 ACCACAGACCC---GCTACTAAAGTCCGTAAGATTAGACAGACTTCTTATCTTACT 1644
Qy      1704 GGTTCACCGTTTAAACATACGAGGGGATCAGTACTTCTCAACAATACATACGAGAC 1763
Db      1645 GGTTCACCATTTAAACCTACGCGGGGATCAGTACTTCAACAAATACATACGAGAT 1704
Qy      1764 GGAGTGGCCCTTGTGTATACCGGTAGCGATCTGAAGCCATTGTGTATGTGCACAT 1823
Db      1705 GGGCGTGAACGTTTGTATACAGATGAGCATGCGAAGCCATGTGTCTGCAACATAT 1764
Qy      1824 CAGATGCGCAGACGACTTGCCCTATGCGCAGACTCGAATGCGGTACCCGATGTC 1883
Db      1765 CAGATGCGCAGACGACTTGCCCTATGCGCAGACTCGAATGCGGTACCAATGTC 1824
Qy      1884 GAAGAAATGAGGCGCATATAGTCCGCTGTATCTATGCGCATCTAGGCTCCGACATCA 1943
Db      1825 GAAGAAATGAGTGCATATATAGTACCACTACTATGTAAATTTAGTTCTTAGACATTTCT 1884
Qy      1944 TCGTATACCTGCGCATATCCCGAATATCTGTATCTCAATGCGCATCTACTCGGCGGC 2003
Db      1885 TCAATATACCTGCGCATATCAAGAAATCTGTATACATCAATGTGATTTATGGGTGAC 1944
Qy      2004 ATGGCCGTCATGCGCGTCAAGCAATGACCAAGAGACAAATTTGCGAACCGCAACA 2063
Db      1945 ATGGCGGTCATGCGCGTCAAGCAATGACCAAGAGACAAATTTGCGAAGTGCACACA 2004
Qy      2064 CGCAATCAATCAATGAGGCGCACCAATGCGCGCACCACTGTCTGAGACCAATCAAG 2123
Db      2005 CGCAATCAATCAATGAGTGTGTGCAACCAATGTGTGCAATGATGACGCGTGTGTGCTAT 2064
Qy      2124 CTCGAT-----CATGCGACTACGAATTTGGCTGTGATGACCGACGACAA 2168
Db      2065 CCGATGCGCAATCAACAGAAACAAAGGATTAAGAAATGGGTCAAGATTTATACAGACAA 2124
Qy      2169 GCTGCGCAAGATTAAACATCATGACCAATCTTTATGAGCGCGTCAAGACAAACGCTG 2228
Db      2125 GCTGCGCAAAATTAACACCAAGCAATCTTTATGAGCGCGTCAAGACCAATGACATG 2184
Qy      2229 GTTATATGAATGAATGTATGTGTCTGAATGACATCATGACAGCGCGTGTGTGAC 2288
Db      2185 GTAGACATGAAGATGTATGTGTCTTAATGATATCATTTGAACAAAGCGGTGTGCGCAT 2244
Qy      2289 AGTGGGGAACCGATCGCGGTGTCTCGTTTACTATTTCCCAACAGAGAGATGACAG 2348
Db      2245 AGTGTGTGTAGTGAACGAGT-----GAGGAGATGACGAA 2280
Qy      2349 GATGGGCGGACGTTCAAGACAGGCACTGAGATGATCTCAAGGATCGATGTGTT 2408
Db      2281 GATGTCACCAATTCAGAGACATGCGCTCGAATCATCTCTAAGAGCATGGAATCTTT 2340
Qy      2409 TGTGTGTGGAATGTGTGTGTGTGTGAATTTCAAGAGTGGTATGCTCATGCTC 2468
Db      2341 TGTGTATGGAATGTGTGTGTGTGTGAATTTCAAGATGGGTGTCTTTATGTG 2400
Qy      2469 TTGCATCCCTTCTGTGAGCTCTTATCAACGCTGTGCAATTTGTGTGAACAAGATGTTCA 2528
Db      2401 TTGCATCCCTTCTGTGAGCTCTTATCAATCCCTGTGTATGTGTGAACAAGATGTTATG 2460
Qy      2529 GCATGATGATCAACGATATGAACAAAGAGATGGAACGCTGTCAAGAGTGGCAACTAT 2588
Db      2461 GCATGATGATCAACGATATGAATCCGAAATTAAGAGAGTGTGAAAGTGTGATCAT 2520
Qy      2589 TTCTTCAACCGCACCTTTGCAATGAGCCACATGAAGCTAATGCGCATGAGCCCAAG 2648
Db      2521 TTCTTCAACCGCACCTTTTGAATGAACCAAGCATGAAGTGTGCGATGAGCCCAAG 2580
Qy      2649 TACTATTTCCAGAGGCTGGAACATCTTGAATCTCATCTGTGCGCTTATGCTATATG 2708
Db      2581 TACTATTTCCAGAGGCTGGAACATCTTGAATCTCATCTGTGCGCTTATGCTATATG 2640
Qy      2709 GAACGGAATCGAGGCTGTGCAAGGCTGTGCTGATGCGTTCCTTCAATGCTGTGCT 2768

```

---

```

Db      2641 GAATTTGGGCTGTGAGGGGTGTGCAAGGCTGTGCGGTGTGAAGTTTGTGTGCTGCT 2700
Qy      2769 GTATTTCAACTGCGCAAGCTTTGGCCCACTTAAATTTACTCATTTTGCATTTGAGAGC 2828
Db      2701 GTATTTCAAAATTTGGCAAAATCTGCGCCCACTCAATTTACTCATTTTGCATTTGAGC 2760
Qy      2829 AACATGGGCGCTTTGGGTATCTGACATTTGTACTTTGATTCATTCATTCATCTTTGCG 2888
Db      2761 ACAAATGGGTGATTTGGGTATCTGACATTTGTACTTTGATTCATTCATTCATCTTTGCG 2820
Qy      2889 GTGATGGAATGCACTGTTGGAAGAATTAATCATGATCAAGAACCGCTTTCCGAT 2948
Db      2821 GTGATGGAATGCACTTTTGGAAAGATTAATGACCAAGAGATGCTTCAAGAGC 2880
Qy      2949 GCGCACTGCGCGCTGGAATTTCAACGACTTTATGCAAGCTTCATGATGTGTTCGG 3008
Db      2881 CATGAATTAACGCGCTGMACTTCAACGACTTCATGACACACTTCATGATGTGTTCGA 2940
Qy      3009 GTGCTGTGCGGAGATGATGAGTGCATGAGGAGCTGATGATGATGAGGAGTGTGCG 3068
Db      2941 GTGCTGTGCGGAGATGATGAGTGCATGAGGAGCTGATGATGATGAGGAGTGTGCG 3000
Qy      3069 TGCAATCCCTTCTTGTGCGCACCGTGTGTCAATCGCAATCTTGTGTACTTAACCTTTTC 3128
Db      3001 TGTATACCTTCTTGTGCGCACCGTGTGTCAATCGCAATCTTGTGTACTTAATCTTTTC 3060
Qy      3129 TTGACCTTGTCTTTGTGCAATTTTGTGCTCATCTGCTTATGAGGCGGATGCGATAC 3188
Db      3061 TTGACCTTGTCTTTGTGCTCATCTGCTTATGAGGCGGATGCGGATGCGGATAC 3120
Qy      3189 GATACGAATTAATAGCGAGGCTTCAATGATGATGCGGATTTAAAGTTGGGTAA 3248
Db      3121 GATACGAATTAATAGCGAGGCTTCAATGATGATGCGGATTTAAAGTTGGGTAA 3180
Qy      3249 CGTAAATTTGTGATTTGTTCAATTAATGATTAATGATTAATGATTAATGATTAATGAT 3308
Db      3181 CGTAAATTTGTGATTTGTTCAATTAATGATTAATGATTAATGATTAATGATTAATGAT 3240
Qy      3309 CAACATCAAGTGTGAGAGACCAACCAATCAATGATTTGAGAGAGATGATGATGAT 3368
Db      3241 CAACCATC-----AGAACATGCGCAT 3261
Qy      3369 AACGAATGAGGCTGTGCGCACGAGATCTGTGCGGCTCATCAAGAGGAGAT 3428
Db      3282 AATGAATGAGGCTGTGCGCACGAGATCTGTGCGGCTCATCAAGAGGAGAT 3321
Qy      3429 AAGGAGAGAGCACTGAGAGTGCATCGGGATCGATGATTAATGATTAATGATTAATGAT 3488
Db      3322 AAGGCGAGAGCCAGCTGTGAGAGTGCATCGGGATCGATGATTAATGATTAATGATTAATGAT 3381
Qy      3489 GACATGAAGACAAACAGCGGAGAAATCAATATCTTAATTAACGCAAGATGATGATG 3548
Db      3382 GATATGAAGAAACAACAGCGGAGAAATCAATATCTTAATTAACGCAAGATGATGATG 3441
Qy      3549 AACTCAATTAACCAACCAAGCAATGAGCTGGAACAGAGCTTAACCAATGAGGTTTGTG 3608
Db      3442 AACTCAATTAACCAACCAAGCAATGAGCTGGAACAGAGCTTAACCAATGAGGTTTGTG 3501
Qy      3609 TTACAGAGAGAGCACTGTGCAAGATTAATCATATGATGATGATGATGATGATGATGAT 3668
Db      3502 ATACAGAGAGAGTACATGTGCAAGATTAATCATATGATGATGATGATGATGATGATGAT 3561
Qy      3669 AAGGAGAGAGCAACAGGCGAGCGGAGAGATGAGGCGGAGAGAGAGAGAGAGAGAGAG 3728
Db      3562 AAGGAGAGAGCAACAGGCGAGCGGAGAGATGAGGCGGAGAGAGAGAGAGAGAGAGAG 3621
Qy      3729 AGCAAGAGAGATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3788
Db      3622 AGCAAGAGAGAGCTTGTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3681
Qy      3789 CCGCTGAGCGGTGATATCATTTATGATG--ACAGAGAGAGATATATGATGATAT 3845
Db      3682 CAGCTGAGTGTGATATCATTTATGATGCGGAAACAGAGAGAGATATATGATGATAT 3741

```

QY 3846 CCAGTATGTCGCCCGATTCGTATTAAGAAATTCGATCTTACCGGTGACGAT 3905  
DB 3742 CCGGCGGACGTGTTCCCGACCTGCTACAGAAATTCGATCTTGGCCGGCGACGAG 3801  
QY 3906 GACTGCGGCTTCGCGAAGATGGGCAATTTACACTGAAAATTTCATTTAATGAA 3965  
DB 3802 GACTCCCGCTTCGCGAAGATGGGCAATTTACACTGAAAATTTCATTTAATGAA 3861  
QY 3966 AATAAATTTTGAACAGCTGTATCACTATGATTTTAAGAGTCTTAGCTTGAGCA 4025  
DB 3862 AATAAATTTTGAACAGCTGTATCACTATGATTTTAAGAGTCTTAGCTTGAGCA 3921  
QY 4026 TTGAAGATGTACATCTGCCAAGAACCCATACCTGACAGATTTTATATATGAC 4085  
DB 3922 TTGAAGATGTACATCTGCCAAGAACCCATACCTGACAGATTTTATCTACATGAC 3981  
QY 4086 AGAATTTTACGTTATATCTTCTTGGAATTTTATCAAGGTGTGGCGCTGAGCTTC 4145  
DB 3982 AGAATTTTACGTTATATCTTCTTGGAATTTTATCAAGGTGTGGCGCTGAGCTTC 4041  
QY 4146 AAGTGTACTTCAACAAACGCGGTGTGGCTGATTTCTGTATGTCAATGATGCTT 4205  
DB 4042 AAGTGTACTTCAACAAACGCGGTGTGGCTGATTTCTGTATGTCAATGATGCTT 4101  
QY 4206 ATCAACTTGTGCTTCACTTGTGAGCTGTGTGTATTTCAAGCTTCAAGATGACGA 4265  
DB 4102 ATCAACTTGTGCTTCACTTGTGAGCTGTGTGTATTTCAAGCTTCAAGATGACGA 4161  
QY 4266 ACGTTAAGACACTGAGACCACTACGTCAGTCGCGATGCCGATGACGAGGATGCTGTC 4325  
DB 4162 ACGTTAAGACACTGAGACCACTACGTCAGTCGCGATGCCGATGACGAGGATGCTGTC 4221  
QY 4326 GTTAATGCGTGTGACAACTATACGTCATCTTCAATGTGTATGTGTCTTATATA 4385  
DB 4222 GTTAATGCGTGTGACAACTATACGTCATCTTCAATGTGTATGTGTGTCTTATATA 4281  
QY 4386 TTTTGGCTAATTTTGGCTATATAGGTGTACAGTCTTGTGGAAATTTTAAAGTGC 4445  
DB 4282 TTTTGGCTAATTTTGGCTATATAGGTGTACAGTCTTGTGGAAATTTTAAAGTGC 4341  
QY 4446 GAGGACATGATGACGAAAGCTCAGCCACGAGATTCATACCAATCGCAATGCTGAG 4505  
DB 4342 AAGATGTATATGACCTGTCTGACGCCATGAAATCTACCGAATCGTAATGCTGAAA 4401  
QY 4506 AGCGAAGACTACAGCTGGGTGAATTCAGCAATGATTCATCTATGATGATGACGCTAT 4565  
DB 4402 AGTAAATCTACCTGGGAAATTCGCAATGAACTTCATCTATGATGATGACGCTAT 4461  
QY 4566 CTGTGCTTTTCCAAAGTGCACCTTCAAGGCTGTGATACAAATCATGAAAGATGCTATC 4625  
DB 4462 CTGTGCTTTTCCAAAGTGCACCTTCAAGGCTGTGATACAAATCATGAAAGATGCTATC 4521  
QY 4626 GATTACGAGAGGTGACAAAGCAACCAATTCGTGAAAGCAATCTACATGATTTATAT 4685  
DB 4522 GATTACGAGAGGTGACAAAGCAACCAATTCGTGAAAGCAATCTACATGATTTATAT 4581  
QY 4686 TTGCTATTTCTCATATTTTGGATCTTTTTCACATCTCAATCTGTTCATTTGGTATC 4745  
DB 4582 TTGCTATTTCTCATATTTTGGATCTTTTTCACATCTCAATCTGTTCATTTGGTATC 4641  
QY 4746 ATTGATATTTTAAATGACAAAGAAAGAAAGCAGGTGATCATTTAGAAATTTTCATACA 4805  
DB 4642 ATTGATATTTTAAATGACAAAGAAAGAAAGCAGGTGATCATTTAGAAATTTTCATACA 4701  
QY 4806 GAAGATCAGAAAGTACTATATATGCTATGTAAGAAAGATGCTCTTAAAAACCTTAAA 4865  
DB 4702 GAAGATCAGAAAGTACTATATGCTATGTAAGAAAGATGCTCTTAAAAACCTTAAA 4761  
QY 4866 GCCATTTCCAAAGCAGGTGCGACCAAGCAATATGCTTTGAAATGTAACGATGAG 4925  
DB 4762 GCCATTTCCAAAGCAGGTGCGACCAAGCAATATGCTTTGAAATGTAACGATGAG 4821

QY 4926 AATTCGATATATCATATATGATATATGCTGAAACAGTTCAACATGACCTCGAT 4985  
DB 4822 AATTCGATATATCATATATGATATATGCTGAAACAGTTCAACATGACCTCGAT 4881  
QY 4986 CTTTACAGATGCGTGCAGACGATTAAGCGGCTCTAGATCTATCTCAATGCAATTCGTA 5045  
DB 4882 CCGTACAGACGCTCGAGGCGGTACAAACATGCTCGACAAATCTCAATGCAATTCGTA 4941  
QY 5046 GTTATTTTCAAGTTCCGAATGTCTATTAATAATATTCGTTTACATATCATATTTTAT 5105  
DB 4942 GTTATTTTCAAGTTCCGAATGTCTATTAATAATATTCGTTTACATATCATATTTTAA 5001  
QY 5106 GAGCATGGAATTTATTTGATGTAGTATGTCATTTTATATCATCTTATGCTTGTACTT 5165  
DB 5002 GAGCATGGAATTTATTTGATGTAGTATGTCATTTTATATCATCTTATGCTTGTACTT 5061  
QY 5166 AGCATATTTTGAAGAGTACTTGTGTGCGGACCTGCTCCGATGCTGCTGCTGCTG 5225  
DB 5062 AGCATATTTTGAAGAGTACTTGTGTGCGGACCTGCTCCGATGCTGCTGCTGCTGCTG 5121  
QY 5226 AAGTGGGCGGCTGCTTCCGACCTGCTGGAAGGAGCCAGAGGATTCGACACTGCTTTC 5285  
DB 5122 AAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5181  
QY 5286 GCGTTGACCATGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5345  
DB 5182 GCGTTAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5241  
QY 5346 TTGATCTTTGCAATTTTGGGATGTGCTTCTTCAAGCAAGTGAAGAGGCGGCAAT 5405  
DB 5242 TTGATCTTTGCAATTTTGGGATGTGCTTCTTCAAGCAAGTGAAGAGGCGGCAAT 5301  
QY 5406 AACGAGCTTACAACTTCAAGACTTGGCCAGACATGATCTGCTCTTTCAGATGCTG 5465  
DB 5302 AATGCTGTATATATTTTAAACATTTGGCCAAAGATATATGCTGTTCAAGATGCT 5361  
QY 5466 ACGTACCGGCTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5525  
DB 5362 ACGTACCGGCTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5421  
QY 5526 CCGGACAGGACAAAGGCTATCCGGCAATTTGGTTCAGGACCGTGGAAATTAAGTT 5585  
DB 5422 CCGGACAGGACAAAGGCTATCCGGCAATTTGGTTCAGGACCGTGGAAATTAAGTT 5481  
QY 5586 CTCTCTCATATCTATATTAAGCTTTTGAATGATATTAATGATATGATCTGCTGAT 5645  
DB 5482 CTCTCTCATATCTATATTAAGCTTTTGAATGATATTAATGATATGATCTGCTGAT 5541  
QY 5646 CTGAGAACTATATGACGACCCGACGAGCTGCAAGAGGCTTACCGACAGACCTAC 5705  
DB 5542 CTGAGAACTATATGACGACCCGACGAGCTGCAAGAGGCTTACCGACAGACCTAC 5601  
QY 5706 GATATGTATATGATGCTGCGAGCAATTCGATCCGAGAGGACCCAGATACATGCTAT 5765  
DB 5602 GATATGTATATGATGCTGCGAGCAATTCGATCCGAGAGGACCCAGATACATGCTAT 5661  
QY 5766 GATCAGCTGCTGCAATTTCTGACGATCTGAGCCCTGCTGCAATTCACAAACCGAAC 5825  
DB 5662 GATCAGCTGCTGCAATTTCTGACGATCTGAGCCCTGCTGCAATTCACAAACCGAAC 5721  
QY 5826 AAGTACAAATCATATGATGACATACCATCTGCGGGTGAACCTCATATGATGCTGTC 5885  
DB 5722 AAGTACAAATCATATGATGACATACCATCTGCGGGTGAACCTCATATGATGCTGTC 5781  
QY 5886 GATCCTGACGCGCTTACGAAAGCTTTTCCGCGAAGGCAATCCGATGAGAGAG 5945  
DB 5782 GATATATGATGCTGCTGACCAAGATCTTTTGGCGGAAAGGATATCCGATGAGAGAG 5841  
QY 5946 ACGGCTGATGCTGATGATGCTGCGCGCGCTGCGATACGAGGCTTACGAGCCGCTCA 6005  
DB 5842 ACGGCTGATGCTGATGATGCTGCGCGCGCTGCGATACGAGGCTTATGCTGCTGCTG 5901  
QY 6006 TCAACGCTGTGGGCTGACGCTGAGAGTACTGCGCGCGCTAATTCAGACGCTGACGA 6065

Db	5912	TCACACCTGTGGCCGCGCAGCGTAGAGATACCTGCGCAAGCTGTATACAGATATGCGTGGCGG	5961
Qy	6066	AAGCAACAAGCGCGCGCGCGAGGGAGGTGGTCTTTTGAGCCGGATACGATCATGCGAT	6125
Db	5962	CGTTACAAGATGCGC-----CCACCCCGAGGAGGTAT	5994
Qy	6126	GGCGGTATCCGGATGCCGGGAGCCCGCGCCCATGAGCAACGACGGCGATGCGCC	6185
Db	5995	GAGGCGGAGCGCGCGTGTGGAGAGATGTGTGTAAGCGCGGTGAAGGTGAAGAGCGAC	6055
Qy	6186	GCTGGTGAAGATGGTAGTGTAAACGGTACTGCAGAGGAGCGCGCGATGCCGATGAGAGT	6245
Db	6055	GGCGCGCGCGGGTGAATGATGTGTGCTCAAGGACAGAGACGCGCGCGCGGAGCC	6114
Qy	6246	AATGTAATTAATCCGCGTGAAGGATGCAGCGCGCGCGAGCAGCAGCAGCAGCAGCGCG	6305
Db	6115	ACATCAACCT-----CAATCCAGATGCCGCGAGAGCAGATGTGTCCAGC	6155
Qy	6306	GCGGCGGCGACGACGACGCGCGGAAATGCCCGAGCGGTAGCCCGGCGACAGACGCGC	6365
Db	6160	GTCGGCGGCGCCCTTATGTATCCGGGCTGTATAGTGGCGGCAAGTAATGCGCGCAAAACGCGC	6219
Qy	6366	GTTCTCGTGGAGAGCGGCGTTCGTACGAAAGACGCGCACAGAGTGTATCATCTCG	6425
Db	6220	GTACTGTGCGAAAGAGATGCTTTTGTTCAAAAAACGCTCATTAAGGTGTATATACATCG	6279
Qy	6426	CGATCGCGAGACATCAAGTTCGGCGACGCGCGGATGTCCTGA	6464
Db	6280	AGATTCGCGGACATACATCAAGACGCGCAAGTGTCTTA	6318

RESULT 9	LOCUS	AR028529	6318 bp	DNA	linear	PAT 29-SEP-1999
AR028529	DEFINITION	Sequence 1 from patent US 5858713.				
AR028529	ACCESSION	AR028529				
AR028529.1	VERSION	GI:5940502				
	KEYWORDS					
SOURCE	ORGANISM	Unknown.				
	REFERENCE	Unclassified.				
	AUTHORS	1 (bases 1 to 6318)				
	TITLE	Soderlund,D.M. and Ingles,P.J.				
	JOURNAL	Calcium permeable insect sodium channels and use thereof				
	FEATURES	Parent: US 5858713-A 1 12-JAN-1999;				
	Source	Location/Qualifiers				
		1..6318				
		/organism="unknown"				
		/mol_type="unassigned DNA"				
ORIGIN						
Query Match		68.3%; Score 4447.8; DB 6; Length 6318;				
Best Local Similarity		82.0%; Pred. No. 0;				
Matches 5298; Conservative		0; Mismatches 1002; Indels 159; Gaps 9;				
QY	24	ATGACAGAAAGATTCGACTCGATATCTGAGGAAAGACGAGTTTGTCGTCCTTAC	83			
DB	1	ATGACAGAAAGATTCGACTCGATATCTGAGGAAAGACGAGTTTGTCGTCCTTAC	60			
QY	84	CGCGAATCATTTGGTGCAATCGAACCAACGATTGCCGTGAACATGAAGACAGAGAG	143			
DB	61	CGCGAATCATTTGGTGCAATCGAACCAACGATTGCCGTGAACATGAAGAGAG	117			
QY	144	CTGGAAGAAAGAGAGCCGAGGAGAGAGTGGCCGCATATGTGTCGAGAAAAACAAAA	203			
DB	118	CTGGAAGAAAGAGAGCCGAGGAGAGAGTGGCCGCATATGTGTCGAGAAAAACAAAA	148			
QY	204	GAATTCGATATGATGACGAGACGAGGATGAAGTCCACAACCGGATCTTACATTGAA	263			
DB	149	AGATTCGATATGATGACGAGACGAGGATGAAGTCCACAACCGGATCTTACATTGAA	207			
QY	264	CAGGGTGCCAACTACTGTTTCGATTGACGAGGACACTTCCGCGGAATGGCTTCACT	323			

[illegible]

Db 1288 GAGAGAGGCTGCCGAGAGGAGCGATACGAAAGCTGAAGAGCGGCGAGCGCAAG 1347  
Qy 1404 GCGGCCAAGTGGAGAGCGGGGCCAATGCGCAAGCTCAAGGCGAGCGAGTGGCGTGGC 1463  
Db 1348 GCGGCCAAGTGGAGAGCGGGGCCAATGAGCTCAGCGGCTAGAGTGCAGCGGAT 1407  
Qy 1464 GCGGAGAGGCTGCACTGCATCCGGAATGGCCAGAGTCCGACGTATTTTGCATCAGC 1523  
Db 1408 GCGGCTGCGGAGCTCGCATCCGAGATGGCAAGATGCCAGTACTCTTTCATTAAGC 1467  
Qy 1524 TATGAGCTATTTGTTGGCGCGAGAGAGGCAAGATGACAAACAAAGAGAAATGTCC 1583  
Db 1468 TATGAGCTATTTGTTGGCGCGAGAGAGGCAAGATGACAAACAAAGAGAAATGTCC 1527  
Qy 1584 ATTCCGAGCGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1643  
Db 1528 ATAGCGAGCGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1587  
Qy 1644 ACCAGACAGACCAAGCTACCAAGTTCGTAAAGTGAAGCAAGACATCTTATCTTACT 1703  
Db 1588 ACCAGACAGACCC---GCTACTAAAGTCCGTAAAGTGAAGCAAGCTTCTTATCTTACT 1644  
Qy 1704 GGTTCACCGTTTAAACATACGAGGGGATCAGTATGTTCTCACAAGTACAGATACGGAGC 1763  
Db 1645 GGTTCACCATTTAACTTACGCGGGGATCAGTATGTTTCAACAAGTACAGATACGAAAT 1704  
Qy 1764 GGAAGGCGCGCTTGGATACCGGATACCGGATACCGGATACCGGATACCGGATACCGGAT 1823  
Db 1705 GGGCGTGGACGCTTTGGTATACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 1764  
Qy 1824 CAGATGCGCAGAGCACTTGGCTTATGCGAGATCAGTACAGTACAGTACAGTACAGTAC 1883  
Db 1765 CAGATGCGCAGAGCACTTGGCTTATGCGAGATCAGTACAGTACAGTACAGTACAGTAC 1824  
Qy 1884 GAAAGAGATGGGGCATCATGATGCGCGGTACTATGAGCAATCAGGCTCCGACACTCA 1943  
Db 1825 GAAAGAGATGGGGCATCATGATGCGCGGTACTATGAGCAATCAGGCTCCGACACTCA 1884  
Qy 1944 TCGATATCTCGCATCAGTCCGGAATTCGTATACCTCAATGCGCATCTACGCGGC 2003  
Db 1885 TCGATATCTCGCATCAGTCCGGAATTCGTATACCTCAATGCGCATCTACGCGGC 1944  
Qy 2004 ATGCGCGCTCATGAGGCGTACAGCAATGACCAAGAGAGCAAAATGGCGACCGCAACCA 2063  
Db 1945 ATGCGCGCTCATGAGGCGTACAGCAATGACCAAGAGAGCAAAATGGCGACCGCAACCA 2004  
Qy 2064 CGCAATCATCATGATGCGGCGCACCAATGCGGCAACCTGTGAGCAACCAATCACAAG 2123  
Db 2005 CGCAATCATCATGATGCGGCGCACCAATGCGGCAACCTGTGAGCAACCAATCACAAG 2064  
Qy 2124 CTGCAAT-----CATGCGACTACGAATTTGGCTTGGAGTGCACGAGCA 2168  
Db 2065 CCCGATGCGCAATCACAAGAGCAAAAGAGATATGAAATGGGTCAGAGATTATACAGACAA 2124  
Qy 2169 GGTGCGAAGTAAACATCATGACATCTTTTATGAGCGCGCTCAGACCAAAAGCGGTG 2228  
Db 2125 GGTGCGAAGTAAACATCATGACATCTTTTATGAGCGCGCTCAGACCAAAAGCGGTG 2184  
Qy 2229 GTTGAATGAAAGATGTGATGCTCTGATGATGATCATCATGAAACAGCGCTGCTGCGAC 2288  
Db 2185 GTTGAATGAAAGATGTGATGCTCTGATGATGATCATCATGAAACAGCGCTGCTGCGAT 2244  
Qy 2289 AGTGGGCGAAGCGATGCGGCTGTCTCCGTTACTATTTCCCAACAGAGAGCGATGAGAG 2348  
Db 2245 AGTGGGCGAAGCGATGCGGCTGTCTCCGTTACTATTTCCCAACAGAGAGCGATGAGAG 2280  
Qy 2349 GATGGGCGAAGCGTCAAAAGACAGAGCACTGAGATGATCTCAAGAGCATCATGATGAT 2408  
Db 2281 GATGGGCGAAGCGTCAAAAGACAGAGCACTGAGATGATCTCAAGAGCATCATGATGAT 2340  
Qy 2409 TGTGTGTGGAAGCTGTGCTGGGTTGGTGAATTTCAAGAGTGGGATGCTCATGCTG 2468  
Db 2341 TGTGTGTGGAAGCTGTGCTGGGTTGGTGAATTTCAAGAGTGGGATGCTCATGCTG 2400

Qy 2469 TTGATCCCTTGTGAGCTCTTCAATCAGCTGTGATTTGTTGTTCAACAGATGTTCAATG 2528  
Db 2401 TTGATCCCTTGTGAGCTCTTCAATCAGCTGTGATTTGTTGTTCAACAGATGTTCAATG 2460  
Qy 2529 GGAATGATATCACAGATATGAAACAGAGATGAAACAGAGATGAAACAGAGATGAAACAG 2588  
Db 2461 GGAATGATATCACAGATATGAAACAGAGATGAAACAGAGATGAAACAGAGATGAAACAG 2520  
Qy 2589 TTCTTACCGGCACTTTGCAATGAGGCAACATGAACTGAAAGTAAAGTAAAGTAAAGTAA 2648  
Db 2521 TTCTTACCGGCACTTTGCAATGAGGCAACATGAACTGAAAGTAAAGTAAAGTAAAGTAA 2580  
Qy 2649 TACTATTTTCAAGAGGCGTGAACATCTTCACTTCAATGATGAGGCTTATGCTATG 2708  
Db 2581 TACTATTTTCAAGAGGCGTGAACATCTTCACTTCAATGATGAGGCTTATGCTATG 2640  
Qy 2709 GAACTGGAGCTGAGAGGCTGCAAGGCTGTCGATGCTGATGCTGCTTCCATGATGCTGCT 2768  
Db 2641 GAACTGGAGCTGAGAGGCTGCAAGGCTGTCGATGCTGATGCTGCTTCCATGATGCTGCT 2700  
Qy 2769 GATTTCAAACTGGCAAGCTTTGCGCCACACTTAAATTTTACTATTTGATTAAGGAGC 2828  
Db 2701 GATTTCAAACTGGCAAAATCATGAGCCCACTCAATTTACTATTTGATTAAGGAGC 2760  
Qy 2829 ACCATGGGCGCTTGGGTTATCTGACATTTGATTTGATTTGATTTGATTTGATTTGAT 2888  
Db 2761 ACCATGGGCGCTTGGGTTATCTGACATTTGATTTGATTTGATTTGATTTGATTTGAT 2820  
Qy 2889 GTGATGGAATGCACTGTTGGAAAGAAATATCATGATCAACAAGACCGCTTCCGAT 2948  
Db 2821 GTGATGGAATGCACTTTCGAAAGAACTATATTTGACCAAGAGATGCTTCAAGAGC 2880  
Qy 2949 GCGGACCTGCGCGCTGGAATCTTACCGGCTTATGACAGGCTCATGATGATGCGGATC 3008  
Db 2881 CATGAAATTCAGGCGTGAACCTTACCGGCTTATGACAGGCTCATGATGATGCGGATC 2940  
Qy 3009 GTGCTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3068  
Db 2941 GTGCTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
Qy 3069 TGCATTCCTCTTCTTCTTGGGCAACCTGTTGATCAGGAACTTGTGTTACTTAACTTTTC 3128  
Db 3001 TGCATTCCTCTTCTTCTTGGGCAACCTGTTGATCAGGAACTTGTGTTACTTAACTTTTC 3060  
Qy 3129 TTTGCGCTGCTTGTTCAAATTTTGGCTCATGATGATGATGATGATGATGATGATGATG 3188  
Db 3061 TTTGCGCTGCTTGTTCAAATTTTGGCTCATGATGATGATGATGATGATGATGATGATG 3120  
Qy 3189 GATACGAATTAATAGCGGAGGCTTCAATGCAATGAGGCTTCAATGCAATGAGGCTTCAAT 3248  
Db 3121 GATACGAATTAATAGCGGAGGCTTCAATGCAATGAGGCTTCAATGCAATGAGGCTTCAAT 3180  
Qy 3249 CGTATATTTGCTGATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 3308  
Db 3181 CGTATATTTGCTGATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 3240  
Qy 3309 CAACCATCAGATGAGAGCAACCAACAGATCAGTTGATTTTGAAGGAGAGCATGCTGAC 3368  
Db 3241 CAACCATC-----AGAACATGCGGAT 3261  
Qy 3369 AACGAACTGAGCTGGGCGACAGAGATCTTGGCGGAGCTTCAATCAAGAGGAGATC 3428  
Db 3262 AATGAACTGAGGTTGGGCTGATGAGCAATGATGAGGAGATGAGGCTTGAACAAAGGAGATG 3321  
Qy 3429 AAGAGAGAGCGCACTGAGAGGCGGATGAGGAGGATGAGATGAGATGAGATGAGATGAG 3488  
Db 3322 AAGAGAGAGCGCACTGAGAGGCGGATGAGGAGGATGAGATGAGATGAGATGAGATGAG 3381  
Qy 3489 GACATGAGAGCAACAGCGGAGAGAAATCAATATCTAAATTAACGACAGATGATGAGC 3548  
Db 3382 GATATGAGAGCAACAGCGGAGAGAAATCAATATCTAAATTAACGACAGATGATGAGC 3441

3549 AACTCAATTAACCAAGACATAGACTGAAACGAGCTAAACCATAGAGTTTGTCC 3608  
3442 AACTCAATTAACCAAGACATAGACTGAAACGAGCTAAACCATAGAGTTTGTCC 3501  
3609 TTACAGAGCAGACACTGCGAGCATTTAATCATATGTTAGCCATTAAGATCGACATTC 3668  
3502 ATACAGAGCAGATGACCTGCGAGCATTTAATCATATGTTAGCCATTAAGATCGACATTC 3561  
3669 AAGAGCAGAGCCACCAAGGCGAGCCGAGACGATGAGGCGAGGAGAGAGCGGACGCC 3728  
3552 AAGAGCAGAGCCACCAAGGCGAGCCGAGACGATGAGGCGAGGAGAGAGCGGACGCC 3621  
3729 AGCAAGAGAGATTTAGTCTGACGAGAGATGAGCAGAGAGGAGGAGATGAGAGAGGAG 3788  
3622 AGCAAGAGAGATTTAGTCTGACGAGAGATGAGCAGAGAGGAGGAGATGAGAGAGGAG 3681  
3789 CCGCTGACGAGTATCATTTATTCATGACGAGAGAGAGATGAGAGAGGAGATGAGAG 3845  
3682 CAGCTGAGATGATGATCATTTATGAGGAGAGAGAGAGAGAGATGAGAGAGGAGATG 3741  
3846 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3905  
3742 CCGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3801  
3906 GACTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3965  
3802 GACTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3861  
3966 AATAAATATTTTGAAGACGAGTATGATGATGATGATGATGATGATGATGATGATG 4025  
3862 AATAAATATTTTGAAGACGAGTATGATGATGATGATGATGATGATGATGATGATG 3921  
4026 TTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4085  
3922 TTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3981  
4086 AGAATATTTTGAAGACGAGTATGATGATGATGATGATGATGATGATGATGATG 4145  
3982 AGAATATTTTGAAGACGAGTATGATGATGATGATGATGATGATGATGATGATG 4041  
4146 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4205  
4042 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4101  
4206 ATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4265  
4102 ATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4161  
4266 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4325  
4162 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4221  
4326 GTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4385  
4222 GTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4281  
4386 TTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTAT 4445  
4282 TTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTATTTTGGCTAT 4341  
4446 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4505  
4342 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4401  
4506 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4565  
4402 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4461  
4566 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4625  
4462 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4521  
4626 GATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4685

4522 GATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4581  
4686 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4745  
4582 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4641  
4746 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4805  
4642 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4701  
4806 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4865  
4702 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4761  
4866 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4925  
4762 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4821  
4926 AATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4985  
4822 AATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4881  
4986 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5045  
4882 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4941  
5046 GTTATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5105  
4942 GTTATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5001  
5106 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5165  
5002 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5061  
5166 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5225  
5062 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5121  
5226 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5285  
5122 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5181  
5286 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5345  
5182 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5241  
5346 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5405  
5242 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5301  
5406 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5465  
5302 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5361  
5466 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5525  
5362 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5421  
5526 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5585  
5422 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5481  
5586 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5645  
5482 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5541  
5646 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5705  
5542 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5601  
5706 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5765



Best Local Similarity 81.8%; Pred. No. 0;  
Matches 528; Conservative 0; Mismatches 1013; Indels 162; Gaps 8

Oy	24	ATGACAGAAAGATTCCGACTCCGATTA	CTCTGAGGAAAGAACGAGTTTGTCCGCTCTTAC	83
Db	1	ATGACAGAAAGATTCCGACTCCGATTA	CTCTGAGGAAAGAACGAGTTTGTCCGCTCTTAC	60
Oy	84	CGCGAATCAATGGTGCMAATCGAACA	CGCATTTGGCCGTCGATGAAAAAGCAGAGG	143
Db	61	CGCGAATCAATGGTGCMAATCGAACA	CGCATTTGGCCGTCGATGAAAAAGGAG	117
Oy	144	CTGGAAAAAGAGAGCCGAGGAGAGT	GGCCGATATGTTCGAAAGAAAAA	203
Db	118	CTGGAAAAAGAGAGCCGAGAGAGC	-----	148
Oy	204	GAAATCCGATATGATGACGAGAGAC	AGAGATGAAGTCCACAAACCGGATCTTAC	263
Db	149	- AGATACATATGATGACGAGAGAC	AGAGATGAAGTCCACAAACCGGATCTTAC	207
Oy	264	CAGGGTGTGCCAATACCTGTTTGA	TTGCGAGGACGCTTCCGCGGAAATTTGACCT	323
Db	208	CAGGGTGTGCCAATACCTGTTTGA	TTGCGAGGACGCTTCCGCGGAAATTTGACCT	267
Oy	324	CCTCTCGAGATATGATCCCTTAC	TACAGCAATGTACTGACATTCGTAGTTGAA	383
Db	268	CCTCTCGAGATATGATCCCTTAC	TACAGCAATGTACTGACATTTGTAGTAA	327
Oy	384	GGAAAAAGATTTTTTGGCTTTTGC	GCATCAAAAGCATGTGGATCTGATCAATTC	443
Db	328	GGAAAAAGATTTTTTGGCTTTTGC	GCATCAAAAGCATGTGGCTCTGATCAATTC	387
Oy	444	CCGATACGTCGTGGGACATTTAC	ATTCATTTAGTCATCCATTTATTCATTC	503
Db	388	CCGATACGTCGTGGGACATTTAT	TTATTTAGTCATCCCTTGTTCGTTATTCATTC	447
Oy	504	ACCACAATTCCTGTCACATCGAT	CCGTGATATGCCGACAAACGCCACGGTTAGTCC	563
Db	448	ACCACTATTCCTAACTAAATGTAT	TTATTTAGTATGACCGACAAACGCCACGGTTCATCC	507
Oy	564	ACTAGAGGATATTCACCGGAAAT	CTACACATTTGAAATCAGCTGTTAAATGATG	623
Db	508	ACAGAGGATATTCACCGGAAAT	CTACACATTTGAAATCAGCTGTTAAATGATG	567
Oy	624	GGTTTCATTTATGCGCCGTTTAC	GTATACGATCTTACAGATGATGATGAAATTTG	683
Db	568	GGTTTCATTTATGCGCCGTTTAC	GTATACGATCTTACAGATGATGATGAAATTTG	627
Oy	684	GTAATAGCTTTAGCTTATGTGAC	ATGCGATATGATTTAGTAACTTACAGACCCCTG	743
Db	628	GTAATAGCTTTAGCTTATGTGAC	ATGCGATATGATTTAGTAACTTACAGACCTTTG	687
Oy	744	ACGTTTAAAGGTGCTGCGAGCG	CTTAAACCGGTAGCATTTGTGCCAGGCTTGA	803
Db	688	ACATTTAAAGGTACCTGCGAGCT	CTGAAAAACCGTAGCATTTGTGCCAGGCTTAA	747
Oy	804	GTGCGCGCGATCATCGATCGG	TGAAGATCTGCGCGATGATTAATCTGACCAT	863
Db	748	GTGCGGTGCTGATTTGAATCTG	TAAAAAATCTGCGCATGTGATTAATTTGACAT	807
Oy	864	TCCCTGTGCGTTCGCGTTGAG	GCCCTACAGATCTAATGCGGCTCTCACCGAGA	923
Db	808	TCCCTGTGCGTTCGCGCTGAT	GCGCTTACAAATCTAATGCGGCTCTAACA	867
Oy	924	TGCAATCAAGAGTTCCCGCTGA	CGGTTCCCTGGGCAATCTGACCGAAGAACTG	983
Db	868	TGCAATTAACGATTCCTCCG	ACGCAAGTGTGGGGCAATCTGACCGAAGAACTG	927
Oy	984	TATCAATCAATCCCAATAGCT	CCCAATTTGATTTCCGAGACGAGGGCATCTCAT	1043
Db	928	CTACACATATACCAACAGTTT	CCATTTGTTTACGAGAACGATGGCGATCATTC	987
Oy	1044	TGCGGCAATATATCCGATG	CGGCGCAATGCGACGAGATTAAGTGTGCTG	1103

Db	988	TCGGGAATGTAATCCGGTCGGGAGCAATGGCGCGCAAAATTACGTCCTCGACAGGCTTC	1047
QY	1104	GGTCGAATCCGAATTATAGGCTACACAGACTTCGATTGGTTCGAGTAGGGCTTCTCTGCC	1163
Db	1048	GGCCCCAATCCCACTACGACTACACCAAGTTTGACATTCGGTGGGCTTCTCTGCG	1107
QY	1164	GCCTTCGGGCTGATGACACAGAACTTCTGGAGGATCTGTACCGAGCTGGTGGTGGCGCC	1223
Db	1108	GCCTTTCGTCACATGACCAGAAATTTCTGGAGGATCTGTATCGACAGCTGCTCGCAAGCA	1167
QY	1224	GCCGGACCATGGGCAATGCTGTTCTTTATATGATCATCATCTTCCATAGGTCATCTATCTT	1283
Db	1168	CTGGACCTTGGCAATAGTGTGTTCTTATATGTCATCTTCTTCTAGGTCATCTATCTT	1227
QY	1284	GTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATGACGAATTTGCCAAAGGAGCCGAA	1343
Db	1228	GTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATATACGAATTTGCCAAAGGAGCCGAA	1287
QY	1344	GAAGAAAGGCTGCCGAAGAGAGGCGATACGTGAAGCGGAAGAGCTGCCCGCCAAA	1403
Db	1288	GAAGAAAGGCTGCCGAAGAGAGGCGATCCGAAACCTGAAGAAAGCGGACGCGCCAG	1347
QY	1404	GGGCGCAAGCTGGAGAGAGCGGGCCCAATGGCGGAGCTCAGGACGAGAGGAGTGGCGCTGCC	1463
Db	1348	GGGCGCAAGCTGGAGAGAGCGGGCCCAATGTAGCACTCAGAGGCTCAGAAATGACGCGAAT	1407
QY	1464	GCCGAAGAGGCTGCACATCGATCCCGGAATGGCCAAAGTCCGACGTATTTCTTGATCAGC	1523
Db	1408	GCCTCTCGGAGGCTCTGCATCCCGAATGGCAAAAGAGTCCACGATCTTGTGATTAAGC	1467
QY	1524	TATAGCTATTTGTTGGCGGCGAGAGAGGCAACGATGACAAACAAGAAAGATGTCC	1583
Db	1468	TATGAACGTGTTGTTGGCGGCGAGAAAGGCAACGATGACAAACAAGAAAGATGTGC	1527
QY	1584	ATTGGAGGCGTTCAGGTGTGAGTCCGGAATCCGTTGACGCTTTATCAAAACAAACAGACACT	1643
Db	1528	ATTAGCAGCGTTCGAAGGTGAATCCGATCCGTTGACGCTTTATCAAAACAAACAGACACT	1587
QY	1644	ACCACAGACACCAAGCTACCAAAAGTTCTGTAAAGTAGACAGACATCTTATCTTACT	1703
Db	1588	ACCACAGACACC--GCTACTAAAGTCCGTAAAGTTAGACAGACTTCTTATCTTACT	1644
QY	1704	GGTTCACCGTTTAACATATACGAGGGGATCAAGTATTCTCAACAGTACAGATATCGGAAC	1763
Db	1645	GGTTCACCATTTAACTTACGCGCGGGATCAAGTATTCAACAAGTACACATATCGAAT	1704
QY	1764	GGAGCTGGCGGCTTGGTATACCCGGTAGAGTCCGATCGTATGACCAATTTGTTATGTCACATAT	1823
Db	1705	GGGCGTGGAGGTTTGGTATACCAAGTAGAGCATCGAAGGCCAATTTGGTATCGCAAAACATAT	1764
QY	1824	CAGGATCCCAAGACGACTTGGCCTATAGCCGAGACCTCGAATCCCGCACCCCGATGTCC	1883
Db	1765	CAGGATCCCAAGACGACTTGGCCTATAGCCGAGACTCGAATCCCGTAAACAACAATGTCC	1824
QY	1884	GAAGAGATGGGGCATCATAGTCCCGTGTACTATAGGCATATAGGCTCCCGCACTCA	1943
Db	1825	GAAGAGATGGTGCATTATAGTACGAGCCTACTATTTGTTATTTAGGTTCTTAAACATTTCT	1884
QY	1944	TCTGTATACCTTGACATCACTGCCGAATATCGTATATCTCACATGCGCATCTTACTCGCGGC	2003
Db	1885	TCAATATACCTTGACATCAATCAAGATATCTGTATATCAATCATGATGGTGTATTTATTTGGGTGCG	1944
QY	2004	ATGGCGGTATATGGGCGGTACGACAAATGACGAAGAGGCAAAATTTGGCAACCGCAACACA	2063
Db	1945	ATGGCGGTATATGGGCGGTACGACAAATGACGAAGAGGCAAAATTTGGCAACCGCAACACA	2004
QY	2064	CGCAATCAATCAATGAGGCGGCAACAATATGGCGGACCACTGTCTGACACCAATTCACAG	2123
Db	2005	CGCAATCAATCAATGAGGCGGCAACAATATGGCGGACCAATGAGGCGGCGGTGTGCTAT	2064
QY	2124	CTCGAT-----CATCGGACTACGAATATGGGCTCGAGTGCACGAGCGAA	2168
Db	2065	CCCATATCCATCAACAAGAAACAAGGATTTATGAATGGGTCCAGGATTTATACAGCGAA	2124

QY 2169 GCTGCAAGATTAACATCATGACAAATCTTTATGAGCCGCTCCAGACACAAAGGCTG 2228  
Db 2125 GCTGGCAAAATTAACACACGACCAATCTTTATGAGCCGCTCCAAATCTAAACAGTG 2184  
QY 2229 GTTGATATGAAGATGATGATGCTGTAATGACATCATGACAGCCGCTGCTGGCAC 2288  
Db 2185 GTAGACATGAAGATGATGATGCTTAAATGATATCATGACAGCCGCTGCTGGCAC 2244  
QY 2289 AGTCGGCAAGCATGCGGCTGCTCCTTACTATTTCCAAACAGAGCAATGACAG 2348  
Db 2245 AGTCGGCTAGTGAACAGAT-----GAGACGATGACGAA 2280  
QY 2349 GATGGCCGACGCTTCAAGACAAAGCAGCTGAGATGATCTTCAAGGCAATGATGTTT 2408  
Db 2281 GATGGCTCCCATTTCAAGACATGCGCTCGAATATCTTAAAGGCAATGAAATCTTT 2340  
QY 2409 TGTGTGTGGACCTGTGCTGGGTTTGTGTAATTTCAAGAGTGGTATGCTCATCTC 2468  
Db 2341 TGTGTATGGACCTGTGCTGGGTTTGTGTAATTTCAAGAGTGGGCTCTTTATTTG 2400  
QY 2469 TTGGATCCCTTCCGACGCTTTCATCAGCTGTCATGTCGTCACAGATGTTCA 2528  
Db 2401 TTGGATCATTTCTGGAGCTCTTCTATACCTGTGATTTGTGTCATACAAATGTTCA 2460  
QY 2529 GCAATGATCAACGATATGAACAAAGAGATGAGACGCTGCTCAAGATGCACTAT 2588  
Db 2461 GCAATGATCATCAACGATATGAACAAAGAGATGAGATGCTGAAAGTGTATAT 2520  
QY 2589 TTCTTCACCGCACCTTTGCAATGAGGCCACATGAAGTAAATGACATGAGCCCA 2648  
Db 2521 TTCTTCACCGCACCTTTGCAATGAGGCCACATGAAGTAAATGACATGAGCCCA 2580  
QY 2649 TACTATTTCCAGAGGCTGGACATCTGCACTTATCTGAGCCCTATATGCTAT 2708  
Db 2581 TACTACTTCCAGAGGCTGGACATCTGCACTTATCTGAGCCCTATATGCTAT 2640  
QY 2709 GAATGAGGCTGGAGGCTGTCAGAGGCTGCTGCTATGCTTCTTCAATGCTGCT 2768  
Db 2641 GAATGAGGCTGGAGGCTGTCAGAGGCTGCTGCTATGCTTCTTCAATGCTGCT 2700  
QY 2769 GTATTCAACTGGGCAAGTCTGGCCCACTTAATTTACTCATTTGATGATGAG 2828  
Db 2701 GTATTCAACTGGGCAAGTCTGGCCCACTTAATTTACTCATTTGATGATGAG 2760  
QY 2829 ACCATGGGCGCTTTGGGTAATCTGCAATTTGATCTTTCATTCATCTTTCG 2888  
Db 2761 ACCATGGGCGCTTTGGGTAATCTGCAATTTGATCTTTCATTCATCTTTCG 2820  
QY 2889 GTGATGGGATGCAATGCTTGGGAAATATATCATGATCAAGAGCCGCTTCCGAT 2948  
Db 2821 GTGATGGGATGCAATGCTTGGGAAATATATCAAGAGGCTTCCGATGATCA 2880  
QY 2949 GGGACCTGGCGCGCTGGAACTTCAACGCACTTATGACAGCTTCATGATGCTTC 3008  
Db 2881 CATGATTTACCGCGCTGGAACTTCAACGCACTTATGACAGCTTCATGATGCTTC 2940  
QY 3009 GTGCTTGGGAGATGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3068  
Db 2941 GTGCTTGGGAGATGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3000  
QY 3069 TGCATTCCTTCTTGGGCAACGCTTTCATGCGGCACTTGGGTAATGATGCTTTC 3128  
Db 3001 TGTATACCTTCTTGGGCAACGCTTTCATGCGGCACTTGGGTAATGATGCTTTC 3060  
QY 3129 TTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTTATCAGGCGGATGAC 3188  
Db 3061 TTAGCTTGTCTTGTCCAAATTTGGCTCATCTAGCTTATCAGGCGGATGAC 3120  
QY 3189 GATACGAATTAATGCGGAGCTTCAATGATGATGCTTCAATGATGCTTCAATGAT 3248  
Db 3121 GATACGAATTAATGCGGAGCTTCAATGATGATGCTTCAATGATGCTTCAATGAT 3180

QY 3249 CGTAAATTTGCTGATTTGTTTCAAGTTAATGCTAACAATTAACAAATTAATGAT 3308  
Db 3181 CGTAAATTTGCTGATTTGTTTCAAGTTAATGCTAACAATTAATTAATGATGAC 3240  
QY 3309 CAACCATGAGTGTAGAGCAACACAGATCACTGATTTGGAGCGAAGCATGCTGAC 3368  
Db 3241 CAACCAT-----AGAACATGCGCAT 3261  
QY 3369 AAGCACTGAGCTGGGCAACGACGATCTTCCGACGCTCATCAAGAGGATGAC 3428  
Db 3262 AATGAATCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 3321  
QY 3429 AAGGACCAACGCACTGAGGATGATGATGATGATGATGATGATGATGATGATG 3488  
Db 3322 AAGGACCAACGCACTGAGGATGATGATGATGATGATGATGATGATGATGATG 3381  
QY 3489 GACATGAGACCAACGAGCGAAGAAATCTAATTAACGCAATGATGATGATG 3548  
Db 3382 GATATGAAAAACCAAGCCCAAGAAATCAAAATTCATTAACCAACGATGATG 3441  
QY 3549 AACTCAATTAACCAACCAAGCAATGATGATGATGATGATGATGATGATGATG 3608  
Db 3442 AACTCAATTAACCAACCAAGCAATGATGATGATGATGATGATGATGATGATG 3501  
QY 3609 TTACAGGACGACGACCTGACATTAATGATGATGATGATGATGATGATGATG 3668  
Db 3502 ATACAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 3561  
QY 3669 AAGGACGAGGACCAAGGCGGACGAGATGATGATGATGATGATGATGATG 3728  
Db 3562 AAGGACGAGGACCAAGGCGGACGAGATGATGATGATGATGATGATGATG 3621  
QY 3729 AGCAAGGATTTAGTCTTCCAGCGAGAACTGGAAGAGGCGGATGCGAGAGG 3788  
Db 3622 AGCAAGGATTTAGTCTTCCAGCGAGAACTGGAAGAGGCGGATGCGAGAGG 3681  
QY 3789 CCGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3845  
Db 3682 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3741  
QY 3846 CCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3905  
Db 3742 CCGGCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 3801  
QY 3906 GACTCGCGCTTGGGCAAGGATGATGATGATGATGATGATGATGATGATGAT 3965  
Db 3802 GACTCGCGCTTGGGCAAGGATGATGATGATGATGATGATGATGATGATGAT 3861  
QY 3966 AATTAATTTTGAACAGCTGATGATGATGATGATGATGATGATGATGATG 4025  
Db 3862 AATTAATTTTGAACAGCTGATGATGATGATGATGATGATGATGATGATG 3921  
QY 4026 TTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4085  
Db 3922 TTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3981  
QY 4086 AGAATATTTACGCTTATATCTTCTGGAATGATGATGATGATGATGATGAT 4145  
Db 3982 AGAATATTTACGCTTATATCTTCTGGAATGATGATGATGATGATGATGAT 4041  
QY 4146 AAGGTACTTCAACCAAGGCTGATGATGATGATGATGATGATGATGATGAT 4205  
Db 4042 AAGGTACTTCAACCAAGGCTGATGATGATGATGATGATGATGATGATGAT 4101  
QY 4206 ATCACTGCTGCTTCACTTGTGAGAGCTGATGATGATGATGATGATGATG 4265  
Db 4102 ATCACTGCTGCTTCACTTGTGAGAGCTGATGATGATGATGATGATGATG 4161  
QY 4266 ACCTTAAGACACTGAGACCACTACGATGATGATGATGATGATGATGATGAT 4325  
Db 4162 ACCTGAGGCGCTTAAGGCAATGATGATGATGATGATGATGATGATGATGAT 4221  
QY 4326 GTTAATGCTGCTGATCAAGCTATACGCTCATCTTCAATGATGATGATGAT 4385

Db 4222 GTGATGGCGTGTTCAGCTATACCTGCTCATCTTCATGTGCTATGTGTGCTGTAT 4281  
Qy 4386 TTTTGGCTAATTTTTCGATTAATGGGTGTACAGCTTTTGTCTGAAAAATTTTAAAGTGC 4445  
Db 4282 TTTTGGCTTATTTTGGCATTAATGGAGTACAGCTTTTGTCTGAAAAATTTTAAAGTGT 4341  
Qy 4446 GAGACATGAAATGGACGAAAGCTCAGCCAGAGATCATACCAATTCGCAATGCCGAG 4505  
Db 4342 AAAGTGGTAATGACACTGTGTGAGCCATGAAATCAACGAAATCGTAATGCCGCAAA 4401  
Qy 4506 AGCGAAGCTACACGTGGGTGAATTCAGCAATGAAATTCGATCATGTAGTGAACGCTAT 4565  
Db 4402 AGTGAATCTACCTCGGAAAAATTCGGCAATGAATTCGATCATGTAGTGAATCGTAT 4461  
Qy 4566 CTGTGCTTTTCCAGTGGCCACTTCAAGGCTGGATACAAATCATGACGATGCTATC 4625  
Db 4462 CTGTGCTTATTTCAAGTGGCCACTTCAAGGCTGGATACAAATCATGACGATGCTATC 4521  
Qy 4626 GATTCAAGAGGTGGACAGCAACCAATTCGTGAAGGAACATCTACATGATTTATAT 4685  
Db 4522 GATTCAAGAGGTGGACAGCAACCAATTCGTGAAGGAACATCTACATGATTTATAT 4581  
Qy 4686 TTGCTATCTTCATCATATTTTGGATCTTTTTCACACTCAATCTGTGATTTGTTATC 4745  
Db 4582 TTGCTATCTTCATCATATTTTGGATCTTTTTCACACTCAATCTGTGATTTGTTATC 4641  
Qy 4746 ATTGATAATTTTAAATGAGCAAAAGAAAGCAAGGTGATCATTAAGATGTTCA 4805  
Db 4642 ATTGATAATTTTAAATGAGCAAAAGAAAGCAAGGTGATCATTAAGATGTTCA 4701  
Qy 4806 GAATATCGAAGAAATCTATTAATGCTATGAAAAAGATGGGCTCTAAAAATCATTTAA 4865  
Db 4702 GAATATCGAAGAAATCTATTAATGCTATGAAAAAGATGGGCTCTAAAAATCATTTAA 4761  
Qy 4866 GCCATTCGAAGACCAAGGTGGCGACCAAGCAATAGCTTTGAAATGATGAACGATAG 4925  
Db 4762 GCCATTCGAAGACCAAGGTGGCGACCAAGCAATAGCTTTGAAATGATGAACGATAG 4821  
Qy 4926 AAATTCGATTAATCAATTAATGATTAATCAATGATGAAATGATGATGATGATGAT 4985  
Db 4822 AAATTCGATTAATCAATTAATGATTAATCAATGATGAAATGATGATGATGATGAT 4881  
Qy 4986 CGTTACATGCTGGGACAGCTATACCGGCTCTAGCTATCTCAATGCAATTTGCTA 5045  
Db 4882 CGTTACATGCTGGGACAGCTATACCGGCTCTAGCTATCTCAATGCAATTTGCTA 4941  
Qy 5046 GTTATTTTCAAGTTCGAATGCTATTAATAAATATTCGCTTTACGATATCATTTTAT 5105  
Db 4942 GTTATTTTCAAGTTCGAATGCTATTAATAAATATTCGCTTTACGATATCATTTTAA 5001  
Qy 5106 GAGCAGTGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
Db 5002 GAGCAGTGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
Qy 5166 AGCGATATTAATGAGAAATCTGCTGTGCTGCGACCTGCTCCAGTGGTGGTGGCG 5225  
Db 5062 AGCGATATTAATGAGAAATCTGCTGTGCTGCGACCTGCTCCAGTGGTGGTGGCG 5121  
Qy 5226 AAAGTGGGCGGTGCTTCGACTGGTGAAGGAGCAAGGGCATTCGAGCATGCTCTTC 5285  
Db 5122 AAAGTGGGCGGTGCTTCGACTGGTGAAGGAGCAAGGGCATTCGAGCATGCTCTTC 5181  
Qy 5286 GCGTGGCGCATGCTGCTGCGGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 5345  
Db 5182 GCGTGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5241  
Qy 5346 TTTCAATCTTGGCATTTTGGCATGCTGCTTTCATGACGTTGAAGAGAGAGAGAGAGAG 5405  
Db 5242 TTTCAATCTTGGCATTTTGGCATGCTGCTTTCATGACGTTGAAGAGAGAGAGAGAGAG 5301  
Qy 5406 AACGAGCTTCAACCTTCAAGCCTTTGGCAGAGCATGATCTGCTCTTCAAGATGCG 5465

Db 5302 AATGCTGTATTAATTTTAAACATTTGGCCAAAGTATGATTTGCTTTCAGATGCT 5361  
Qy 5466 AGCTGACCGGTTGGATGTGTACTGAGCGCAATTAATCAATGAGAAAGATGCGATCA 5525  
Db 5362 ACCTGACCGGTTGGATGTGTACTGAGCGCAATTAATCAATGAGAAAGATGCGATCA 5421  
Qy 5526 CCGGACCGGCAAGAGGCTATCCGGGCAATGTGTGCTGAGGACCGTTGAAATACGTT 5585  
Db 5422 CCGGACCGGCAAGAGGCTATCCGGGCAATGTGTGCTGAGGACCGTTGAAATACGTT 5481  
Qy 5586 CTCTCTCATCTAGTATTAATGATTTTGAATGATTAATGATGATGATGATGATGATGAT 5645  
Db 5482 CTCTCTCATCTAGTATTAATGATTTTGAATGATTAATGATGATGATGATGATGATGAT 5541  
Qy 5646 CTGAGAACTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5705  
Db 5542 CTGAGAACTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5601  
Qy 5706 GACATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5765  
Db 5602 GATATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5661  
Qy 5766 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5825  
Db 5662 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5721  
Qy 5826 AAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
Db 5722 AAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
Qy 5886 GACATCTCGAGCGCTTAAAGAGCTTCTTGGGGAAGGGCAATCCGATGAGAGAG 5945  
Db 5782 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
Qy 5946 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
Db 5842 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
Qy 6006 TCAAGCTGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6065  
Db 5902 TCAAGCTGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5961  
Qy 6066 AAGCAAGAGCGCGCGGCGAGGAGTGGCTCTTTGAGCCGATACGATACATGCGAT 6125  
Db 5962 CGTTACAAAGATGCT----- 5976  
Qy 6126 GCGGCTGATCCGATGCGGCGGAGCCGCGCGCGATGAAGCAAGCAAGCGATGCGCC 6185  
Db 5977 CCACCCAGAGGCTGATGAGGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6036  
Qy 6186 GCTGTGAGAGTGTGATGTTAACGTTATCTGAGAGAGAGCTGCGATGAGAGT 6245  
Db 6037 GAGGCTGAAGGCGGACGCGCGCGCGCGATGATGATGATGATGATGATGATGATGATGAT 6096  
Qy 6246 AATGTAATAGTCCGCGTGAAGATGACGCGCGCGCGAGAGAGAGAGAGAGAGAGAG 6305  
Db 6097 GAGGCTGAAGGCGGACGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6156  
Qy 6306 GCGGCGGCGAG 6365  
Db 6157 GGTGGCGGCGCTTATGCTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6216  
Qy 6366 GTTCTGTGAG 6425  
Db 6217 GTACTGTGAG 6276  
Qy 6426 CGATGCGGAG 6484  
Db 6277 AGATGCGGAG 6315

RESULT 11  
AR028530

LOCUS AR028530 6315 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 2 from patent US 5858713.  
 AR028530  
 VERSION AR028530.1 GI:5940503  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 6315)  
 Soderlund D.M. and Ingles P.J.  
 TITLE Calcium permeable insect sodium channels and use thereof  
 JOURNAL Patent: US 5858713-A 2 12-JAN-1999;  
 FEATURES  
 source 1..6315  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 68.1%; Score 4434.2; DB 6; Length 6315;  
 Best Local Similarity 81.8%; Pred. No. 0;  
 Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;

```

QY 24 ATACAGAAATCCGATCGATATCTGAGAGAAAGCGAGTTGTTCCGCTTACC 83
DB 1 ATACAGAAATCCGATCGATATCTGAGAGAAAGCGAGTTGTTCCGCTTACC 60
QY 84 CGGAAATCATTTGTCGAAATCGAACACGATTCGCGCTGAACATGAAAGAGAG 143
DB 61 CGGAAATCATTTGTCGAAATCGAACACGATTCGCGCTGAACATGAAAGAG 117
QY 144 CTGAGAAAGAGAGAGCGGAGAGAGAGTCCCGATATGTCGCAAGAAAAA 203
DB 118 CTGAGAAAGAGAGAGCGGAGAGAGTCCCGATATGTCGCAAGAAAAA 148
QY 204 GAAATCCGATATGATGACGAGAGACGAGATGAAAGTCCACACCGATCCCTTAA 263
DB 149 -AGATACGATATGATGACGAGAGACGAGATGAAAGTCCACACCGATCCCTTAA 207
QY 264 CAGGCTGCGCAATACCTGTTGATTCGAGGAGGCTTCCCGCGGAATTGGCTCCACT 323
DB 208 CAGGCTGCGCAATACCTGTTGATTCGAGGAGGCTTCCCGCGGAATTGGCTCCACT 267
QY 324 CCTCTGAGATATGATGATCCCTTACAGAGATGATGATGATGATGATGATGAT 383
DB 268 CCTCTGAGATATGATGATCCCTTACAGAGATGATGATGATGATGATGATGAT 327
QY 384 GAAAGAGATATTTTCTGCTTCTGATCAAAAGCAATGATGATGATGATGATGAT 443
DB 328 GAAAGAGATATTTTCTGCTTCTGATCAAAAGCAATGATGATGATGATGATGAT 387
QY 444 CCGATAGCTGCTGCGCATTTAATTTAGTGAATCCATTTATTTTCCATTCATC 503
DB 388 CCGATAGCTGCTGCGCATTTAATTTAGTGAATCCATTTATTTTCCATTCATC 447
QY 504 ACCCAATTCGTCATCTGATCTGATGATTAAGCGACCAAGCCCAAGCTTGAATCC 563
DB 448 ACCCAATTCGTCATCTGATCTGATGATTAAGCGACCAAGCCCAAGCTTGAATCC 507
QY 564 ACTGAGTATATTCACCGGATCTACACATTTGAATGAGTGAATGATGATGATGAT 623
DB 508 ACTGAGTATATTCACCGGATCTACACATTTGAATGAGTGAATGATGATGATGAT 567
QY 624 GATTTCATTTATGCGCGTTTACGATTTTGAAGATGATGATGATGATGATGATGAT 683
DB 568 GATTTCATTTATGCGCGTTTACGATTTTGAAGATGATGATGATGATGATGATGAT 627
QY 684 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743
DB 628 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
QY 744 ACGTTAGGCTGCTGAGCGCTTAAACCGTAGCATTTGTCAGAGCTTGAAGCATC 803
DB 688 ACGTTAGGCTGCTGAGCGCTTGAACCGTAGCATTTGTCAGAGCTTGAAGCATC 747

```

```

QY 804 GTGGCGCCGCTCATGCAATCGGTGAGAAATCTGGCGGATGATTAATCCGACCATGTC 863
DB 748 GTGGCTGTGTCATGAAATCTGTAATAAATCTAGCGATGATTAATTTGTAACAATGTTT 807
QY 864 TCCCTGTGGGTGTGGCGTGAATGAGGCTTACAGATCTATATGGCGTCTCCAGAGAG 923
DB 808 TCCCTGTGGGTGTGGCGTGAATGAGGCTTACAGATCTATATGGGTCTTAAACCAAAAG 867
QY 924 TGCATCAAGAAATTCGCGTGAACGCTTCTGGGCAATCTGACCGACGAAATCTGGAC 983
DB 868 TGCATTAACGATTCCTCCCTGACGCGAGTTGGGCAATCTGACCGAGTAAACGAGTTT 927
QY 984 TATCAATTCGCAATAGCTCCCAATTTGATTTCCGAGAGAGAGGATCTCATTTCCGTTA 1043
DB 928 TATCAATTCGCAATAGCTCCCAATTTGATTTTACGAGAAAGATGCGAGTCTATCCGGTG 987
QY 1044 TCGGCAATATATCCGCTGCGGCGCAATGCGACGACATTAAGTGTGCTGCAAGGGGTTT 1103
DB 988 TCGGCAATATATCCGCTGCGGCGCAATGCGGCGCAATTAAGTGTGCTGCAAGGGGTTT 1047
QY 1104 GGTTCGAATCCGAATTAATGCTTACACAGCTTCCATTTGTTGGATGAGGCTTCCGTCC 1163
DB 1048 GGTTCGAATCCGAATTAATGCTTACACAGCTTCCATTTGTTGGATGAGGCTTCCGTCC 1107
QY 1164 GCTTCCGCTGATGACACAGGACTTTCGAGAGATCTGACAGCTGCTGCTGAGGCTCC 1223
DB 1108 GCTTCCGCTGATGACACAGGACTTTCGAGAGATCTGACAGCTGCTGAGGCTCC 1167
QY 1224 GCGGACATATGACACAGGACTTTCGAGAGATCTGACAGCTTTCGAGGCTTTCATCTT 1283
DB 1168 GCTGACCTGACACAGGACTTTCGAGAGATCTGACAGCTTTCGAGGCTTTCATCTT 1227
QY 1284 GTGATTTGATTTGGCCATTTGTCATGATGATGATGATGATGATGATGATGATGATGAT 1343
DB 1228 GTGATTTGATTTGGCCATTTGTCATGATGATGATGATGATGATGATGATGATGATGAT 1287
QY 1344 GAAAGAGAGCTGCGCAAGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1403
DB 1288 GAAAGAGAGCTGCGCAAGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1347
QY 1404 GCGGCAATGAGAGAGGCGGCAATGCGAGGCTTACGAGGAGGAGGAGGAGGAGGAGGAG 1463
DB 1348 GCGGCAATGAGAGAGGCGGCAATGCGAGGCTTACGAGGAGGAGGAGGAGGAGGAGGAG 1407
QY 1464 GCGGCAATGAGAGGCTGATCCGAAATGCGCAAGGCTTACGAGGAGGAGGAGGAGGAGGAG 1523
DB 1408 GCGGCAATGAGAGGCTGATCCGAAATGCGCAAGGCTTACGAGGAGGAGGAGGAGGAGGAG 1467
QY 1524 TATGACTATTTGTTGGCGGAGAGAGGCAATGATGACAAACAAAGAGAGATGTC 1583
DB 1468 TATGACTATTTGTTGGCGGAGAGAGGCAATGATGACAAACAAAGAGAGATGTC 1527
QY 1584 ATTGAGAGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1643
DB 1528 ATTGAGAGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
QY 1644 ACCAAGACACCAAGCTACCAAGTTCGTAAGTGAAGACGACATCTTATCTTACCT 1703
DB 1588 ACCAAGACACCC--GCTACTAAGTCCGTAAGTGAAGACGACATCTTATCTTACCT 1644
QY 1704 GATTTCACGTTTAACTACGACGAGGAGTACGTAATTTCTCAACAGTACAGATGCGGAAC 1763
DB 1645 GATTTCACGTTTAACTACGACGAGGAGTACGTAATTTCTCAACAGTACAGATGCGGAAC 1704
QY 1764 GAGAGTGGCGCTTGTGATACCCGATGAGATGATGATGATGATGATGATGATGATGATGAT 1823
DB 1705 GAGAGTGGCGCTTGTGATACCCGATGAGATGATGATGATGATGATGATGATGATGATGAT 1764
QY 1824 CAGGATCCGAGAGCACTTGCCTTATGCGAGATGCGAGATGCGATCCGATCCGATGTC 1883
DB 1765 CAGGATCCGAGAGCACTTGCCTTATGCGAGATGCGAGATGCGATCCGATCCGATGTC 1824

```

QY 1884 GAAGAGATGGGGCCATGATGCGCGGTACTATGCGAATCTTAGGGCTCCGACACTCA 1943  
 DB 1825 GAGAGAAATGGTGCATTAATGATACAGCTACTATGTAATTTAGGTTCTTAGACATCTT 1884  
 QY 1944 TCGATATCCTGCGATCAGTCCGAAATATGTAATCTGATCAGATGCGGATCTACCGGCGAC 2003  
 DB 1885 TCATATACCTGCGATCAATCAAGAAATCTGTAATCATCAATGGATTTATATGAGTGGC 1944  
 QY 2004 ATGGCGCTATGGGGCTGACGCAATGACCAAGAGAGCAAAATGGCGACCGCAACCA 2063  
 DB 1945 ATGGGGCCATATGGGTCAGCACAATGACCAAGAGAGCAAAATTCGAGTGCACACA 2004  
 QY 2064 CGCAATCATCATGATGGGGCCCAATGGCGGACCACTGCTGAGACCAATGACAG 2123  
 DB 2005 CGCAATCATCATGATGGTCTGCAACCAATGGGCAATGATGCGCGGGTGGCTAT 2064  
 QY 2124 CTCGAT-----CATGCGACTACGAATTTGGCTGAGTGCAGGACGCA 2168  
 DB 2065 CCCGATGCGCAATCAAGAGAAACAAAGGATATGAAATGGGTCAAGATTATACAGACGA 2124  
 QY 2169 GCTGCGAAGATTAAATCATATGACATCTTTATGAGCCCGTCCAGACACAAACGGTG 2228  
 DB 2125 GCTGCGAAATTAACACACACACATCTTTATGAGCCCGTCCAAATCAAAACAGTG 2184  
 QY 2229 GTTGATGAAAGATGATGCTGCTGAAATGACATCATGCAAGCGCGCTGCTGGAC 2288  
 DB 2185 GTAGACATGAAGATGTAATGCTTAAATGATATCATTTGAACAAAGCGCTGGTGGAT 2244  
 QY 2289 AGTCGGGCAAGCATCGCGGTCTCCGTTTACTATTTCCAAAGAGAGCATGACAG 2348  
 DB 2245 AGTCGTCTATGACGAGT-----GAGGACATGACGA 2280  
 QY 2349 GATGGGCGGACGTTCAAAAGACAGGCACTGCAAGTATCTTCAAGGCAATGATGTTT 2408  
 DB 2281 GATGGTCCCAATTCAGACATCGCCCTCGAATATCTTAAAGGATCGAAATCTTT 2340  
 QY 2409 TGTGTGGGACGTGTGCTGGGTTTGTGAATTCAGAGTGGGTATCGCTCATCGTC 2468  
 DB 2341 TGTGTGGGACGTGTGTGGTGTGTTAAATTCAGAAATGGGCTCTCTTAATGTG 2400  
 QY 2469 TTGATCCCTTCTGCGACTCTTTCATCAAGCTGTCATTTGTCGCAACGATGTTCAAG 2528  
 DB 2401 TTGATCATTCGTGGAGCTCTTTCATTAACCTGTGTATTTGGTCAATACATATGTTCA 2460  
 QY 2529 GCATGATTCACACAGATATGAACAGAGATGACCGGTCTCAAGATGGCAAT 2588  
 DB 2461 GCCATGATTCATCAAGCATGATCCGAAATTTGGAAGATGGCTGAAAGTGTAACTAT 2520  
 QY 2589 TTCTTCAACGCGCACTTTGCCATGAGGCGCAACGAAGCTAATGGCCATGAGCCCAAG 2648  
 DB 2521 TTCTTCAACGCGCACTTTGCCATGAGGCGCAACGAAGCTAATGGCCATGAGCCCAAG 2580  
 QY 2649 TACTATTTCAAGAGGGCTGGAACATCTTTCGACTTATTCGTCGAGCCCTATCGTATG 2708  
 DB 2581 TACTATTTCAAGAGGGCTGGAACATCTTTCGACTTATTCGTCGAGCCCTATCGTATG 2640  
 QY 2709 GAATCGGACTGAGAGGTGTCCAGGGTGTCTCGTATGCGTCTTTCGATGCTGCGT 2768  
 DB 2641 GAATCGGACTGAGAGGTGTCCAGGGTGTCTCGTATGCGTCTTTCGATGCTGCGT 2700  
 QY 2769 GTATTCAAATGCGCAATCTTGGCCCACTTATATTCATTTGCAATTTGGAAGGCG 2828  
 DB 2701 GTATTCAAATGCGCAATCTTGGCCCACTTATATTCATTTGCAATTTGGAAGGCG 2760  
 QY 2829 ACATGAGGCGCTTGGTATCTGACATTTGATCTTTCATTTGCAATTTGGAAGGCG 2888  
 DB 2761 ACATGAGGCGCTTGGTATCTGACATTTGATCTTTCATTTGCAATTTGGAAGGCG 2820  
 QY 2889 GTGATGGAATGCACTGTTGGAAAGATATATCATGATCAAGAGCGGCTTTCGAT 2948  
 DB 2821 GTGATGGAATGCACTTTCGAAAGATATATATGACCAAGAGTGGCTTTCGAT 2880  
 QY 2949 GCGGACCTGCGCGCTGGAATCTTACCGAATTTATGACAGCTTCAATATGTTCCG 3008

DB 2881 CATGAATTAACCGCGCTGGAATTTCAACGACTTTCATGCAACACTTATATGTTCCGA 2940  
 QY 3009 GTGCTTCGAGAGATGAGTCAAGTCCATGAGGATGCAATGATGAGGCGATGCTCG 3068  
 DB 2941 GTGCTTCGAGAGATGAGTCAAGTCCATGAGGATGCAATGATGAGGCGATGCTCG 3000  
 QY 3069 TGCATTCCTCTTCTTGGCCACCGTGTATCGGCAATCTTGGTACTTAACTTTTC 3128  
 DB 3001 TGTATACCTCTTCTTGGCCACCGTGTATCGGCAATCTTGGTACTTAACTTTTC 3060  
 QY 3129 TTAGCTTCTTCTTGGCCACCGTGTATCGGCAATCTTGGTACTTAACTTTTC 3188  
 DB 3061 TTAGCTTCTTCTTGGCCACCGTGTATCGGCAATCTTGGTACTTAACTTTTC 3120  
 QY 3189 GATACGAATTAATAGCGGCGCTTCAATGAAATGCGGATTTAAAGTGGTTAAG 3248  
 DB 3121 GATACGAATTAATAGCGGCGCTTCAATGAAATGCGGATTTAAAGTGGTTAAG 3180  
 QY 3249 CGTATATGCTGATGTTTCAATGATATGTAATGCAATTAATGCAATTAATGAT 3308  
 DB 3181 CGTATATGCTGATGTTTCAATGATATGTAATGCAATTAATGCAATTAATGAT 3240  
 QY 3309 CAACCATGAGGTGAGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3368  
 DB 3241 CAACCAT-----GAAACATGCGAT 3261  
 QY 3369 AACGAATGAGGTGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3428  
 DB 3262 AATGAATGAGGTGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3321  
 QY 3429 AAGGACGAGGACCACTGAGAGTGGCCATCGGGATCGGATGCAATTAATGCAAT 3488  
 DB 3322 AAGGACGAGGACCACTGAGAGTGGCCATCGGGATCGGATGCAATTAATGCAAT 3381  
 QY 3489 GACATGAAGAACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3548  
 DB 3382 GATATGAAGAACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3441  
 QY 3549 AACTCAATTAACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3608  
 DB 3442 AACTCAATTAACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3501  
 QY 3609 TTAACGAGGACCACTGAGAGTGGCCATCGGGATCGGATGCAATTAATGCAAT 3668  
 DB 3502 ATACAGGACGATGACCTGAGGACCACTGAGAGTGGCCATCGGGATCGGATGCAAT 3561  
 QY 3669 AAGGACGAGGACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3728  
 DB 3562 AAGGACGAGGACCAACGAGGACCAACCAATCAGTTGATTTGAGGAGAGAGATGATG 3621  
 QY 3729 AGCAAGGAGATTAAGTCTTGAAGAGAACTGAGGAGGAGGAGGAGGAGGAGG 3788  
 DB 3622 AGCAAGGAGATTAAGTCTTGAAGAGAACTGAGGAGGAGGAGGAGGAGGAGGAGG 3681  
 QY 3789 CCGCTCGAGGAGTATCATTTATTCATGCT---ACACGAGGAGATTAATGCAAT 3845  
 DB 3682 CAGCTGAGTGTGATCATCATTCATTCATGCT---ACACGAGGAGATTAATGCAAT 3741  
 QY 3846 CCAGCTGATTTGCTGCGCGGATTTGATCAATTAAGAAATTTGCAATTTAGCGGATGAT 3905  
 DB 3742 CCGGCGAGCTTTTCCGAGCTGATCAATTAAGAAATTTGCAATTTAGCGGATGAT 3801  
 QY 3906 GACTCGCGTCTTGGCAAGATGAGGCAATTAAGGAGGAGGAGGAGGAGGAGGAGG 3965  
 DB 3802 GACTCGCGTCTTGGCAAGATGAGGCAATTAAGGAGGAGGAGGAGGAGGAGGAGG 3861  
 QY 3966 AATTAATTTTGAACAGCTGTTATCATATGATTTTATGATGATGATGATGATG 4025  
 DB 3862 AATTAATTTTGAACAGCTGTTATCATATGATTTTATGATGATGATGATGATG 3921  
 QY 4026 TTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4085



Qy 6246 AATGAATAGTCCGGTGAAGATGACGCGCGCGGACGACGACGACGACGCGGCG 6305  
Db 6097 GGAGCCATATACCCACAGATCCAGATCCGCGGAAGAGATGTGTCCAGCGCCGCGCAT 6156  
Qy 6306 GCGCGCGGACGACGACGCGCGGAGATCCGCGAGCGGTAGCGCGCGGCGACGACGCGCC 6365  
Db 6157 GGTGCGCGCCCGCTTATGTCGCGGCTGTGTATGTGCGCGGACGTAATGTGCGCGCAACGCGCC 6216  
Qy 6366 GTTCTCTGTGAGAGGACGCGGTTCGTACGAAAGACGCGCACAGGTGTCTATCCATCG 6425  
Db 6217 GTACTGTGTGAAAGGATGTGTGTTCACAAAACGCTCATTAAGGTGTATATACATCG 6276  
Qy 6426 CGATCGCGGACGATCAGCTCGCGGACGCGGCGATGTCTGA 6464  
Db 6277 AGATCGCGGACGATCAGCTCAGGACGCGGAGATGTCTGA 6315

RESULT 12  
AY663385 6317 bp mRNA linear INV 14-JUL-2004  
LOCUS Aedes aegypti voltage-dependent para-like sodium channel mRNA,  
DEFINITION partial cds, alternatively spliced.  
ACCESSION AY663385  
VERSION AY663385.1 GI:50080865  
KEYWORDS  
SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
Stegomyia.  
1 (bases 1 to 6317)  
Wu, J.-H. and Zhao, T.-Y.  
Direct Submission  
Submitted (21-May-2004) Department of Vector Biology and Control,  
Microbiology and Epidemiology Institute, 20 Dongda Street, Fengtai  
District, Beijing 100071, China  
Location/Qualifiers  
1. 6317  
/organism="Aedes aegypti"  
/mol\_type="mRNA"  
/db\_xref="taxon:7159"  
/note="alternatively spliced"  
/codon\_start=1  
/product="voltage-dependent para-like sodium channel"  
/protein\_id="AA069681.1"  
/db\_xref="GI:50080865"  
/translation="DEDEDGEGPODSTLEGGVPIPVMOGSPPELSTPLBIDSY  
VANGRTFVYVSKGDIREFSATNMLYVDPNPRIYVLAIVLHPLEFPIITLITN  
CITLIMBETPTVESTVEVTFGTITTFESAVKMAAGFILOPTTILBDAKNNMLDVFVIAL  
AVTMGIDLGNLALRTFRVRLAKTVAIVGLKTIAGVAVESVKNLMDVILITMPSL  
SVFLMGIDITMGVLTOKICEPLDGSWMGLSDENMGRFNNNSMNFESTGDTPLC  
GNSGAGCGCEBEGYICLOGYNDPNYGYSPFTGWAFFSARLMTODWENLYOLVLR  
SAGWHMLFFIIVIFLGSFYLVNLIALVANSYDELGRAEESBAEALREABEA  
AAKAKLEAOAAAAAANPRLASPSPSGSHSYELFNOKGDNKNEKRSRSG  
LESSEITRTTATATAGTAKAKVSAASISLPSGSPNLRGSGRSQPTIRNGR  
FVGVGSDRKLPLVSTIYLDADENLPTADSNVAVPMSENALIVPVYVLAHGRSHS  
YTSQSRISYSTSHDILGAMTKESRLRNSANTNHSIVPPNMSGPMASVYDNNHG  
QRDPMGQDCTDEAGKIKHNDNPIESPOTVDMKVMVNLNDIIEQAGRHRSAD  
HGVSIVYPTEDDEDGPTFKDKALEFPMRIIVDCVMWLFQEWALFVDF  
FVELFITLIVNTLFMALDHDMDPMERMLKSGNYEFTPTPIEATMKLIAMPKY  
YFOGWNIFDPIVALSLLELGGVGLSTLRSPRLRVKAKSNPTLNLISING  
RTKALGNLTVLCTIITFTVAMGMLFGKRTIDVDFPKDLPRKMTDPMHSFLA  
VFRVLCGEWISMDMCLVGVSCIPFLATVVIIGNLVNLFLALLSNGSSLSA  
PTADNEITLKIARISRFNMIKSNIANLAKVKONLQIOLISVQAGAGVPCIS  
AEHGBNELTLPDILADGLKGVKEHNOLEVAIDGMEFTIHGDLNKGKKNOLM  
NNSKYIGNSINHODNKLHEHNRGMSLDDPDAISIKSYGSHNRPKDKSHPDC  
TMGEKEDVSKDGLDELDRCDEGSLDEGLIHADEDEVIBSPKDCPPNC  
YKKEPVLAGDDAPFMOGMANLRLKTFOLINKFTETAVITLISLALBVDHLP  
HRPILODLVLYMDRIETVIFPLEMLIKLALGFRTNACMDPILIVMVLICIFML  
SLGAGGIOAFKTKTLTALRLPAMSMQMRVVVNLVVALISIFVNLVLCIFML  
IFALINGVOLFAKGYKCVDKNTLSHEIIPDVNAVENTWENSPPNPFVGAAYL  
CLFOVATPKMIQIMNDAIDREVGKQIRRTNITMYLYFVFPIIFGSPFLNLFIV

FEATURES  
SOURCE

CDS

IIIDNEOKKXAGGSLMEFTEDDCKYYNAMKMKXSKPLKAIPEPRMRPOAIVEIV  
TNKPEPDIIMLFIFGRNMLTWLTHYKOTDPTFSATLDYLMIFCITFSECCMKIPALR  
YHIFIEPMNLFDFVNTSLIGLVLSLIDIEFTIETPILRVARAKGRVRLYKAGK  
GIRTLPLALMSLPALFNI CLLPFLVMEFALFPMSPFMKVDKSGLDVNLFTGQ  
SMILLFQMSSTAGMDVLDGIIINEDECIPENDMGYFGNCSATIGITVLAIVISF  
LIVINMYLAVLENYSOATEDEVOGLNDPDNDYIEIMQCPDGTGYIRDOJSLFL  
DVAREPLOIHKNPNKYKTIISMDIPICRDMNCCVILALTLDPFARKGNPIAEFTALIG  
EVQARPEVEGIEFVASTLMKREYICARVIOHAKRKERAGGGGDDPTDADND  
DGDGGGAGGGSAGGCVTSRPGGGSIVGGGTPESSGGGSQANLGVVEHNLSP  
KESPDGNNDPGRQTAVALVESDGPVTRNGHVRVHSRSPITSRADV"

Query Match 54.3%; Score 3536.4; DB 3; Length 6317;  
Best Local Similarity 74.0%; Pred. No. 0; Mismatches 1561; Indels 72; Gaps 11;  
Matches 4655; Conservative 0;

Qy 216 GATGACGAGCAGCAGAGATGAAGTCCACCAACCGATCTCACTTGAACAGAGGTGCGCA 275  
Db 1 GATGACGAGCAGCAGAGATGAAGTCCACAGCGGACTCCACACTCGACAGAGAGTGCCA 60  
Qy 276 ATACCTGTTCGATTCGACAGGCGAGCTTCCCGCGGAATTTGCTTCATCTCTCGAGAT 335  
Db 61 ATCCCGGTTCCGAATGCAAGGCGAGCTTCCCTCCGGAATTTGGCTCCACCGCTTCGAGAT 120  
Qy 336 ATCGATCCCTACTACAGCAATGTACTGACATTTGCTAGTGTGAAGCAAGAAAGATATT 395  
Db 121 ATCGACGACTTATTCGCAATCAAGACGACATTCGTAGTGTGAAGCAAGAAAGATATT 180  
Qy 396 TTTGCTTTTCGATCCAAAGCAATGTGATGCTGATCCATTCATTCATCCGATACGTCGT 455  
Db 181 TTTGCTTTTCGACGACCAATGATTAATGTACTGATCCGTTCAATCCATACGTCGTGC 240  
Qy 456 GTGCGCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 515  
Db 241 GTAGCTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 300  
Qy 516 GTCAACGACATCCGATGATATGCGCAACAGCGGCGGTTGATCCAGAGGTGATA 575  
Db 301 ACCAATGTATATGATGATATGATATGATATGATATGATATGATATGATATGATATGAT 360  
Qy 576 TTCAACCGAATCTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 635  
Db 361 TTCAACCGCATCTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 420  
Qy 636 TGCCGTTTACGATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 695  
Db 421 CAACGTTTACTTATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
Qy 696 GCTTATGACATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755  
Db 481 GCATATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Qy 756 CTGAGAGGCTTAAACCGTACGATTCGACAGCTTGAAGACATTCGCGCGCTC 815  
Db 541 CTAGAGCTGCAAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
Qy 816 ATCAATCGGTGAAGATTCGCGGATGATGATGATGATGATGATGATGATGATGATGATG 875  
Db 601 ATTAGAGTCGTTAAGATTCGAGAGATGATGATGATGATGATGATGATGATGATGATG 660  
Qy 876 TTCCGTTGATGGGCTACAGATCTTATATGCGGCTGACCGGAGAGTGATCAAGAG 935  
Db 661 TTTCCTTAAAGGGCTGACAGATCTACATGCGGCTGACGAGAGTGATCAAGAG 720  
Qy 936 TTCCGCTGACGAGGTTCTGCGGCAATCTGACCGAGCAAGCTGGAATCAATTCGCG 995  
Db 721 TTCCGCTGACGAGGTTCTGCGGCAATCTGACCGAGCAAGCTGGAATCAATTCGCG 780  
Qy 996 AATAGCTCAATTTGATTCGAGAGCAGAGGATCTCATTTCCGTTATGCGCAATTA 1055  
Db 781 AATAGCTCAATTTGATTCGAGAGCAGAGGATCTCATTTCCGTTATGCGCAATTCG 837  
Qy 1056 TCCGCTGCGGCGCAATGACGAGATTAAGTGTGCTGACAGGAGTTTGTGCGAATCG 1115

Db 838 TCGGCTGCTGCGCAATGCGAGAGATATTTGTTTACAGGTATGAGATATCA 897  
Qy 1116 AATTATGCTACACAGCTTCGATTGCTTGATGAGGCTTTCTGTCGCTTCGGCTG 1175  
Db 898 AATTAGCGGATATCAAGTTGATCTTCGATGAGGCAATCTTATCTGCTTTCGCTA 957  
Qy 1176 ATGACAGAGACTTTCGGAGAGATCTGACAGCTGATGTCGCGCCGCGAGCATG 1235  
Db 958 ATGACCAAGATTTCTGGAGAACTTTATCACTGCTGTTAGATCAGCTGAGCCGTG 1017  
Qy 1236 CACATGCTGCTTATATGATCATCTTCTTAGTTCAATCTTCTTGAATTTGAT 1295  
Db 1018 CACATGCTTCTTCAATGATTTATCTTCTGCTGCTTCTTCACTTGAATTTGAT 1077  
Qy 1296 TTGGCCATTTGTCGATGCTGATGAGATGCAATGCAAGAGAGGCGGAGAGGCT 1355  
Db 1078 TTGGCCATTTGTCGATGCTGATGAGATGCAATGCAAGAGAGGCGGAGAGGCT 1137  
Qy 1356 GCCGAGAGAGGCGATACGTGAAAGCGAGAGAGCTGCGCGCAAGCGGCAAGCTG 1415  
Db 1138 GCCGAGAGAGAGGCTTTCGGAGAGCGAGAGAGAGCTGAGGAAAGCGGCAAACTC 1197  
Qy 1416 GAGAGCGGCGCAATGCGAGGCTCAGGACAGCGAGATGCGCTGCGCGGAGAGGCT 1475  
Db 1198 GAGGCGC-----AAGCAGGCGAGCGGCGGCG 1224  
Qy 1476 GCACTGATCCGGAATGCGCAAGTCCGACG---TATTCTGATCAGCTATGAGCTA 1532  
Db 1225 GCAACCAACCGGAGATGCGCAAGGCGGCTGCGACTTTCTGCGACACTGAGCTG 1284  
Qy 1533 TTTGTTGCGCGGAGAGAGGCGCAACGATGACAAACAAGAGAGATGTCATTCGAGC 1592  
Db 1285 TTGCTGAACCGAGAGAGGCGCAACGACAAACAAGAGAGATGTCATTCGAGC 1344  
Qy 1593 GTGAGTGTGATGCGAGTGTGAGGCTTATCAAGAGCAACCGAGACCTACCAAGCA 1652  
Db 1345 GAAAGATTTGATGCTGTGAGGAAATCAACAAGAACCGGCAACGCTACTGAGCT 1404  
Qy 1653 CACCAAGCTACCAAGTTGTAAGTGAAGCAAGCATCTTATCTTACCTGTTCA 1712  
Db 1405 GGC---ACTGCAAAAGCCCGTAAGTGAAGCGGCTTCACTTATTAACGTTTCA 1461  
Qy 1713 TTTAATATGCGAGGAGATCAAGTATCTCAACAATGACAGTACGGAAGCGTGGC 1772  
Db 1462 TTTATCTTCTGTAAGAGATCTAGAGATCAATCATGTTACATGTAAGTGAAGGA 1521  
Qy 1773 CG---CTTTGATATCCCGGTAGAGGATGTAAGCATGATGATGTCACATATCAGAT 1829  
Db 1522 CGTTTCGCGGCTGCTGTGAGGATGAAACATTTGTAATCTTCAACATATCTGAT 1581  
Qy 1830 GCCCAGAGCACTTCCCTATGCGAGCACTGCAATGCGCTGACCCCGATGCGAGAG 1889  
Db 1582 GCAAGAAACATTTGCTCATACGCGGATGATGAAAGCGGCTGACACCATATCTGAGGAA 1641  
Qy 1890 AATGAGGCAATATGTCGCTGATATGAGGATGTAAGGCTCCGAGCACTCATGAT 1949  
Db 1642 AATGATGCAATCTGTTCAAGTATATGATGTAATTTAGTTGCGCATTTCACTGAT 1701  
Qy 1950 ACCCTGATCAGTCCCGAATATGTAATCTTCAATGCGATCTTCACTGCGGCGATGCGC 2009  
Db 1702 ACATGCAATCATGCGCATCTGTAACATGCAAGCGGAGCTGCTGCGGCGATG--- 1758  
Qy 2010 GTCATGCGGCTGAGCAATGACCAAGAGAGCAATTTGCGACACCGCAACACGCAAT 2069  
Db 1759 ---AGAGAGAGCGACTGCGGAAACGCTGCGCGCGCAACACCAATCATCTGAT 1815  
Qy 2070 CAATATGAGGCGCAACCAATGCGGCAACCTGCTGAGACCAATCAAGCTGAT 2129  
Db 1816 CCGCGCGCAACATGCTGCGCGCAACATGCTTCACTGAGAGCAACCAAG---GGG 1872  
Qy 2130 CATCGCACTACGAATTTGCTGAGTGAAGCAAGAGCTGCGCAAGATTAACATCAT 2189

Db 1873 CAGCGAGACTTGTATATGCTCAAGACTGTACAGACGAAAGCTGGCAAAATTAACACAC 1932  
Qy 2190 GACAACTCTTTATGACCCGCTCAGACACAAAGGTGTTGATATGAAGATGTATG 2249  
Db 1993 GACAACTCTTATGACCCCTCTCAACACAAACGTAATGATGAAGACGCTGATG 1992  
Qy 2250 GTCTGAATGATATGGAACAGGCGCTGTGGGCAAGTGGGGAAGGATGCGGCT 2309  
Db 1993 GTTTAAACGATATCATGAGCAAGCTGTGTGGGCAATGAGTATGATGATATGA 2052  
Qy 2310 GTCTCGTTTACTATTTCCCAACAGAGACATGACAGATGAGGAGCGTCAAGAC 2369  
Db 2053 GTCTCTGTTTACTATCTCCCAACAGAGACGACAGAGAGGCTCAACGTTCAAGAC 2112  
Qy 2370 AAGGCACTGAGATGATCTCAAGAGCATGATGTTTGTGTGTGAGAGCTGCTGG 2429  
Db 2113 AAGGCTGTGAGTGTGAGATGAGATGCAAGCTTCTGTGTGTGAGAGCTGCTGG 2172  
Qy 2430 GTTTGTTGAATTTTCAGAGTGGGATGCTCATGCTTTCGATCCCTTCTGAGCTC 2489  
Db 2173 GTGTGCTGAATTTTCAGAGTGGGATGCTCATGCTTTCGATCCCTTCTGAGCTC 2232  
Qy 2490 TTCAATCAAGCTGTGATGCTCAACAGATGTTCAAGATGATGATCAACAGATATG 2549  
Db 2233 TTCAATCAAGCTGTGATGCTCAACAGATGTTCAAGATGATGATGATGATGATG 2292  
Qy 2550 AACAGAGATGGAACGCTGTCAAGAGTGGCACTTCTTCAACGCGCACTTGGC 2609  
Db 2293 GACCCGAGATGAGAGGCGGCTCAAGAGTGTATCTTCTTCAACGCGCACTTGGC 2352  
Qy 2610 ATGAGGCGCACCATGAGGCTATGCGCAAGAGCGGCAAGTATTTCCAGAGGCTG 2669  
Db 2353 ATGAGGCGCACCATGAGGCTATGCGCAAGAGCGGCAAGTATTTCCAGAGGCTG 2412  
Qy 2670 AACATCTTGAATTTATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGAT 2729  
Db 2413 AACATCTTGAATTTATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGAT 2472  
Qy 2730 CAGGCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2789  
Db 2473 CAGGAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2532  
Qy 2790 TGCCCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2849  
Db 2533 TGCCCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2592  
Qy 2850 CTGACATTTGATCTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2909  
Db 2593 CTGACATTTGATCTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2652  
Qy 2910 GGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2969  
Db 2653 GGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2712  
Qy 2970 TTACGCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3029  
Db 2713 TTACGCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2772  
Qy 3030 GAGTTCATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3089  
Db 2773 GAGTTCATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2832  
Qy 3090 ACCGTTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3149  
Db 2833 ACCGTTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2892  
Qy 3150 TTGGCTCATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3209  
Db 2893 TTGGCTCATCTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2952  
Qy 3210 GCGTTCAATGAATTTGCGGATTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3269  
Db 2953 GCGTTCAATGAATTTGCGGATTTCAACTGATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3012

QY 3270 AAGTTAATCGTAACAAATGACAAATCAATTAAGTATCAACCATCGATGAGAGACC 3329  
Db 3013 AAGTTGCGAAAAACAGTTAAACAGCAAGATGCGTCCGTCCGACCCGACG-----GC 3066  
QY 3330 AACGATCAGTTGGATTGGAGCGAGAGCATGCTGACCAAGCACTGAGCTGGAGCCAC 3389  
Db 3067 AAAGGGATATGTCATGATCTCTGCAAGCATGCTGATGAAATGAGCTGAAATTAATCTCA 3126  
QY 3390 GACGATCTCTGCGGACGCGCTCATCAAGAGGGGATCAAGAGCAGACGCACTGAG 3449  
Db 3127 GATGATACATGCGCGACGCGGCTGCTCAAGAAAGGCTCAAGAGACACAAACAGCTGAG 3186  
QY 3450 GTGGCATCGGGGATCGGATGGAATTCACGATACCGCGACATGAAGAACAAGCCG 3509  
Db 3187 GTGGCATCGGCGAGCGGATGAGATTCAAGATACCGCGACCTGMAAACAAGGCGAAG 3246  
QY 3510 AAGAAATCCAATATCTAATTAACGCAAGATGATGGCAACTCAAT---TAACCAACCA 3566  
Db 3247 AAGAAACAAACAGCTGATGAACAATTCAGAGTGATAGCAATTTCTATTATGATATCA 3306  
QY 3567 GACATGACCTGGAACACAGCTAAACCATAGAGGTTGTCCTTACAGACGACGACCT 3626  
Db 3307 GATATAATTAAGACAGAACTGAATCATAGAGCATGCTCTTGACAGACGATGATCT 3366  
QY 3627 GCCAGCTTAATCTCATATGCTAGCCATAGAAATGCAACCATTCAGAGACGACGACAG 3686  
Db 3367 GCCAGTAAAGTCTTATGAGAGTCAACAAGATCCCTCTTCMAAGAGAAAGCCACAA 3426  
QY 3687 GCGACGCGCGAGACGATGAGAGGCGAGAGAGACGCGACGAGCAAGAGGATTTAGT 3746  
Db 3427 GCGACGCGCGAAACGATGAGAGGCGAAAGAAAGCTGACGTCAGACAGAGACCTTAGA 3486  
QY 3747 CTGACAGAGAACTGAGACGAGAGGCGAATGCGAGAGGCGCTGACGCTGATATC 3806  
Db 3487 ATTATGAAAGCTTAGAGATGAGTGCATGCGAGAGGCTCCATTGATGAGCAACTG 3546  
QY 3807 ATTATGATGACACGAGAGATATCTCATGATGAATTCAGAGCTATTTGCTCCCGCAT 3866  
Db 3547 ATCATCCAGCGCGACGAGAGCAAGCTGATGAGAGCTCACACGAGCGAGCTGTTGCCGAC 3606  
QY 3867 TCGTACTATAAGAAATTTCCGATCTTAGCCGTCGATGACGTCGCGCTTCTGCAAGA 3926  
Db 3607 AATTGCTACAAAATTTCCGCTCTGCGACGAGGACGACGATGCCATTTCTGCGAGGCG 3666  
QY 3927 TGGGCAATTTACGATGAAAACTTTTCAATTAATTGAAAAATTAATTTTGAACAGCT 3986  
Db 3667 TGGGCAATTTGCGACTGAAAACTTTTCACTCATCGAAGCAAGTACTTTGAGACGCGC 3726  
QY 3987 GTTATCACTATGATTTTAAATGATGCTTAGCTTTGCAATTAAGAAATGATGCTGCA 4046  
Db 3727 GTTATCAAGATGATTTGCTAGATGATTTGCTGCTGCTGAGAGATGCTATTCCTCC 3786  
QY 4047 CAAGAACCCTACTGACGAGATATTTTATATATGACAGAAATTTTACGCTATATTC 4106  
Db 3787 CATGACCAATCTGCGAGAGCTCTGATCAATGACAGATATTTCAAGGATATTTT 3846  
QY 4107 TTTCTGAAATGTTAATCAAGTGTGCGCTGCGCTTCAAAAGTATCTTCAACAACGCG 4166  
Db 3847 TTTCTGAGATGTTAATCAAGTGTGCGCTGCGCTTTTCAAGTTTACTTTACGAAGCGC 3906  
QY 4167 TGTGTTGCTGCTGATTTGCTGATTTGCTATGCTATGCTTATCAACTTGTGCTTCACTT 4226  
Db 3907 TGTGTTGCTGCTGATTTGCTATGCTATGCTATGCTTATCAACTTGTGCTTCACTC 3966  
QY 4227 GTTGAAGCTGTGATTTCAAGCTTCAAGACTATGCAAGCTTAAGAGCACTGAGACCA 4286  
Db 3967 TGTGAAGCTGTGATTTCAAGCTTCAAGACTATGCAAGCTTGAAGCACTGAGACCG 4026  
QY 4287 CTACGTCATGTCCTCGTATGCAAGGCAATGAGGCTGCTGTTAATGCGCTGATCAAGCT 4346  
Db 4027 CTACGTCATGTCCTCGTATGCAAGGCAATGAGGCTGCTGTTAATGCTGATGCTGACAGCT 4086

QY 4347 ATACGTCATCTTCAATGCTATGCTGCTGCTAATTTTGGCTAATTTTGGCTAATTTTGGCTAAT 4406  
Db 4087 ATACGTCATCTTCAATGCTATGCTGCTGCTAATTTTGGCTAATTTTGGCTAATTTTGGCTAAT 4146  
QY 4407 ATGGGTGACAGCTTTTGTGCGAAAAATTTTAAAGTGCAGAGCATGATATGCGACAG 4466  
Db 4147 ATGGGTGACAGCTTTTGTGCGAAAAATTTTAAAGTGCAGAGCATGATATGCGACAGAGCATG 4206  
QY 4467 CTCAGCAAGATCATCAAAATGCAATCTGCGAGAGCGAGAACTACAGCTGGTG 4526  
Db 4207 CTGTGCAAGATCATCTCCGATGTAACCGTGGCGCTGAGAACTACAGCTGGTG 4266  
QY 4527 AATTCAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4586  
Db 4267 AACTGCGGATGAACTTGACACAGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4326  
QY 4587 ACTTCAAGAGCTGATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4646  
Db 4327 ACGTTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4386  
QY 4647 CAACCAATGCTGAAACGACATCTAATGATTTATTTATTTATTTATTTATTTATTTATTTAT 4706  
Db 4387 CAGCGATTCGCGAGACCAACATCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 4446  
QY 4707 GGATCTTTTCAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4766  
Db 4447 GGATCTTTTCAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4506  
QY 4767 AAGAAAAAGAGGTGATCATTAAGAAATGTTCAAGAGAGATGAGAGAAAGTACTAT 4826  
Db 4507 AAGAAAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4566  
QY 4827 AATGCTATGAAAAATGAGGCTCTAATAAACATTAAGCAATTCAGACCAAGGTG 4886  
Db 4567 AAGCCATGAAAAAGTGGCTGCAAGAGCGCTGAAAGCTATTCACGCGCTAGGTGG 4626  
QY 4887 CGACCAAGAGATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4946  
Db 4627 CGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4686  
QY 4947 TTATTTATGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5006  
Db 4687 TTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4746  
QY 5007 TATAAGCGGCTCTGAGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 5066  
Db 4747 TTACGCGGCTGCTGAGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 4806  
QY 5067 CTATTAATAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5126  
Db 4807 CTGATGAAGATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4866  
QY 5127 GTATAGTGTGCTATTTATCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 5186  
Db 4867 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4926  
QY 5187 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5246  
Db 4927 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4986  
QY 5247 CTGATGAAG 5306  
Db 4987 CTGATGAAG 5046  
QY 5307 GCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5366  
Db 5047 GCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5106  
QY 5367 ATGCTGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5426  
Db 5107 ATGCTGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5166  
QY 5427 ACCTTTGGCAGAGCATGATCTGCTCTTCAAGATGCGAGCTGAGCGGCTGGAGTGT 5486







Db 4191 CGAGATCATTCGGATGTGAAACGGCTGGTGGCGGAGAACTACACGTGGAGAACTCCCC 4250  
 Qy 4535 AATGAATTCATCATCTGTAAGTAAACGGATCTGTGCTTTTCCAACTGGCCACTTCAA 4594  
 Db 4251 GATGAATTCACCAACGTGGGAAAGCGTACTGTGTCTGTTCCAGGTGGCAACGTTCAA 4310  
 Qy 4595 AGGCTGGATAGAAATCATGAAGATGATGATTCAGAGAGGGTGGCAAGCAACCAAT 4654  
 Db 4311 GGGCTGGATCCAGATAGAAAGATGCAATGACTCGGGAGGGTGGCAAGCAACCAAT 4370  
 Qy 4555 TCGTGAAGCAACATCTACATGATTTATTTATTTCTGATCTTCATCATATTTGATCTT 4714  
 Db 4371 TCGGAGACCAACATCTACATGATCTTACTGTTCTTCATCATCTTCCGCTT 4430  
 Qy 4715 TTTCACTCATCTGTTCTGTTCTGTTGTTATTTATTTATTTAAATGCAAGAAAA 4774  
 Db 4431 CTTCACCTCAACCTGTTTCATCGGTGTCATCATCAACCTTCAACGAGCAAGAAAA 4490  
 Qy 4775 AGCAGTGGATCATTAAGAAATGTTTCAATGACAGAAAGATGCAAGAAAGTACTAATGCTAT 4834  
 Db 4491 AGCGGTGGCTCGCTGGAAATGTTTCAATGACAGAAAGTCAAGAAAGTACTAAGCAAT 4550  
 Qy 4835 GAAAAAGATGGGCTCTAAAAAACCAATTAAGCCATTCAGAACCAAGGTGGCGACCA 4894  
 Db 4551 GAAAAAGATGGGCTCGAAGAAAGCGGTAAAGCTATCCCTGGGCTAGGTGGCGACCA 4610  
 Qy 4885 AGCAATAGTCTTTGAAATAGTAAACGATTAAGAAATTCATATATCATTTATTTATTCAT 4954  
 Db 4611 AGCAATAGTATTCGAAATAGTAAACGATTAAGAAATTCATATATCATTTATTTATTCAT 4670  
 Qy 4955 TGTGTCGAACATGTTTCAACATGACCCGTGATCGTTAGATGGGTGGACAGATTAAGC 5014  
 Db 4671 CGGGTTCAACATGTTGACATGACGCTGATCATCAAGACAGACGAGACGTTCAAGTGC 4730  
 Qy 5015 GGTCTAGATCATCTCATGCGATTAATGATTTATTTTCAATTCAGATGCTATTAATA 5074  
 Db 4731 GGTCTAGATCATCTCATGATTAATGATTTATTTTCAATTCAGATGCTATTAATA 4790  
 Qy 5075 AATATTCGCTTTAGATATCACTATTTTATTTAGACCATGAATTTATTTATTTATTTAT 5134  
 Db 4791 GATATTCGCTGGGTGACCACTACTTCATCAACCGTGAACCGTTCGATTCGATTCG 4850  
 Qy 5135 TGTATTTTATCATCTTAAATGTTTCTGATAGGATTTATTCAGAGATCTTCGATTC 5194  
 Db 4851 GGTATCTGTCATTTTAAATGTTTCTGATAGGATTTATTCAGAGATCTTCGATTC 4910  
 Qy 5195 GCCACCTGCTCCGAGTGTGCGTGTGGCGAAAGTGGCGGCTCTTCAGATGTTGAA 5254  
 Db 4911 GCCACGTTGCTCCGAGTGTGCGTGTGGCGAAAGTGGCGGCTCTTCAGATGTTGAA 4970  
 Qy 5255 GGGAGCCCAAGGCAATTCGACATGCTCTTTCGCTGGCATGTCGCTGGCGGCTGTT 5314  
 Db 4971 GGGGCGCAAGGATTCGCAAGTGTGCTGTTGCGTGTGGCGCATGTCGCTGGCGGCTGTT 5030  
 Qy 5315 CAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5374  
 Db 5031 CAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5090  
 Qy 5375 CTTCATGCACTGTAAGAGAAAGACGCGCATTAAGACGCTTCAACATTCAGACCTTTGG 5434  
 Db 5091 CTTCATGCACTGTAAGAGAAAGACGCGCATTAAGACGCTTCAACATTCAGACCTTTGG 5150  
 Qy 5435 CCAAGACATGATCTGCTCTTTCAAGATGTCAGCTCAAGCCGTTGGATGGTGTACTGGA 5494  
 Db 5151 CCAAGACATGATCTGCTCTTTCAAGATGTCAGCTCAAGCCGTTGGATGGTGTACTGGA 5210  
 Qy 5495 CGCCATTTCAATGAGAAAGATGATCAACCGGACGAGCAAAAGGCTATCCGGGCAA 5554  
 Db 5211 CGGATTCATCAACAGAGCAAGTCTGCTCCCGGATTAAGACAGAGGTTTACCTTGGGAA 5270  
 Qy 5555 TTGTGTTCAAGCAACGTTGGAATTAAGTTTCTCTCATACCTAGTTATTAAGCTTTT 5614  
 Db 5271 CTGCGGGTGGCTAGATCGGATCAAGTACTTGTGTAAGATCTTGTATTAAGCTTTT 5330

Qy 5615 GATAGTTATTAATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5674  
 Db 5331 GATGTTATTAATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5390  
 Qy 5675 GGTGCAAGAGGTTTAAACCGACGACGACTACGATGATGATGATGATGATGATGATGATGATGAT 5734  
 Db 5391 GGTGCAAGAGGTTTAAACCGACGACGACTACGATGATGATGATGATGATGATGATGATGATGAT 5450  
 Qy 5735 CGATCCGAGGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5794  
 Db 5451 CGATCCGAGGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5510  
 Qy 5795 GGAAGCCCGCTGCAAGATCCCAACCGAACAAGTACAAGTACATATGATGATGATGATGATGATGAT 5854  
 Db 5511 GGAACACCGCTGCAAGATCCCAACCGAACAAGTACAAGTACATATGATGATGATGATGATGATGAT 5570  
 Qy 5855 CATCTGTCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5914  
 Db 5571 CATCTGTCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5630  
 Qy 5915 CTTTCCGAGGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5974  
 Db 5631 CTTTCCGAGGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5690  
 Qy 5975 CCGGATTAAGAGGCTTACAGACCGCTCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6034  
 Db 5691 CCGGATTAAGAGGCTTACAGACCGCTCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5750  
 Qy 6035 CTTGCGCCGCTTATTCAGACGCTGCGCAACCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6094  
 Db 5751 CTTGCGCCGCTTATTCAGACGCTGCGCAACCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5810  
 Qy 6095 GTCTTTGAGCCGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6154  
 Db 5811 GTCTTTGAGCCGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5864  
 Qy 6155 GCCCGATGAAGCAACCGACCGGATGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6214  
 Db 5865 TGTGTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5924  
 Qy 6215 TGCAGAGAGAGCTGCGCAT---GCCGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 6271  
 Db 5925 AGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5984  
 Qy 6272 AGCGCGCGCGCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 6331  
 Db 5985 TTTCAAGGCTTAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6044  
 Qy 6332 TCCCGAGAGCGGTTAGCGCCGCGGCAACGACCGGCTTCTGCTGAGAGACGACGCGGTTCT 6391  
 Db 6045 TGGCAATTAATGATCTTCAAGGCGCTCAACGCGCGCTCTGATTAAGATGATGATGATGATGAT 6104  
 Qy 6392 GACGAGAGAGCGGCAACGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6451  
 Db 6105 AACTTAAGAGGTTAGCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6164  
 Qy 6452 GGCAGATGTTGACGACGAGGCTGCGCCCGCTTCAAGATGCA 6494  
 Db 6165 GGCAGATGTTGACGACGAGGCTGCGCCCGCTTCTGATTTCA 6207

RESULT 14  
 BGU73584  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BGU73584 6096 bp mRNA linear INV 19-MAR-1997  
 Blatella germanica para sodium channel mRNA, complete cds.  
 U73584.1 GI:1657985  
 Blatella germanica (German cockroach)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Orthopteroidea; Dictyoptera; Blattellaria; Blatelloidea;



[illegible]

QY	2301	GATGCGGTGTCTCCGTTTACTATTTC	CCAA	CAGAGACGATGACGAGATG	GGCCGACG	2360
Db	2173	GAAATGGAAGCTCCATCTATTATTTC	CCGACAGACGAAATGACGAG	---	GGTCCAA	2229
QY	2351	TTCAAAGCAAGGCACTCGAAGTACT	CTCAAAGGATCGATGCTTTTGTGTGG	AGAC		2420
Db	2230	GTTAAAGGAAGGCTGTAGCTATATG	TATGATCGAAGATTCACATCTTCTG	CTGCTGATG	GGAT	2289
QY	2421	TGTTGCTGGGTTTGTTGAAATTTCA	GGAGGATACGCTACGCTTCGATCC	CTTC		2480
QY	2230	TGTTGCTGGCTCTGCTGCTCACTT	CCAGAAATAGTCCGCTCTTGTGTT	GAACCCCTT		2349
Db	2481	GTCGAGCTCTTCATCAGCGCTGTG	ATGCTGTCACGATGTTCAAGCATG	GAATGGAATGAT	CAC	2540
QY	2350	GTCGAGTTGTTCAATCACCTTTG	CACTTGTGTGCTAATACATGTT	CATGGCCCTCGACAC		2409
Db	2541	CACGATATGAACAAGAGATGGAAC	GGGTGCTCAAGATGGAACATATTT	CTTCAACGCGC		2600
Db	2410	CACGACATGATTAAGACATGGAAT	AGAGCTCTCAAGATGGAACATATTT	CTTCAACGCGC		2469
QY	2601	ACCTTTGCGATCGAGGCGCACCAT	ATAGCTATAGGCGCATAGGCCCA	AGTACTATTTCCAG		2660
Db	2470	ACCTTTGCGATTTAGGCGGACGCT	CATAGTTGATGACATAGACCTTA	AGTACTACTTCCAG		2529
QY	2661	GAGGCGTGGACATCTTTCGACTTC	ATATCGTGGCCCTATCGCTATTTG	GAACCTGGGACCTC		2720
Db	2530	GAAAGATGAACATTTTGTGATTT	CATCATTTGTCATCTTCTGTG	GAATAGGGCTT		2589
QY	2721	GAGGCTGCCAGGCTCTGTCCGTA	TGCGTTCCCTTGATGCTGCTGTAT	CAAACTG		2780
Db	2590	GAAAGTGTCCAAAGGTCTGTCCG	CTCCGATCGTTCAGATTTGTTGA	AGGCTTCAAACTT		2649
QY	2781	GCGAAGCTTGAGCCACACATTA	ATTATCTCATTTGATTAAGGA	CGCACATAGGGCGCT		2840
Db	2650	GCGAAGCTTTGAGCCAGAGCTGA	ATCTCTCATATTCATAGGGTAAC	CTTGTGTGCT		2709
QY	2841	TTGGGTATCTGACATTTTGTACT	TTTGATTAATCATCTTTCGATG	AGATGAGGATG		2900
Db	2710	CTGGGTAACTGACCTTTGTGCTT	TGTATATCATTTTCACTTTG	CCGTCAAGGGATG		2769
QY	2901	CAACTGTTGGAANAATATATCAT	GATCACAGAGCCGCTTTCGATG	AGCGACCTGCGC		2960
Db	2770	CAACTTTTGGCAAAATATATAT	ATGATTAATGTTGAAGTGTTC	CCGACGAGGATATG	CCG	2829
QY	2961	CGCTGGAATCTCACCCGACTTT	ATAGACAGGCTTACATGATCG	GTGTCGGGTGCTGTGGA		3020
Db	2830	AGATGGAACCTTACGAGCTTCA	TGACATCATATGATTTGTTC	CGAAGTGTGTGCGG		2889
QY	3021	GAATGGAATCGAGTCATGTGGG	ACTGACATGATGAGGGGACATG	CTCGTSCATTTCCCTTC		3080
Db	2880	GAGTGAATAGAGTTATGTGGAG	ATTGATGCTTGTGGAACCTGTG	CTGCAATCCGCTTC		2949
QY	3081	TTCTTTGGCAACGTTGTCTAT	CGCAACTTGTGGTACTTAACCT	TTTCTTAAGCCTTGCTT		3140
Db	2950	TTCTTTGGCACTGTGCTCATTT	GAGAACTTGTGTGTGAAACCT	CTTCTTGAGCCTTGCTG		3009
QY	3141	TTGTTCAAATTTTGGCTCAT	TAGCTTATACGCGCGCATCTG	CCGATTAACGATATAA		3200
Db	3010	CTGACGAACCTTTGGTTATCT	CAATCTGTGAGCCCAACAGCT	CAATATGAAACCAACAG		3069
QY	3201	ATATCCGAGGCGCTTCATTCGA	ATTGGCGGATTTAAAGTTGG	GGTTAAGCGGTATATTTGCT		3260
Db	3070	ATTGCTAGGCAATTTGAGCG	TTTCTCAAGATTTCTTTA	CTGATTAAGCGTATAGCGGCTTA		3129
QY	3261	GATTGTTTCAAGTTAATACG	TAAACAATATGCAATCAATCA	AGATCAACCATCAAGT		3320
Db	3130	AAAGTGGCAAAATATGTTG	CGTCAAAATTAACCAATCA	AGTATCCGATTCAGACG	CAAGAT	3189
QY	3321	GAGAGACCAACCAAGATCA	GTTGATTTGGAGGGAAGAG	ATGCTGACCAACATCTG	AG	3380
Db	3190	GCCC-----ATGAGG	TATACAGACCTTTGAC			3216

QY 3381 CTGGCCACAGCAGATCTCTCCGACGCGCTCAT-----CAAGAGGGGATCAAG 3431  
|||  
Db 3217 CTCACAGCGGATGAATCTCTGGCCGATGGAATCTGTATATAGACAAAGAGGTCCAAAG 3276  
QY 3432 GAGCAACCGCACTGAGAGGTGGCCATCGGGGATCGGATGGAATTCAAGATACAGCGGAC 3491  
3277 GAGCAACCGCACTGAGAGGTGGCCATCGGGGATCGGATGGAATTCAAGATACAGCGGAC 3336  
QY 3492 ATGAACAACAACAGCCGAGAAATCCAAATATCTAAATACGCAACGATGATGGCAAC 3551  
3337 CTGAAAAACAGGTGAAGAAAGCAAGCTGATGATGAACGACGAAAGGTGATCGCAAT 3396  
QY 3552 TCAATTAACCAACAAGACAAATAGACTGGAACAGACTAAACATAGAGTTTGTCTTA 3611  
3397 TCTTTAATCATTAAGACCAATCGAATGAAAGTGTGACTATCTACAAATCGG----- 3450  
QY 3612 CAGAGACGACACTCGCAGCACTTAACTCATATGATGACCAATGAAGTCAACCATTCAG 3671  
3451 CAGAGACGAGATCTTTGAGCACAAGGCTCATATGAAAGTCAAAAAACCTCCATACAAAG 3510  
QY 3672 GACGAGACCAACAGGCGACGCGCAGACGATGAGAGGCGAGAGAGCGCAGCGCAGC 3731  
3511 GATGACGCAATAGGGAAGTGCAGAGACTATGATGAGGAGGAGAAAGATGCAAGC 3570  
QY 3732 AAGGAGATTTAGTCTCGACAGAGAACTGGAACGAGAGGCGCAATGCGAGAGGCGCG 3791  
3571 AAGAGATCTCATCAAG 3630  
QY 3792 CTGACGAGTATATCATTTATTCATGACACAGCAGAGATATCTCATGATATTCAGCT 3851  
3631 GAGAGACAGATGATGATGATGATGACAGGCACTGAGGACGTATGATGATGATGATG 3690  
QY 3852 GATTGCTCCCGGATTCGTAATAGAAATTTCCATCTTACCGGTGACGATGCTG 3911  
3691 GATGCTGCTCTGATCACTGCTATAGCGCTTCCCTTCTGCTGAGAGAGAGCTCT 3750  
QY 3912 CCGTTCGAG 3971  
3751 CCGTTCGAG 3810  
QY 3972 TATTTGAAACAGCTGTTATCATATGATTTTAAATGATAGCTTACCTTGGCATAGAA 4031  
3811 TACTTGAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3870  
QY 4032 GATGATCATCTGCAACAAAGACCATACTGAGAGATTTTAACTATATGACAGATA 4091  
3871 GATGATCATCTGCAACAAAGACCATACTGAGAGATTTTAACTATATGATGATGATG 3930  
QY 4092 TTTAGGTTATATCTTCTGGAATGTTATCAAGTGTGGCGCTCGCTTCAAGTG 4151  
3931 TTTAGGTTATATCTTCTGGAATGTTATCAAGTGTGGCGCTCGCTTCAAGTG 3990  
QY 4152 TACTTCAACAACGCGTGTGTGTGCTCGATTTGCTGATTTGCTGATGCTGCTTATCAC 4211  
3991 TACTTCAACAATGCTGTGTGTGTGCTGATTTGCTGATTTGCTGATGCTGCTTATCAC 4050  
QY 4212 TTTGTTGTTTCACTTGT 4271  
4051 TTTGTTGTTTCACTTGT 4110  
QY 4272 AGAGCACTGAGACACTGCTGCAATGCTCCGTAATGACAGGCGATGAGGCTGCTGTAAT 4331  
4111 AGGCGCTTAAAGCTCTTAAAGGCTATGCTTAAGATGACGAGGAGTGAAGGCTGTAAC 4170  
QY 4332 GCGCTGTACAACTATACCGTCCATCTTCAATGCTGCTATGCTGCTGCTGCTGCTGCT 4391  
4171 GCTTGTGTGCAAGCCTCCAGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4230  
QY 4392 CTAATTTTGCATATAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4451  
4231 CTCACTTTTGCATATAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4290  
QY 4452 ATGATGACAG 4511

Db 4291 TCCAACTTACCACTTTTGAAGCAGCAATATCATTTCTGACAGAAATGCTGATGCTGAA 4350  
QY 4512 AACTACAGTGGTGAATTCAGCAATGAATTTGATCATGTAGTAAAGCTATCTGTGC 4571  
4351 AACTACAGTGGTGAATTCAGCAATGAATTTGATCATGTAGTAAAGCTATCTGTGC 4410  
QY 4572 CTTTTCAGTGGGCACTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4631  
4411 CTTTTCAGTGGGCACTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4470  
QY 4632 CGAGAGTGGACAAACCAATTCGTGAAACGAACTCTACATGATATTTATTTGCTA 4691  
4471 AGAGAGCTCAATTAACAGCAATGAGGAAACGAACTCTACATGATCTTCTGCTG 4530  
QY 4692 TTTCTCATATATTTGATCTTTTTCACCTCACTCACTCACTCACTCACTCACTCACTCACT 4751  
4531 TTTCTCATATCTTTGCTGCTATTTTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4590  
QY 4752 AATTTTAAATGACCAAAAGAAAAAGAGGTGATCATTAAGAAATGTTGATGACAGAGAT 4811  
4591 AACTTTAATGACCAAAAGAAAAAGAGAGGCTGCTTAAGATGTTTATGATGATGATGAT 4650  
QY 4812 CAGAAAAAGTACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4871  
4651 CAGAAAAAGTACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4710  
QY 4872 CCAAGACCAAGTGGCGACCAAGCAATATGCTTTGAATGTAACGATTAAGAAATTC 4931  
4711 CCAAGACCAAGTGGCGACCAAGCAATATGCTTTGAATGTAACGATTAAGAAATTC 4770  
QY 4932 GATATATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4991  
4771 GATATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4830  
QY 4992 GATGCTGCGACAGTATAGCGGCTCTAGACTATCTCAATGCGATATTCGATGATGAT 5051  
4831 CAACAGTCCAGAGAGTCCAGCAGCAGCTTCTGATGATGATGATGATGATGATGATGATGAT 4890  
QY 5052 TTTAGTTCCGAATGCTATTAATAAATTCGCTTACATGATGATGATGATGATGATGATGATGAT 5111  
4891 TTTAGTTCCGAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4950  
QY 5112 TGGAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5171  
4951 TGGAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5010  
QY 5172 ATTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5231  
5011 ATTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5070  
QY 5232 GGCAGTGTCTTGCATGCTGAG 5291  
5071 GGCAGTGTCTTGCATGCTGAG 5130  
QY 5292 GGCATGCTGTGCGGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5351  
5131 GCTATGCTTGTGCAAGGCTCTTCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5190  
QY 5352 TTTGCACTTTTGGGAGTGTGCTTCAATGCAAGTAAAGGATGAGGCTGATGATGATGATGAT 5411  
5191 TTTGCACTTTTGGGAGTGTGCTTCAATGCAAGTAAAGGATGAGGCTGATGATGATGATGATGAT 5250  
QY 5412 GTCTACAACTTCAAGACCTTTTGGCAGAGAGATGATGATGATGATGATGATGATGATGATGAT 5471  
5251 GTCTACAACTTCAAGAGCTTTTGGCAGAGATGATGATGATGATGATGATGATGATGATGATGAT 5310  
QY 5472 GCGGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5531  
5311 GCTGAT 5370  
QY 5532 AGGAGCAAGAGCTATCGGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5591



QY	384	GGAAAGATATATTTTGGCTTTCTTGCAATCAAAAGCAATGGATGCTGATTCATTCAAT	443
Db	325	GGAAAGATATTTTCCGGTTCAAGTGGCAAGAGCCATGGATTTTGGACCATTCAC	384
QY	444	CCGATAGGTGGTGGCCATTTCATCTATGATGATCCATCAATATTTCCATATTCATC	503
Db	385	CCGATTCGAGGGTGGCCATCTACATTTTGGTTCACCCTTGTTCTCACTTCATCAAT	444
QY	504	ACCACAATTCGTCAACCTGCATCTCGATGATATATGCGCAACGGCCACGGTTAGTCC	563
Db	445	ACCAACATTTTAAACAACCTGCATCTTCATCATCATGATGATCAACACCCCAATATAGTCC	504
QY	564	ACTAGGTGATATCAACCGAAATCTACATTTTGAATCAAGCTGTATTAAGTATGGACGA	623
Db	505	ACTAGGATTAATTTTACTGGCATCTACACATTTTGAATCGGCGTTTAAAGTATGGGAAA	564
QY	624	GGTTTCATTTTATGCCCCGTTTACGTATCTTAGAGATGCAATGAAATGGCTGATCTGTAT	683
Db	565	GGTTTCATTTACTCAGCCATTTCAAGTACTTAGAGATTCATGAACTGGCTGGACCTTCGTAT	624
QY	684	GTAATAGCTTTAGCTTATATGACCAATGGGATATGATTTAGTATATAGAGAGCCCGGCA	743
Db	625	GTAATAGCTTTAGCTTACGTAACTATGGGATGATTTAGAAACCTGGCGGCTTTGCCA	684
QY	744	ACGTTTGGGGTGTGCGAGCGCTTAAACCGTATGACCATTTGTGCGAGGCTTGAAGACATC	803
Db	685	ACGTTTGAAGGTGTCTCCAGCTTTGAAGACGTGTCTATTTGTTCAGGTTTGAAGACATTT	744
QY	804	GTCGGCGCGTCATCGAATTCGTTGAAGATATTTGGCGCATGTGATATATCCGACCATGTC	863
Db	745	GTTGGCGCTGTGATTTGAATCTGTAAAGAACTCGGCGATGTGATATCTCCACCATGTTC	804
QY	864	TCCGCTGCGGTGTGCGCTGATATGGGCTACAGATCTATATATGGCGCTCACCGAAG	923
Db	805	TGCTCTCTCGTGTTTGCTTTATATGGGGTCCAGATTTAATAGGGTGTCTCACGCAAG	864
QY	924	TGCATCAAGATTTCCGCTGAGCGTTCTGTGGGCAATCTGACCGACAGAACTGGGAC	983
Db	865	TGCATCAAAAATTTCCCATTAATATGTTTCATGGGGGAAATTAATATGATGAATCTGCAT	924
QY	984	TATCAATTCGCAATAGCTCCAAATGTGATTTCCGAGACGAGGCGATCTCATTTCCGTTA	1043
Db	925	GCAATTTTGCATGTAACAACAACATCTGTACTTTCCGAAAGGTGACACAAAGTTCCACTG	984
QY	1044	TGCGCAATATATTCGGTGTGCGGGCAATGCAACGACTTATGTTGTGCTGCGAGGGTTT	1103
Db	985	TGTGGGAATTCATTCAGAGAGCTGTGTCAATGTCACCTGATTAACAATGTCTCCAGGGCTTT	1044
QY	1104	GGTCCGAATCCGAATTAATGGCTACACAGACTTCGATTTGGTCCGAGTGGGCTTTCCTGTC	1163
Db	1045	GGAGAAATTCACACATATGTTTACACAGATTTCAATAGTTTGGTTGGGACTTCCTCTCG	1104
QY	1164	GCCTTCCGGCTGATGACACAGACTTCTGGAGAGATCTGTACCAAGCTGTGTGGCGGCC	1223
Db	1105	GCCTTCAGCTGATGACCCAGGATTTATGGAGAACTTTATCAGCTGTGTATGAGATCT	1164
QY	1224	GCGCGACATGCAATGTGTCTTTTATGATCAATCACTTCCTAAGGTCAATTTATCTT	1283
Db	1165	GCTGGGCGCTGCAATATGCTGTCTTCATGTGCATCACTTCTTAAGCTCAATCTAATCTT	1224
QY	1284	GTCATATTTGATTTGGCCATTTGTCCCATGTCGATGCAATTTGCAATTTGCAAGAGCCGAA	1343
Db	1225	GTCATATTTGATTTGGCCATTTGTCCCATGTCGATGCAATTTGCAATTTGCAAGAGCTGAG	1284
QY	1344	GAGGAAGAGCTGCGCAAGAGAGGCGATATCTGAAGGGAAGAAAGCTGCCCGCCAAA	1403
Db	1285	GAGGAAGAGAGCTGCGCAAGAGAGGCTTGAAGGGAAGGGAAGAGCAGCTTGTCCGAAA	1344
QY	1404	GCGGCCAAGCTGGAAGAGGCGGCAATGCGAGGCTCAGGCGACGACGCGGATGCGGCTCC	1463
Db	1345	GAGGCGAAAATTTAAGACAAAGCGATTAATCTGGACGACAAAGATTTGACGACGACGACAA	1404
QY	1464	GCGGAAGAGGCTGCACTGCAATCCGGAATATGCGCAAGATCCGAGGTATTTCTTGATCAAGC	1523

Db	1405	GAAC	TAGCTGCGGCGCAAAATCTAGCAAAATCTCCCTCGGAAAGTTGCTCTGT-----AGT	1458
Qy	1524	TATG	ACTATTTTGTGTGCGCGCAAGAGGCAACGATGACAAACAACAAAGAGATGTCC	1583
Db	1459	TATG	ATTGTTATTAATATAAAAGACGGCAATATATGACAAACAAAGGAGAACTGAGC	1518
Qy	1584	ATTG	CGAGCGTCGAGGTGAGTTCGAGTCTGGTGAAGCTTATACAAAGACACACGACCT	1643
Db	1519	ATCC	GAGCGAAGGCGGGGACTCG-----ATAGCGCAACAAAGGA	1560
Qy	1644	ACCA	CGACACCAACCAACTTACCAAAAGTTCGTAAAGTAGACACACATCTTATCTTACCT	1703
Db	1561	AGAG	TGGGTGCAATATGTAACGGCGATCAGAAAGTATAGCGCGCAAGTTTGAAGTCAACA	1620
Qy	1704	GGTT	CAACCTTTAACTATGCGGATCAGAGGATCCCAAGTAGATCATCACTTTCAATTAGAAAC	1680
Db	1621	GGCT	CACTTTCAACCATCGCGGATCCCAAGGATCCCAAGTAGATCATCACTTTCAATTAGAAAC	1680
Qy	1764	GAG	CGTGGCCG---CTTTGGTATACCCGGTAGAGATTCGTAAAGCATGGTATTTGCAACA	1820
Db	1681	GGA	CGTGGAAAGTTCGTGGGCCCACTGGGTGATCGAAACCCCTAGTACTTTTAAAG	1740
Qy	1821	TATC	AGGATGCCAGACGACTTGCCCTATGCGAGACACTCGAATGCGTCACCCGATG	1880
Db	1741	TACT	CGATCCACAAAGAACATCTTCTTATGACAGATGACGTGCAATGCAATACACTATG	1800
Qy	1881	TCCG	AAGAAATGGGCGCATCATAGTGCCTCGTACTATAGGCACTTAAGCTTCCGACAC	1940
Db	1801	TCAG	AGAGATGGAGCAATGATGTGATACAGTTTATTAACGCGCCTCGGTTCCAGACAC	1860
Qy	1941	TCAT	CGTATACCTCGGACTCAAGTCCCGAAATATCGTATATCTCCATGCGCATCTTACTCGG	2000
Db	1861	TCAT	CTTATCATATACACGATCCAGATATCTTCAACGCTCTCATGGGAGCCTCGTGGGT	1920
Qy	2001	GGCA	TGGCCGTCATGGGCGTCAGACAAATGACCAAGAGACAAATTTGCGCAACCGCAAC	2060
Db	1921	G-----	CAGGCAACAAATCTCAAGCAACAGATCATGCACTGCGACGCTCGTTCA	1968
Qy	2061	ACAC	CGAATCATATAGTGGGCGCAACAAATGGGCGACCACTGTCTGACACCAATACAC	2120
Db	1969	GTTG	GCA-----CAACCTTCAAGTGTCTAATTTCAACACATATATGA	2014
Qy	2121	AAGC	TCATCGCGCACTACGAATTTGGCTGGAGTGCACGACGAAGCTGCGAAGATT	2180
Db	2015	ATGC	GTGACG-----GACAGTATGATGAGCGGTGAAGACA	2052
Qy	2181	AAAC	ATATGACATCTCTTTTATGAGCCCGTCACACACAAACCGGTGTGATATGAAA	2240
Db	2053	AAGCA	CACTGCAATCATATCTATTTGAACAAATGACGAACCTAACATTTGTTGATATGAAT	2112
Qy	2241	GATG	ATGATCGCTGATGATGATCATCATGAAACAGCGCTGGTGGCAACATCGGGCAAC	2300
Db	2113	GATG	TATATGATGATGATGATGATATATATGAAACACACTCTGGACGACGATGAGCCAGT	2172
Qy	2301	GATC	CGCGGTGTCTCGTTACTATTTCCCAACAGAGACGATGACAGAGATGGGCCGACG	2360
Db	2173	GAA	CACTGAGACTCCATCTATTTATTTCCCGACACACAAAGATGACAG--GGTCAACA	2229
Qy	2361	TTCA	AAAGCAAGCACTCGAAGTATCTCAAAAGGATTCGATGCTGTTTGTGTGGGAC	2420
Db	2230	GTTAA	AGGAAGGTGTATGCTATATGATATGAGAGATATCACAATCTTCTGGTGTGGAT	2289
Qy	2421	TGTT	CTGGTGTGTAATTTCAGAGTGGGATTCGCTCATGCTTCTGATCTCTTC	2480
Db	2290	TGTT	CTGGTCTGTGCTGCTCAAGTCCAAAGATAACGTGCGCCCTCTGTGTTTGAACCTTTT	2349
Qy	2481	GTCA	GCTCTTCAATACGCTGTGCAATTTGTGTCAACAGATGTTCAAGGCAATGATATAC	2540
Db	2350	GTTG	AGTTGTTTATACCTTTGCAATTTGTGTCAATATACCTGTTCAATGCCCCGACAC	2409
Qy	2541	CACG	ATATGAACAAAGATGGAACGCGTGTCTCAAGATGGCAATATTTCTTCAACGCC	2600

D 2410 CAGCAGATGATAAAGCATGATTAAGGCTCTCAAGGTGGCAACTATTTCTGACAGCG 2469  
Q 2601 ACCTTTGGCATGAGGCCCATGAGTAAATGGCCATGAGCCCCCAAGTACTATTTCCAG 2660  
D 2470 ACCTTTCGCAATGAGGCGACCTCAAGTGAATGACAAATGAGCCCTAAGTACTACTTCAG 2529  
Q 2661 GAGGGCTGGAAACATCTTGCATTTATGCGTGGCCCATGCGATTGGAACTGGGACTC 2720  
D 2530 GAAAGATGGAACATTTTGAATTCATATGTGACATTCCTTGGCGAAATGGGCTT 2589  
Q 2721 GAGGGTCCAGGGTCTGCTCCGATTTGGCTTCTTTCGATTTGCTGCGTATTCAACTG 2780  
D 2590 GAAAGTCCCAAGTCTGTCTGCTGATCGTTCAGATTTGTGAGAGCTTCAACTT 2649  
Q 2781 GCCAAGTCTGGCCCACTTAATTTACTCATTTTGGATTATGGAACGCAATGGGCGCT 2840  
D 2650 GCGAAGCTTGGCCGACGCTGAATCTGCTCATTTTCATCATGGGTAGAAAGTGTGCT 2709  
Q 2841 TTGGGTATCTGACATTTGTACTTTGATTCATTCATCTTTCATCTTGGGTATGGAATG 2900  
D 2710 CTGGGTAACTGACCTTGTGTGTGTATTAATTCATCTTTCATCTTGGGTATGGAATG 2769  
Q 2901 CAACGTTCGGAAGAAATTAATCATGATCAAGGACCGCTTTCGGAATGGACCTGCG 2960  
D 2770 CAACCTTTGGCAAAATTAATTAATGATTAATGTAAGCTTTCCTGACGGGATATGCG 2829  
Q 2961 CGCTGAACTTACCGACTTTATGCAAGCTTCATGATCGTGTTCGGGTCTCTGCGGA 3020  
D 2830 AGATGGAATTTAGGACTTCATCATCTCATGATGATGTGTCCGAGTGTGCGG 2889  
Q 3021 GAATGATCGAGTCAATGTGGGACGTCGATGATGCGGCGATGTCTGTGATCCCTC 3080  
D 2890 GAGTGAATGAGTCTATGTGGGATTTGATGTCTTGTGAGACTGTCTGTGATCCCTC 2949  
Q 3081 TTCTTGGCCACCGTGTATCGCAATCTTGTGATCTTAACTTTTCTTACCTTGTCT 3140  
D 2950 TTCTTGGCCACGTCGTATGGAACCTTGTGTGTGAACTTCTTCTTGTGCTTGTG 3009  
Q 3141 TTGTCCAAATTTGGCTCATCTAGCTTATCAGCGCGACGTCGCAATACGATACGAATAA 3200  
D 3010 CTCGCAACTTGGTATCAATCTGTCAGCCCAACAGCTGACAAATGAAACCAACAG 3069  
Q 3201 ATAGCGAGGCTCAATCGAATGGCCGATTTAAAGTTGGGTAAAGCGTAATATGCT 3260  
D 3070 ATAGCTAGGATTTGAGCGTTCTCAAGATTTCTTAACTGGAATAAACGTAAGCGCTA 3129  
Q 3261 GATTGTTCAAGTAAATAGTAACAAATTTGACAAATTAAGTATCAACATCAAGT 3320  
D 3130 AACGTGGCAAAATGTTGCGTGCCTAATTAACATGATTCGATCAGACCGCAT 3189  
Q 3321 GAGAGACCAACAGATCAATGATTTGAGCGAAGAGATGTGACAAAGAACTGGAG 3380  
D 3190 GCC-----ATGAGCTGACACGCACTTGAC 3216  
Q 3381 CTGGGCCACAGAGATCTTCCGACGCGCTCAT-----CAGAAGGATCAAG 3441  
D 3217 CTCACACGAGTAATCTTGGCGATGGAATCGTATATAGACAAGAAAGATGCAAG 3276  
Q 3432 GAGCAGACGCACTGAGAGTGGCCATCGGGATCGATGGAATTCAGATCAAGCGAC 3491  
D 3277 GAGAGACGAGTGGAGAGTGGCGATAGAGATGGAATGAGTTCAACATCAAGAGAT 3336  
Q 3492 ATGAGAACCAAGCCGAGAAATTCAAATATCTAAATACGCAAGATGATGGCAAC 3551  
D 3337 CTGAAACCAAGCTGAAAGAGCAAGCTGATGTAAGCAAGAAAGTATGGCAAT 3386  
Q 3552 TCATTAACCAAGCAATAGACTGGAACAGAGCTAAACATAGAGTTTCTCTTA 3611  
D 3397 TCTTGAATCTAATAGCAATCGATAGAAAGTGTGATCTATCTACAAATCGG----- 3450  
Q 3612 CAGAGCAGCAGACTGCGACATTAATCAATATGATGATGATGATGATGATGATGATGAT 3671  
D 3451 CAGAGCAGGATATCTTTGAGACAGGGGTCAATATGGAAGTCAAAAAACCGTCAATCAG 3510

Q 3672 GACGAGCCCAAGGGCAGCGCCGACGATGGAAGGCGGAGAAACCGGACCGCAC 3731  
D 3511 GATGACGCCAATAAGGAGAGGACAGACTATGATGGGGAGGAAAGAAAGATGCAAGC 3570  
Q 3732 AAGAGATTTAGGCTCTGACGAGGAACTGGAACGAGGAGGCGAATGAGAGGAGCGC 3791  
D 3571 AAGAGATCTCATTAAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3630  
Q 3792 CTCACGATGATATCATTAATTCATGACACAGCAGAGATTAATCTCATGATTAATCA 3851  
D 3631 GAGAGGACATGATTAATGATGAGGACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3690  
Q 3852 GATTGCTGCCCGATTTGATTAATGAAATTTCCATCTTACCGGAGGAGGAGGAGGAG 3911  
D 3691 GATTGCTGCTGATTAATGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3750  
Q 3912 CCGTTCTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3971  
D 3751 CTTTCTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3810  
Q 3972 TAATTTGAAACAGCTGTTATCATATGATTTTAATGATGAGCTTACCTTGGCATTA 4031  
D 3811 TACTTGAACGCTGTGATCAGATGATCTGCTTACGATCTGACGAGGAGGAGGAGGAG 3870  
Q 4032 GATGATCATCTGCAACAAAGCCATCTGAGGATTTTATTAATTAATGAGGAGGAG 4091  
D 3871 GATGATCATCTGCTCATGACCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3930  
Q 4092 TTACGTTATATCTCTTGGAAATGTTAATCAAGGAGGAGGAGGAGGAGGAGGAGGAG 4151  
D 3931 TTACGTTATATCTCTTGGAAATGTTAATCAAGGAGGAGGAGGAGGAGGAGGAGGAG 3990  
Q 4152 TACTTCAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4211  
D 3991 TACTTCAACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4050  
Q 4212 TTGCTGCTCATCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4271  
D 4051 TTGCTGCTCATCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4110  
Q 4272 AGAGCACTGAGACCACTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4331  
D 4111 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4170  
Q 4332 GCGCTGATCAAGGATATACGATCATCTTCAATGATGATGATGATGATGATGATGAT 4391  
D 4171 GCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4230  
Q 4392 CTAAATTTTGCATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4451  
D 4231 CTCAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4290  
Q 4452 ATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4511  
D 4291 TCACCTCTACCACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4350  
Q 4512 AACTACAGTGGGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4571  
D 4351 AACTACAGTGGGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4410  
Q 4572 CTTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4631  
D 4411 CTCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4470  
Q 4632 CGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4691  
D 4471 AGAGAGCTCATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4530  
Q 4692 TTCTTCAATATTTGGATCTTTTCACTCAATCTGTTCAATGAGGAGGAGGAGGAGGAG 4751  
D 4531 TTCTTCAATATTTGGATCTTTTCACTCAATCTGTTCAATGAGGAGGAGGAGGAGGAG 4590

QY 4752 AATTTAATGACAAAGAAAAAGCAGGTGATCATTAAGATGTTCAATGACAGAGAT 4811  
 DB 4591 AACTTTAATGACAAAGAAAAAGCAGAGGTGCTAGATGTTCAATGACAGAGAT 4650  
 QY 4812 CAGAAAAAGTACTATATATGCTATGAAAAAGTGGCTTAAAAAACCTTAAAGCATT 4871  
 DB 4651 CAGAAAAAGTACTATATGCTATGAAAAAGTGGCTTAAAAAACCTTAAAGCATT 4710  
 QY 4872 CCAAGACCAAGGAGGAGCAGCAAGCAATAGTCTTGAATAGTAAACCAATGAATTC 4931  
 DB 4711 CCCAGGCCAAGTGGAGAGCCAGAGCCATTGTTGAAATCTGCACAGACAAAGAAATTT 4770  
 QY 4932 GATATATCATTAATGTTATTCATGATGCTGACATGTTCAACATGACCTCGATGTTAC 4991  
 DB 4771 GACATATCATCATGTTGTTTCATTGGCTTAAACATGTAACATGATCTGATGATCAT 4830  
 QY 4992 GATGCTGCGACACGTTAAACGGGCTCTAGACTATCTGAATGCGATTTGAGTATT 5051  
 DB 4831 CAAACAGTCGAAAGAGTTCAGCCAGCTTCTGATTACTGAACTGATCTTCATCTGATC 4890  
 QY 5052 TTCAGTTCGATGCTATTAATAAATATTCGCTTTACGATATCATATTTTATGACCA 5111  
 DB 4891 TTGAGTTCCGAGTGTCTGATGAATATTCGCCCTCAGATACCACTTCAAGAACCA 4950  
 QY 5112 TGAATTTATTTGATGATGATGATGTTGATTTTATTCATCTTAGTCTTGTACTAGCGAT 5171  
 DB 4951 TGGAACTCTTGTGATTTGATGATGATGATCTATCTATATTTGAGTCTGATGATGATG 5010  
 QY 5172 AATATGAGAAAGTACTGATGCGCGAGCCCTGCTCCAGTGTGCGTGGGAAAGTG 5231  
 DB 5011 ATCATGAGAAATCTTGTGTGTGCTGCTACCTGCTGAGTGTGAGAGTGCGAAAGTG 5070  
 QY 5232 GGCCTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5291  
 DB 5071 GATGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5130  
 QY 5292 GCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5351  
 DB 5131 GCTATGCTTGTGCGAGGCTCTTCAATATCTGCTACTACTACTACTACTACTACTACT 5190  
 QY 5352 TTTGCAATTTTGGCATGCTGCTTCTCATGCACTGAGAGAGAGAGAGAGAGAGAGAG 5411  
 DB 5191 TTTGCCATCTTGGCATGCTTCTCATGCACTGAGAGAGAGAGAGAGAGAGAGAGAG 5250  
 QY 5412 GTCTACAACTTGAACCTTTGGCAGAGATGATCTGCTCTTTCAGATGATGATGATG 5471  
 DB 5251 GTGTACAACTTGAACCTTTGGCAGAGATGATCTGCTCTTTCAGATGATGATGATG 5310  
 QY 5472 GCCGTTGGGATGGTGTACTGAGCGCATTTATCATGAGAGAGAGAGAGAGAGAGAG 5531  
 DB 5311 GCTGATGGATGGTGTACTGAGCGCATTTATCATGAGAGAGAGAGAGAGAGAGAG 5370  
 QY 5532 AGCGACAAAGGCTATCCGGGCAATTTGCTTCAAGCACTGAGAGAGAGAGAGAGAG 5591  
 DB 5371 AGCGAGATTTGCTATCCGGGAGAGATGATCTGCTCTTTCAGATGATGATGATG 5430  
 QY 5592 TCATATCTAT 5651  
 DB 5431 TCATATCTAT 5490  
 QY 5652 AACTATAGTCAAGCCAG 5711  
 DB 5491 AATTAATCTCCAG 5550  
 QY 5712 TACTATGATCTGGCAGCAATTTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5771  
 DB 5551 TACTATGATCTGGCAGCAATTTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5610  
 QY 5772 CTGTCCGAATTCCTGAG 5831  
 DB 5611 CTGTCCGAATTCCTGAG 5670  
 QY 5832 AAGATCATATGATGAG 5891

DB 5671 AAGATGCTGATGAG 5730  
 QY 5892 CTCGAGCCCTTACGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5951  
 DB 5731 TTGATGCTTGAAG 5790  
 QY 5952 GAGATGCTGA---GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6008  
 DB 5791 GAGTGGAGTGAAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5850  
 QY 6009 ACGTGTGCGTCAAG 6068  
 DB 5851 ACGTGTGCGGAG 5910  
 QY 6069 CACAAAGCGCGGAG 6128  
 DB 5911 CACAAAGCAAG 5967  
 QY 6129 GGTGATCCGAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6159  
 DB 5968 CCGAGCTTCAAG 5998

Search completed: May 9, 2005, 12:19:12  
 Job time : 2688 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 02:50:45 ; Search time 3084 Seconds  
(without alignments)  
12501.711 Million cell updates/sec

Title: US-08-554-424-7  
Perfect score: 6513  
Sequence: 1 TCTAGACGTTGCGCCGATAG.....ACGCGATATTAGCTTGA 6513

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

13: 1: N\_Geneseq\_16Dec04: \*  
2: 2: geneeqn1980s: \*  
3: 3: geneeqn1990s: \*  
4: 4: geneeqn2000b: \*  
5: 5: geneeqn2001bs: \*  
6: 6: geneeqn2002as: \*  
7: 7: geneeqn2002bs: \*  
8: 8: geneeqn2003bs: \*  
9: 9: geneeqn2003bs: \*  
10: 10: geneeqn2003cs: \*  
11: 11: geneeqn2003ds: \*  
12: 12: geneeqn2004as: \*  
13: 13: geneeqn2004bs: \*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6513	100.0	6513	2	AA118966	AA118966 Drosophil
2	6513	100.0	6513	2	AA173238	AA173238 Drosophil
3	6209.6	95.3	6517	4	AB115853	AB115853 Drosophil
4	6163.8	94.6	6519	2	AA8152500	AA8152500 Calcium p
5	4447.8	68.3	6318	2	AAAV06259	AAAV06259 Musca dom
6	4447.8	68.3	6318	2	AAAV02498	AAAV02498 Calcium p
7	4434.2	68.1	6315	2	AAAV06050	AAAV06050 Musca dom
8	4434.2	68.1	6315	2	AAAV02499	AAAV02499 Calcium p
9	1021.4	15.7	6586	2	AAV58423	AAV58423 PN4 sodiu
10	1021.4	15.7	6007	2	AAV58421	AAV58421 Tetradocy
11	1019.4	15.7	6007	10	ABH742021	ABH742021 Toxicity
12	1019.4	15.7	6586	13	AD516302	AD516302 Rat volt
13	993	15.2	5977	2	AAV58420	AAV58420 Tetradocy
14	993	15.2	6556	2	AAV58419	AAV58419 PN4 sodiu
15	993	15.2	6556	12	ADP71901	ADP71901 Renal to
16	977.2	15.0	7555	2	AA081338	AA081338 Cardiac s
17	974	15.0	6503	13	AD516304	AD516304 Cow volt
18	957.2	14.7	6021	6	AB124240	AB124240 Rat volta
19	956.4	14.7	7555	2	AAQ05831	AAQ05831 Cardiac s
20	944.8	14.5	7052	2	AAAT7805	AAAT7805 cDNA enco

[illegible]

from 3 overlapping regions of para cDNA isolated by PCR amplification using primers (see also AAT18987-92) based on a published para sequence. Recombinant host cells (E.coli, yeast mammalian or insect) expressing the Drosophila para VASC can be used to isolate para VASC in biologically active form. Antisense constructs can block expression of the gene

XX Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 U; 0 Other;

Query Match 100.0%; Score 6513; DB 2; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCTAGACGTTGGCGCATAGACATGACAGAAAGTTCCGACTCGATATCTGAGAAAGAAC 60  
1 TCTAGACGTTGGCGCATAGACATGACAGAAAGTTCCGACTCGATATCTGAGAAAGAAC 60  
61 GCAGTTTGTCCGTCCTTTACCGCGAATCATTTGGTGCMAATCGAATCGAATGCGG 120  
61 GCAGTTTGTCCGTCCTTTACCGCGAATCATTTGGTGCMAATCGAATCGAATGCGG 120  
121 CTGAAACATGAAAAGCAGAGAGCTGGAAGAAAGAGCCGAGGAGAGAGTCCGCGAT 180  
121 CTGAAACATGAAAAGCAGAGAGCTGGAAGAAAGAGCCGAGGAGAGAGTCCGCGAT 180  
181 ATGGTCCCAAGAAAAAACAAGAAATCCGATATGATGACAGAGACGAGAGATGAAAGT 240  
181 ATGGTCCCAAGAAAAAACAAGAAATCCGATATGATGACAGAGACGAGAGATGAAAGT 240  
241 CACAAACCGGATCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 300  
241 CACAAACCGGATCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 300  
301 TCCCGCGGAATTTGGCTCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
301 TCCCGCGGAATTTGGCTCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
361 TGACATTCGATGTTGTAAGCAAGAAAGATATTTTTCGTTTCTGCAATCAAAAGCAA 420  
361 TGACATTCGATGTTGTAAGCAAGAAAGATATTTTTCGTTTCTGCAATCAAAAGCAA 420  
421 TGTGATGTCGTGATCCATTCATCCGATACGTCGTGTCGCAATTCATTCATTCATTC 480  
421 TGTGATGTCGTGATCCATTCATCCGATACGTCGTGTCGCAATTCATTCATTCATTC 480  
481 CATTAATTTTCCCTATTCAATCAACACCAATTCCTGCACTGATCTGATGATATGC 540  
481 CATTAATTTTCCCTATTCAATCAACACCAATTCCTGCACTGATCTGATGATATGC 540  
541 CGACAAACCGCAACGCTTGAATCACTGAGTGAATTCACCGGAATCTACCATTTGAT 600  
541 CGACAAACCGCAACGCTTGAATCACTGAGTGAATTCACCGGAATCTACCATTTGAT 600  
601 CAGCGTTAAAGTATGACAGAGGTTCAATTTATGCGCTTTACGTAATCTTGAAGATG 660  
601 CAGCGTTAAAGTATGACAGAGGTTCAATTTATGCGCTTTACGTAATCTTGAAGATG 660  
661 CATGGAATTTGCTGACCTTCTGATATGCTTTAGCTTATGTCACATGAGGATATGAT 720  
661 CATGGAATTTGCTGACCTTCTGATATGCTTTAGCTTATGTCACATGAGGATATGAT 720  
721 TAGGTAATCTGACAGCCCTGCGAAGCTTTAGGTTCTGAGACGCTTTAAACCGTAGCA 780  
721 TAGGTAATCTGACAGCCCTGCGAAGCTTTAGGTTCTGAGACGCTTTAAACCGTAGCA 780  
781 TTGTCCAGAGCTTGAAGACATGTCGCGCGCTGATCGAATCGGTGAAGATCTGCGCG 840  
781 TTGTCCAGAGCTTGAAGACATGTCGCGCGCTGATCGAATCGGTGAAGATCTGCGCG 840  
841 ATGTGATTAATCTGACATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
841 ATGTGATTAATCTGACATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
901 AATATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

901 AATATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
961 ATCTGACCGACAGAAAGTGGGACTATCAAAATCGCAATGCTCCAAATTTGTAATCCGAGG 1020  
961 ATCTGACCGACAGAAAGTGGGACTATCAAAATCGCAATGCTCCAAATTTGTAATCCGAGG 1020  
1021 ACAGAGGCAATCTCATTTCCGTTATGCGGCATATATCCGCTGCGGGGCAATGCGAGCA 1080  
1021 ACAGAGGCAATCTCATTTCCGTTATGCGGCATATATCCGCTGCGGGGCAATGCGAGCA 1080  
1081 ATTAGTGTCGTGACAGGGGTTTGGTCCGAATCCGAATATGATGCTACACAGCTTCGATT 1140  
1081 ATTAGTGTCGTGACAGGGGTTTGGTCCGAATCCGAATATGATGCTACACAGCTTCGATT 1140  
1141 CGTTGGAATGGCTTTCTGTCGCGCTTCCGCTGATGACACAGGACTTCTGGAGAGATC 1200  
1141 CGTTGGAATGGCTTTCTGTCGCGCTTCCGCTGATGACACAGGACTTCTGGAGAGATC 1200  
1201 TGTACCACTGCTGTTGCGCGCGCGCGACATGAGCAATGCTGTTATATGATCA 1260  
1201 TGTACCACTGCTGTTGCGCGCGCGCGACATGAGCAATGCTGTTATATGATCA 1260  
1261 TCTTCTAGGTTCAATCTATCTTGTGAAATTTGATTTGGCCATTGTCATGCTGATG 1320  
1261 TCTTCTAGGTTCAATCTATCTTGTGAAATTTGATTTGGCCATTGTCATGCTGATG 1320  
1321 ACGAATTCGAAAGAAAGGCGCGAAGAAAGAGAGCTGCCGAAGAGGCGAATTCGTAAG 1380  
1321 ACGAATTCGAAAGAAAGGCGCGAAGAAAGAGAGCTGCCGAAGAGGCGAATTCGTAAG 1380  
1381 CGGAAGAGCTGCGCGCGCGCGAAGAGGCGCGAAGAGGCGCGAATTCGTAAG 1440  
1381 CGGAAGAGCTGCGCGCGCGCGAAGAGGCGCGAAGAGGCGCGAATTCGTAAG 1440  
1441 AGGACAGCGAGATGCGGCTGCGCGCGAAGAGGCTGCACTGCAATCCGAAATGCGCAAGA 1500  
1441 AGGACAGCGAGATGCGGCTGCGCGCGAAGAGGCTGCACTGCAATCCGAAATGCGCAAGA 1500  
1501 GTCCGACGATATTTTTCGATCACTGATGAGCTTTTGTGCGCGCGAAGAGGCGAAGATG 1560  
1501 GTCCGACGATATTTTTCGATCACTGATGAGCTTTTGTGCGCGCGAAGAGGCGAAGATG 1560  
1561 ACAACAAAGAAAGAGATGTCATTCGAGAGCTCGAGGTGAGTGGAGTGGTGAAGCG 1620  
1561 ACAACAAAGAAAGAGATGTCATTCGAGAGCTCGAGGTGAGTGGAGTGGTGAAGCG 1620  
1621 TTATACAAAGACACAGACCTTACCAACAGCACACAGCAACCAAGTTCTGTAAGTGA 1680  
1621 TTATACAAAGACACAGACCTTACCAACAGCACACAGCAACCAAGTTCTGTAAGTGA 1680  
1681 GCAAGCAATCCTTATCCTTACCTGATGACCGTTTAACTACAGCAGAGGATCACTGATT 1740  
1681 GCAAGCAATCCTTATCCTTACCTGATGACCGTTTAACTACAGCAGAGGATCACTGATT 1740  
1741 CTCAAGATACAGATACAGAACGAGAGCTGCGCTTTGATATACCGGTAGCGATGCTA 1800  
1741 CTCAAGATACAGATACAGAACGAGAGCTGCGCTTTGATATACCGGTAGCGATGCTA 1800  
1801 AGCCATTGATATGCTCAACATATCAGAGATGCCAGAGCACTTGCCCTTATGCCAGAGCT 1860  
1801 AGCCATTGATATGCTCAACATATCAGAGATGCCAGAGCACTTGCCCTTATGCCAGAGCT 1860  
1861 AGCCATTGATATGCTCAACATATCAGAGATGCCAGAGCACTTGCCCTTATGCCAGAGCT 1920  
1861 AGCCATTGATATGCTCAACATATCAGAGATGCCAGAGCACTTGCCCTTATGCCAGAGCT 1920  
1921 GCAATTCAGGCTCCGACACTCATCTGATACCTGCAATGATGCTGCTGCTGCTGCTGCTG 1980  
1921 GCAATTCAGGCTCCGACACTCATCTGATACCTGCAATGATGCTGCTGCTGCTGCTGCTG 1980  
1981 CAGATGCGGATCTACTGCGGCGCATGCGCTGATGCGCGCTGATGAGCAATGCAAGAGGA 2040

Db 1981 CACATGGGAGTCTACTGCGCGGCAATGGCCGCTCATGGCGCTCAGCACAATGACAAAGAGA 2040  
Qy 2041 GCAAATTGGCGAATCCGCAACACGCAATCAATGATGAGGCGCAACCAATGGCGCACCA 2100  
Db 2041 GCAAATTGGCGAATCCGCAACACGCAATCAATGATGAGGCGCAACCAATGGCGCACCA 2100  
Qy 2101 CCTGTGAGACCAATCACAAGGCTTCATCGGAGTCAAGAAATGGGCTGAGATGCA 2160  
Db 2101 CCTGTGAGACCAATCACAAGGCTTCATCGGAGTCAAGAAATGGGCTGAGATGCA 2160  
Qy 2161 CGAGCAGAGCTGGCAGATTAACATCATGACAAATCTTTATGAGCCGCTCCAGACAC 2220  
Db 2161 CGAGCAGAGCTGGCAGATTAACATCATGACAAATCTTTATGAGCCGCTCCAGACAC 2220  
Qy 2221 AAAAGGTGTGATATGAAAGATGTATGATGCTGATGATGATCATCATGAGCAGGCTG 2280  
Db 2221 AAAAGGTGTGATATGAAAGATGTATGATGCTGATGATGATCATCATGAGCAGGCTG 2280  
Qy 2281 GTGCGGACAGTGGGCAAGCGATGGCGGTGATCGTTACTATTTTCCCAAGAGAGC 2340  
Db 2281 GTGCGGACAGTGGGCAAGCGATGGCGGTGATCGTTACTATTTTCCCAAGAGAGC 2340  
Qy 2341 ATGACGAGATGGGCGGACGTTCAAAGACAAAGGACCTGAAATGATCTCAAAGGCAATG 2400  
Db 2341 ATGACGAGATGGGCGGACGTTCAAAGACAAAGGACCTGAAATGATCTCAAAGGCAATG 2400  
Qy 2401 ATGTGTTTTGTGTGGGAGCTGTGCTGGGTTGTGAAATTTTCAAGAGTGGGTATGCG 2460  
Db 2401 ATGTGTTTTGTGTGGGAGCTGTGCTGGGTTGTGAAATTTTCAAGAGTGGGTATGCG 2460  
Qy 2461 TCAATGCTTCGATCCCTGTGTGAGGCTTCATCAGCGTGTGATGTTGTGCAACGCA 2520  
Db 2461 TCAATGCTTCGATCCCTGTGTGAGGCTTCATCAGCGTGTGATGTTGTGCAACGCA 2520  
Qy 2521 TGTTCATGCGAATGATCAACGAGATGAAACAAGAGATGAAAGCGGTGCTCAAGATG 2580  
Db 2521 TGTTCATGCGAATGATCAACGAGATGAAACAAGAGATGAAAGCGGTGCTCAAGATG 2580  
Qy 2581 GCACATATTTCTTCAACGCGCACCTTTGCAATGAGGCGACCATGAACTAATGCGCATGA 2640  
Db 2581 GCACATATTTCTTCAACGCGCACCTTTGCAATGAGGCGACCATGAACTAATGCGCATGA 2640  
Qy 2641 GCGCCAGATCTATTTCCAGAGGCGCTGGAACATCTTGCATTTGATTTGCTGAGCCCTAT 2700  
Db 2641 GCGCCAGATCTATTTCCAGAGGCGCTGGAACATCTTGCATTTGATTTGCTGAGCCCTAT 2700  
Qy 2701 CGCTATTGGAATGGAATCTGGAAGGCTGCAAGGCTGCTGCTGATTTGGTTCTTTGAT 2760  
Db 2701 CGCTATTGGAATGGAATCTGGAAGGCTGCAAGGCTGCTGCTGATTTGGTTCTTTGAT 2760  
Qy 2761 TGTGCGGTATTAATACTGGCCAAATGCTTTGGCCCACTTAATTTACTATTTGATTA 2820  
Db 2761 TGTGCGGTATTAATACTGGCCAAATGCTTTGGCCCACTTAATTTACTATTTGATTA 2820  
Qy 2821 TGGAGCGCACATGAGGCGCTTTGGGTAATGACATTTTGTACTTTGATTAATCATCTTCA 2880  
Db 2821 TGGAGCGCACATGAGGCGCTTTGGGTAATGACATTTTGTACTTTGATTAATCATCTTCA 2880  
Qy 2881 TCTTTGCGGTATGGAATGCACTGTTGGAAGAAATTAATCATGATCACAAGACCGCT 2940  
Db 2881 TCTTTGCGGTATGGAATGCACTGTTGGAAGAAATTAATCATGATCACAAGACCGCT 2940  
Qy 2941 TTCCGAGATGGGACCTGCGCGGCTGGAACCTTCAACGCACTTTATGCAACAGCTTCATGATG 3000  
Db 2941 TTCCGAGATGGGACCTGCGCGGCTGGAACCTTCAACGCACTTTATGCAACAGCTTCATGATG 3000  
Qy 3001 TGTTCGAGGAGCTGTGGGAGAAATGATGAGTGCATGAGGGAATGAGTGAAGTGGGCG 3060  
Db 3001 TGTTCGAGGAGCTGTGGGAGAAATGATGAGTGCATGAGGGAATGAGTGAAGTGGGCG 3060  
Qy 3061 ATGTCTGTGATCCCTTCTTCTTGGGCAACGTTGTCATGCGCAATCTTGTGTACTTA 3120  
Db 3061 ATGTCTGTGATCCCTTCTTCTTGGGCAACGTTGTCATGCGCAATCTTGTGTACTTA 3120

Qy 3121 ACCTTTTCTTAACCTTGCTTTTGTCAATTTTGGCTCATCTAGCTTAATCAGCCGCACTG 3180  
Db 3121 ACCTTTTCTTAACCTTGCTTTTGTCAATTTTGGCTCATCTAGCTTAATCAGCCGCACTG 3180  
Qy 3181 CCGATTAACGATAGGAATTAATAGCGAGGCTTCAATGCAATTTGGCGGATTTAAAGTT 3240  
Db 3181 CCGATTAACGATAGGAATTAATAGCGAGGCTTCAATGCAATTTGGCGGATTTAAAGTT 3240  
Qy 3241 GGGTTAAGCGTAATATTTGCTGATTTGTTCAAGTTAATACGTAAACAAATGCAAAATCAA 3300  
Db 3241 GGGTTAAGCGTAATATTTGCTGATTTGTTCAAGTTAATACGTAAACAAATGCAAAATCAA 3300  
Qy 3301 TAAATGATCAACCATGAGTGAAGAGACCAACGATCAGTTGATTTTGGAGCGAAGAC 3360  
Db 3301 TAAATGATCAACCATGAGTGAAGAGACCAACGATCAGTTGATTTTGGAGCGAAGAC 3360  
Qy 3361 ATGATGCAACGAACTGAGTGGGCGACGACGATCTCGCCGAGCGGCTCATCAAGA 3420  
Db 3361 ATGATGCAACGAACTGAGTGGGCGACGACGATCTCGCCGAGCGGCTCATCAAGA 3420  
Qy 3421 AGGGGATCAAGAGCAGACGCAACTGAGAGTGGCATCGGGGATCGGATGGAATTCAGA 3480  
Db 3421 AGGGGATCAAGAGCAGACGCAACTGAGAGTGGCATCGGGGATCGGATGGAATTCAGA 3480  
Qy 3481 TACACGCGGACATGAAAGAAACAACAGCCGAAAGAAATCTAAATTAACCAACGA 3540  
Db 3481 TACACGCGGACATGAAAGAAACAACAGCCGAAAGAAATCTAAATTAACCAACGA 3540  
Qy 3541 TGATTTGCACTCAATTAACCAACCAAGACAAATGACTGGAACAGACTAAACCATGAG 3600  
Db 3541 TGATTTGCACTCAATTAACCAACCAAGACAAATGACTGGAACAGACTAAACCATGAG 3600  
Qy 3601 GTTTGTCTTTACAGAGCAGACGACACTGCAAGATTTAATCTATATGTAGCCATTAAGATC 3660  
Db 3601 GTTTGTCTTTACAGAGCAGACGACACTGCAAGATTTAATCTATATGTAGCCATTAAGATC 3660  
Qy 3661 GACCATTTCAAGAGCAGAGGCAACAGGCGACGCGGACGAGATGAGGCGAGAGAAC 3720  
Db 3661 GACCATTTCAAGAGCAGAGGCAACAGGCGACGCGGACGAGATGAGGCGAGAGAAC 3720  
Qy 3721 GCGAGCGCAGCAAGAGAAATTAATGATGAGGAGAACTGGAACGAGAGGCGAATGCG 3780  
Db 3721 GCGAGCGCAGCAAGAGAAATTAATGATGAGGAGAACTGGAACGAGAGGCGAATGCG 3780  
Qy 3781 AGGAGGCGCGCTGACGATGATTAATCAATGACACGACGAGATATATCTGATG 3840  
Db 3781 AGGAGGCGCGCTGACGATGATTAATCAATGACACGACGAGATATATCTGATG 3840  
Qy 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTAATTAAGAAATTTCCGATCTTGAACGCGTG 3900  
Db 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTAATTAAGAAATTTCCGATCTTGAACGCGTG 3900  
Qy 3901 ACGATGACCTGCGGTTGTGGCAAGGATGGGCAATTTAGCATGAAGAACTTTCAATTA 3960  
Db 3901 ACGATGACCTGCGGTTGTGGCAAGGATGGGCAATTTAGCATGAAGAACTTTCAATTA 3960  
Qy 3961 TTGAAATTAATATTTTGAACAGCTGTTATCACTATGATTTTAATGATGACTTACCTT 4020  
Db 3961 TTGAAATTAATATTTTGAACAGCTGTTATCACTATGATTTTAATGATGACTTACCTT 4020  
Qy 4021 TGGCATTAAGAAATGATCATCTGCGACAAAGACCCATATGCGAGATATTTTATATCTATA 4080  
Db 4021 TGGCATTAAGAAATGATCATCTGCGACAAAGACCCATATGCGAGATATTTTATATCTATA 4080  
Qy 4081 TGGACGAATATTTTACGTTATATTTCTTGTGAAATGTTAAATCAAGTGTGGGCGCTG 4140  
Db 4081 TGGACGAATATTTTACGTTATATTTCTTGTGAAATGTTAAATCAAGTGTGGGCGCTG 4140  
Qy 4141 GCTTCAAGTGTATCTTCAACCAACGCGGTGTGTGCTGATTTGATGATTTGATGAT 4200  
Db 4141 GCTTCAAGTGTATCTTCAACCAACGCGGTGTGTGCTGATTTGATGATTTGATGAT 4200

QY 4201 CGCTTACACTTCGTCCTTCACTTGTGAGCTGCTGATTCAGCCCTTCAAGACTA 4260  
Db 4201 CGCTTACACTTCGTCCTTCACTTGTGAGCTGCTGATTCAGCCCTTCAAGACTA 4260  
QY 4261 TCGGAACGTTAAGAGCACTGAGACCACTACGTCGCCATGTCCTGATGCGGGGCAAGGG 4320  
Db 4261 TCGGAACGTTAAGAGCACTGAGACCACTACGTCGCCATGTCCTGATGCGGGGCAAGGG 4320  
QY 4321 TCGTCGTTAATGCGCTGATCAAGCTATACCGTCATCTTCAATGTCATGTCGTC 4380  
Db 4321 TCGTCGTTAATGCGCTGATCAAGCTATACCGTCATCTTCAATGTCATGTCGTC 4380  
QY 4381 TATATTTTGGCTATTTTTTGGCCATATGCGTGTACAGCTTTTGTCTGAAAAATTTTA 4440  
Db 4381 TATATTTTGGCTATTTTTTGGCCATATGCGTGTACAGCTTTTGTCTGAAAAATTTTA 4440  
QY 4441 AGTGGAGACATGATGAGACCAAGCTACGACGAGATCAACCAATCGCAATGCGCT 4500  
Db 4441 AGTGGAGACATGATGAGACCAAGCTACGACGAGATCAACCAATCGCAATGCGCT 4500  
QY 4501 GCGAGAGCGAAGTCACTACGTCGGTGAATTCAGCAATGATTTGATGATGATGATG 4560  
Db 4501 GCGAGAGCGAAGTCACTACGTCGGTGAATTCAGCAATGATTTGATGATGATGATG 4560  
QY 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACTTCAAGGCTGATGATCAATCATGAGATG 4620  
Db 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACTTCAAGGCTGATGATCAATCATGAGATG 4620  
QY 4621 CTATGATTCAGAGAGAGTGAACAGCAACCAATTCGTGAAACGAACTCATGATAT 4680  
Db 4621 CTATGATTCAGAGAGAGTGAACAGCAACCAATTCGTGAAACGAACTCATGATAT 4680  
QY 4681 TATATTTTGGCTATTTTTTGGCCATATGCGTGTACAGCTTTTGTCTGAAAAATTTTA 4740  
Db 4681 TATATTTTGGCTATTTTTTGGCCATATGCGTGTACAGCTTTTGTCTGAAAAATTTTA 4740  
QY 4741 TTTATCATGATTAATTTAATGAGCAAAAGAAAGAGAGTGTGATCTTGAATGTTCA 4800  
Db 4741 TTTATCATGATTAATTTAATGAGCAAAAGAAAGAGAGTGTGATCTTGAATGTTCA 4800  
QY 4801 TGAAGAGATCAAGAAAAAGTACTATATGCTATGAAAAAGATGGGCTCTAAAAAACAT 4860  
Db 4801 TGAAGAGATCAAGAAAAAGTACTATATGCTATGAAAAAGATGGGCTCTAAAAAACAT 4860  
QY 4861 TAAAGCCATTCAGAACCAAGGTGGGACCAAGCAAGATGTTTGAATGTTAAGCCG 4920  
Db 4861 TAAAGCCATTCAGAACCAAGGTGGGACCAAGCAAGATGTTTGAATGTTAAGCCG 4920  
QY 4921 AATAGAAATTCGATATATCATATGTTATCATTTGCTGAAATGTTCAACATGACCC 4980  
Db 4921 AATAGAAATTCGATATATCATATGTTATCATTTGCTGAAATGTTCAACATGACCC 4980  
QY 4981 TCGATCGTTACGATGCGTCGACACGATTAACGCGGTCCTAGACTATCTCAATGCAAT 5040  
Db 4981 TCGATCGTTACGATGCGTCGACACGATTAACGCGGTCCTAGACTATCTCAATGCAAT 5040  
QY 5041 TCGATGATTTTCACTTCCGAATGCTATTAATAAATTTGCTTGAATGATCATAT 5100  
Db 5041 TCGATGATTTTCACTTCCGAATGCTATTAATAAATTTGCTTGAATGATCATAT 5100  
QY 5101 TTTATGAGCCATGATTAATTTGATGATGATGATGATGATTTTCACTTGAATGCTG 5160  
Db 5101 TTTATGAGCCATGATTAATTTGATGATGATGATGATGATTTTCACTTGAATGCTG 5160  
QY 5161 TACTTACGATATTTATGAGAAATGCTTGTGTCGCGGACCTGCTCGAATGCTGCTG 5220  
Db 5161 TACTTACGATATTTATGAGAAATGCTTGTGTCGCGGACCTGCTCGAATGCTGCTG 5220  
QY 5221 TGGGGAAGTGGGCGGCTGCTTGAAGTGGAGGCAAGGCAATTCGACATGCTG 5280  
Db 5221 TGGGGAAGTGGGCGGCTGCTTGAAGTGGAGGCAAGGCAATTCGACATGCTG 5280  
QY 5281 TCTTGGCGTGGCAATGTCGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTG 5340

Db 5281 TCTTGGCGTGGCAATGTCGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTG 5340  
QY 5341 TCAATGATCTTTTCCCAATTTTGGCAATGTCGTCCTTCAATGCACTGAGAGAGAGAGCG 5400  
Db 5341 TCAATGATCTTTTCCCAATTTTGGCAATGTCGTCCTTCAATGCACTGAGAGAGAGAGCG 5400  
QY 5401 GCATTAACGAGTGTACAACTTCAAGACCTTTGGCCAGAGATGATCTGCTCTTCA 5460  
Db 5401 GCATTAACGAGTGTACAACTTCAAGACCTTTGGCCAGAGATGATCTGCTCTTCA 5460  
QY 5461 TGTGACGTCAGCGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
Db 5461 TGTGACGTCAGCGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
QY 5521 ATCCACCGGACGAGCAAAAGGCTATCCGGGCAATGTTGTTCAAGCGACCTTGGATA 5580  
Db 5521 ATCCACCGGACGAGCAAAAGGCTATCCGGGCAATGTTGTTCAAGCGACCTTGGATA 5580  
QY 5581 CGTTCTCTCTCATACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
Db 5581 CGTTCTCTCTCATACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
QY 5641 TCATTTCTGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
Db 5641 TCATTTCTGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
QY 5701 ACTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
Db 5701 ACTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
QY 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
Db 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
QY 5821 CGAACAAGTACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
Db 5821 CGAACAAGTACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
QY 5881 GGTGTCATCTCTGAGCGGCTTCAAGAAAGCTTCTTGGCGGAGAGGCAATCCGATG 5940  
Db 5881 GGTGTCATCTCTGAGCGGCTTCAAGAAAGCTTCTTGGCGGAGAGGCAATCCGATG 5940  
QY 5941 AGGAGACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
Db 5941 AGGAGACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
QY 6001 TCTCATCAACGCTGTGCGTCAAGCTGAGAGATGATGATGATGATGATGATGATGATG 6060  
Db 6001 TCTCATCAACGCTGTGCGTCAAGCTGAGAGATGATGATGATGATGATGATGATGATG 6060  
QY 6061 GGGGAAAGCAAGAGCGCGCGGAGAGAGAGTGTGCTTGAAGCGGATGATGATGATG 6120  
Db 6061 GGGGAAAGCAAGAGCGCGCGGAGAGAGAGTGTGCTTGAAGCGGATGATGATGATG 6120  
QY 6121 GCGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
Db 6121 GCGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
QY 6181 CGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
Db 6181 CGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
QY 6241 AGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
Db 6241 AGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
QY 6301 CGCGCGCGGCGGAG 6360  
Db 6301 CGCGCGCGGCGGAG 6360  
QY 6361 CGCGCGCTTCTGAG 6420

Db 6361 CCGCGCTTCGTGAGAGCGCGGTTCTGTGACGAGAACCGCCACAGAGTGTCATCC 6420  
Qy 6421 ACTGCGATCGCCGAGCATCAGTCGCGGACGCGGATGTCTGAGCAGGCGCTGCCCC 6480  
Db 6421 ACTGCGATCGCCGAGCATCAGTCGCGGACGCGGATGTCTGAGCAGGCGCTGCCCC 6480  
Qy 6481 CCTTCAGAGTGCACGCGAGTATTAGCTCTAGA 6513  
Db 6481 CCTTCAGAGTGCACGCGAGTATTAGCTCTAGA 6513  
RESULT 2  
AAT33238  
ID AAT33238 standard; cDNA; 6513 BP.  
XX  
AC AAT33238;  
XX  
DT 15-OCT-1996 (first entry)  
XX  
DE Drosophila para voltage-activated sodium channel cDNA.  
XX  
KM Para voltage-activated sodium channel; insecticide;  
KM archinide; pesticide; neuroprotective; ischaemia; antagonist; therapy;  
KM monoclonal antibody; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN MO9614860-A1.  
XX  
PD 23-MAY-1996.  
XX  
PF 06-NOV-1995; 95WO-US014262.  
XX  
PR 10-NOV-1994; 94US-0038702.  
XX  
PA (MERI) MERCK & CO INC.  
XX  
PI Van Der Ploeg LHT, Warmke JW;  
XX  
DR WPI; 1996-259563/26.  
XX  
PT Mono-specific antibodies to voltage-activated cation channel - also new  
PT cation channel DNA, useful for identifying channel modulators,  
XX potentially useful partic. as insecticide and neuroprotective agents.  
XX  
PS Claim 17, Page 39-43; 55pp; English.  
XX  
XX A full-length cDNA clone (AAT33238) codes for the Drosophila para voltage  
CC -activated sodium channel (VASC), a protein responsible for the fast  
CC depolarizing phase of the action potential that underlies electrical  
CC signaling in neurons, muscles, etc. The cDNA clone was obtd. from 3  
CC overlapping regions of para cDNA isolated by PCR amplification using  
CC primers (see also AAT33239-44) based on a published para sequence.  
CC Recombinant host cells (E.coli, yeast mammalian or insect) expressing the  
CC Drosophila para VASC can be used to identify modulators of insect VASCs,  
CC useful as insecticides and archinides. VASC antagonists can be used as  
CC neuroprotective agents for treatment of ischaemia in humans  
XX  
SQ Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 U; 0 Other;  
Query Match 100.0%; Score 6513; DB 2; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 CTGAACATGAAAGAGAGAGCTGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAT 180  
Qy 181 ATGTCGGAAGAAAAAAGAAAAAAGAAATCCGATATGATGACAGAGACAGAGATGAAGTC 240  
Db 181 ATGTCGGAAGAAAAAAGAAAAAAGAAATCCGATATGATGACAGAGACAGAGATGAAGTC 240  
Qy 241 CACAACCGGATCTTACATCTTGAACAGGAGTGAGCAATTCGTTTGAATGACAGGACACT 300  
Db 241 CACAACCGGATCTTACATCTTGAACAGGAGTGAGCAATTCGTTTGAATGACAGGACACT 300  
Qy 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
Db 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
Qy 361 TGAATTCGTAGTTGTAAGCAAGAAAGATATTTTGGCTTTTGTGATCAAAAGCA 420  
Db 361 TGAATTCGTAGTTGTAAGCAAGAAAGATATTTTGGCTTTTGTGATCAAAAGCA 420  
Qy 421 TGTGAGTCTGATCCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 480  
Db 421 TGTGAGTCTGATCCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 480  
Qy 481 CATTAATTTCCCTATTCATCATCAACAATTCCTGTCATCTGATCCCTGATGATATGC 540  
Db 481 CATTAATTTCCCTATTCATCATCAACAATTCCTGTCATCTGATCCCTGATGATATGC 540  
Qy 541 CGACAGGCCCAAGGTTAGTCCAGTGAAGTATTCACCGAATCTACATTTGAT 600  
Db 541 CGACAGGCCCAAGGTTAGTCCAGTGAAGTATTCACCGAATCTACATTTGAT 600  
Qy 601 CAGCTGTTAAGTATGAGTCCAGGTTTCAATTTATGCGGTTTATGAGATG 660  
Db 601 CAGCTGTTAAGTATGAGTCCAGGTTTCAATTTATGCGGTTTATGAGATG 660  
Qy 661 CATGGAATTTGGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 720  
Db 661 CATGGAATTTGGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 720  
Qy 721 TAGGTAATCTAGACAGCCCTGGAAAGTTTAAAGTGCTGCAAGCGTTAAACCGTAGCA 780  
Db 721 TAGGTAATCTAGACAGCCCTGGAAAGTTTAAAGTGCTGCAAGCGTTAAACCGTAGCA 780  
Qy 781 TTGTGCAAGCTTGAAGAACCATGCTGCGCCCGCATCGAATCGTGAAGATCTGGCG 840  
Db 781 TTGTGCAAGCTTGAAGAACCATGCTGCGCCCGCATCGAATCGTGAAGATCTGGCG 840  
Qy 841 ATGTGATTTATCTGACCATGTTCTCCCTGCGGTTTCCGTTGATGAGGCTACAGATCT 900  
Db 841 ATGTGATTTATCTGACCATGTTCTCCCTGCGGTTTCCGTTGATGAGGCTACAGATCT 900  
Qy 901 ATATGAGCGTGTCTACCGAGAGTGCATCAAGAGTTCCGCTGAGCGTTCTTGGGCA 960  
Db 901 ATATGAGCGTGTCTACCGAGAGTGCATCAAGAGTTCCGCTGAGCGTTCTTGGGCA 960  
Qy 961 ATCTGACCGAGAGAACTGGAATCTATCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1020  
Db 961 ATCTGACCGAGAGAACTGGAATCTATCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1020  
Qy 1021 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATCCGTTGCGGCGCAATGCGACAGC 1080  
Db 1021 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATCCGTTGCGGCGCAATGCGACAGC 1080  
Qy 1081 ATTAAGTGTGCTGACAGGAGTTTGTTCGAATCGAATTAATGCTACACAGCTTGAT 1140  
Db 1081 ATTAAGTGTGCTGACAGGAGTTTGTTCGAATCGAATTAATGCTACACAGCTTGAT 1140  
Qy 1141 CGTTGAGTGGGCTTTCTGTCCGCTTCCGCTGATGACACAGACTTTTGGAGATC 1200  
Db 1141 CGTTGAGTGGGCTTTCTGTCCGCTTCCGCTGATGACACAGACTTTTGGAGATC 1200  
Qy 1201 TGTACAGCTGTGTTGTGCGCGCGGACATGAGCAATGCTGTTCTTATAGTATCA 1260  
Db 1201 TGTACAGCTGTGTTGTGCGCGCGGACATGAGCAATGCTGTTCTTATAGTATCA 1260

Db 1201 TGTACAGCTGCTGTTGGCGGCGCCGCGACATGCGCATGCTGTTCTTTATAGTCATCA 1260  
QY 1261 TCTTCTAGGTTCAATCTATCTTTGTAATTTGATTTTGGCATTTGTTCCATGCTGATG 1320  
Db 1261 TCTTCTAGGTTCAATCTATCTTTGTAATTTGATTTTGGCATTTGTTCCATGCTGATG 1320  
QY 1321 ACGAATTTGCAAGGAAGCCGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
Db 1321 ACGAATTTGCAAGGAAGCCGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 CGGAAGAAGCTGCGCGCGCCAAAGCGCCAAAGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
Db 1381 CGGAAGAAGCTGCGCGCGCCAAAGCGCCAAAGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
QY 1441 AGGACAGCGAGTGGCGCTGCGCGCGGAAGAGCTGCACTGCAATCGGAAATGCGCAAGA 1500  
Db 1441 AGGACAGCGAGTGGCGCTGCGCGCGGAAGAGCTGCACTGCAATCGGAAATGCGCAAGA 1500  
QY 1501 GTCCGAGCTATTTGTCATGAGCTATGAGCTATTTGTTGGCGGCGGAAGAGGCGAAGATG 1560  
Db 1501 GTCCGAGCTATTTGTCATGAGCTATGAGCTATTTGTTGGCGGCGGAAGAGGCGAAGATG 1560  
QY 1561 ACAACAACAAGAGAAGATGTCATTCGAGCGTCGAGGTGAGTGGAGTGGTGAAGCG 1620  
Db 1561 ACAACAACAAGAGAAGATGTCATTCGAGCGTCGAGGTGAGTGGAGTGGTGAAGCG 1620  
QY 1621 TTATACAAAGACAACGACCTTACCAAGACCAACCAAGTTCACAAAGTTCTGTAAGTGA 1680  
Db 1621 TTATACAAAGACAACGACCTTACCAAGACCAACCAAGTTCACAAAGTTCTGTAAGTGA 1680  
QY 1681 GCGACGATGCTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
Db 1681 GCGACGATGCTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
QY 1741 CTCAACAAGTACAGATACGGAACGAGCGTGGCTTTGATATCCCGATGAGCATGTA 1800  
Db 1741 CTCAACAAGTACAGATACGGAACGAGCGTGGCTTTGATATCCCGATGAGCATGTA 1800  
QY 1801 AGCATTTGCTATTTGTCACATATCAGAGTGGCGGACGACTTGGCTTATGCGGACGACT 1860  
Db 1801 AGCATTTGCTATTTGTCACATATCAGAGTGGCGGACGACTTGGCTTATGCGGACGACT 1860  
QY 1861 GGAATGCGCTGACCCGCGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Db 1861 GGAATGCGCTGACCCGCGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
QY 1921 GCAATCTAGGCTCCGCACTCATCTGATATCTTCCGATCAGTCCCGAATATCTGATATCT 1980  
Db 1921 GCAATCTAGGCTCCGCACTCATCTGATATCTTCCGATCAGTCCCGAATATCTGATATCT 1980  
QY 1981 CAGATGGCGATCTATCTGGCGGCACTGGCGGCTCATGGCGGCTCATGGCGGCTCATGG 2040  
Db 1981 CAGATGGCGATCTATCTGGCGGCACTGGCGGCTCATGGCGGCTCATGGCGGCTCATGG 2040  
QY 2041 GCAAAATTTGCGCAACCGCAACGCAATCATGAGTGGCGGCGCAACCAATGCGGCGCA 2100  
Db 2041 GCAAAATTTGCGCAACCGCAACGCAATCATGAGTGGCGGCGCAACCAATGCGGCGCA 2100  
QY 2101 CCGTGTCTGACACCAATCAAGCTGATCATGCGATCGAATGGAATTTGGCTTGAAGTGA 2160  
Db 2101 CCGTGTCTGACACCAATCAAGCTGATCATGCGATCGAATGGAATTTGGCTTGAAGTGA 2160  
QY 2161 CGGACGAAGCTGCGCAAGATTTAAATCATGATGCAATCTTTTATGAGAGCGCTGCAAGCAC 2220  
Db 2161 CGGACGAAGCTGCGCAAGATTTAAATCATGATGCAATCTTTTATGAGAGCGCTGCAAGCAC 2220  
QY 2221 AAAAGGCTGTTGATATGAAGATGATGCTGATGATGATGATGATGATGATGATGATGATG 2280  
Db 2221 AAAAGGCTGTTGATATGAAGATGATGCTGATGATGATGATGATGATGATGATGATGATG 2280  
QY 2281 GTGCGGCAAGTGGCGAAGGAGTGGCGGTGCTTCCGTTTATCTATTTCCAAACAGAGAGCG 2340  
Db 2281 GTGCGGCAAGTGGCGAAGGAGTGGCGGTGCTTCCGTTTATCTATTTCCAAACAGAGAGCG 2340

QY 2341 ATGACGAGATGCGCGCGACGTTCAAGAGACGACCTGAGATGATCTTCAAGGCGATCG 2400  
Db 2341 ATGACGAGATGCGCGCGACGTTCAAGAGACGACCTGAGATGATCTTCAAGGCGATCG 2400  
QY 2401 ATGATGTTTGT 2460  
Db 2401 ATGATGTTTGT 2460  
QY 2461 TCAATGCTTTCATGATCTTGTGAGCTGCTTTCATGACGCTGTGATGTTGTGTGATGACA 2520  
Db 2461 TCAATGCTTTCATGATCTTGTGAGCTGCTTTCATGACGCTGTGATGTTGTGTGATGACA 2520  
QY 2521 TGTTCATGCGAATGATATCAACGATATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Db 2521 TGTTCATGCGAATGATATCAACGATATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
QY 2581 GCAACTATTTCTTCAACGCACTTTGCGATGAGGCGCACTATGAGCTATGAGCATGA 2640  
Db 2581 GCAACTATTTCTTCAACGCGCACTTTGCGATGAGGCGCACTATGAGCTATGAGCATGA 2640  
QY 2641 GCGCCAAAGTATATTTCCAGAGAGGCTGGAACATCTTCACTTATGCTGAGCTGAT 2700  
Db 2641 GCGCCAAAGTATATTTCCAGAGAGGCTGGAACATCTTCACTTATGCTGAGCTGAT 2700  
QY 2701 CGCTATTTGGAACGAGGACCTGAGGAGTGCAGAGGCTGTCGCTGATGAGCTGCTTGCAT 2760  
Db 2701 CGCTATTTGGAACGAGGACCTGAGGAGTGCAGAGGCTGTCGCTGATGAGCTGCTTGCAT 2760  
QY 2761 TGTGCGGTGATTTCAACTGCGCAAGTCTTGGCCCACTTATTTACTATTTGATTA 2820  
Db 2761 TGTGCGGTGATTTCAACTGCGCAAGTCTTGGCCCACTTATTTACTATTTGATTA 2820  
QY 2821 TGGGACGACCATGCGGCGCTTGGGATATGATCATTTGATCTTGTGATATATCACTTTGA 2880  
Db 2821 TGGGACGACCATGCGGCGCTTGGGATATGATCATTTGATCTTGTGATATATCACTTTGA 2880  
QY 2881 TCTTTGCGGTGATGGAATGCAACGTTGCGAAAGAAATATCATGATCAAGAGACGCGCT 2940  
Db 2881 TCTTTGCGGTGATGGAATGCAACGTTGCGAAAGAAATATCATGATCAAGAGACGCGCT 2940  
QY 2941 TTTCCGATGCGCACTGCGCGCTGGAACCTTCCAGCTTATGACACGCTTATGATCG 3000  
Db 2941 TTTCCGATGCGCACTGCGCGCTGGAACCTTCCAGCTTATGACACGCTTATGATCG 3000  
QY 3001 TGTTCGCGGTGCTCTGCGGAGATGATGAGTGCATGTGGGACTGTCATGATGATGATG 3060  
Db 3001 TGTTCGCGGTGCTCTGCGGAGATGATGAGTGCATGTGGGACTGTCATGATGATGATG 3060  
QY 3061 ATGTCGTGATCTTCCCTTCTTCTTGGGCAACGTTGTGATCGGCAATCTTGTGTGATCTTA 3120  
Db 3061 ATGTCGTGATCTTCCCTTCTTCTTGGGCAACGTTGTGATCGGCAATCTTGTGTGATCTTA 3120  
QY 3121 ACCCTTTCTTGAAGCTTGTGCTTGTGCTATTTTGGCTATCTGATCTTATGACGCGGAC 3180  
Db 3121 ACCCTTTCTTGAAGCTTGTGCTTGTGCTATTTTGGCTATCTGATCTTATGACGCGGAC 3180  
QY 3181 CCGATTAACGATATGATTAATATGCGGAGGCTTCAATGGAATTTGGCGGATTTAAAGTT 3240  
Db 3181 CCGATTAACGATATGATTAATATGCGGAGGCTTCAATGGAATTTGGCGGATTTAAAGTT 3240  
QY 3241 GGGTTAAGCGATATTTGCTGATTTGTTCAAGTTAATAGTAAACAATTTGACAAATCAAA 3300  
Db 3241 GGGTTAAGCGATATTTGCTGATTTGTTCAAGTTAATAGTAAACAATTTGACAAATCAAA 3300  
QY 3301 TAAATGATCAACCATGAGTGAAGAGCAACCAATCAAGTTGATTTGAGCGGAAGAGC 3360  
Db 3301 TAAATGATCAACCATGAGTGAAGAGCAACCAATCAAGTTGATTTGAGCGGAAGAGC 3360  
QY 3361 ATGTTGACAAACGATGAGGCTGCGGCAAGAGATCTTCCGCGAGCGGCTCATCAAGA 3420  
Db 3361 ATGTTGACAAACGATGAGGCTGCGGCAAGAGATCTTCCGCGAGCGGCTCATCAAGA 3420

OY	3421	AGGGGATCAAGGAGCAGACCGCACTGGAGTGGCCATGGGGATGGATGGAATTCACGA	3480
Db	3421	AGGGGATCAAGGAGCAGACCGCAACTGGAGTGGCCATGGGGATGGATGGAATTCACGA	3480
OY	3481	TACACGGCGCACAATGGAAGAACCAACAGCCGCAAGAAATCCAAATATCTTAATTAACGACGA	3540
Db	3481	TACACGGCGCACAATGGAAGAACCAACAGCCGCAAGAAATCCAAATATCTTAATTAACGACGA	3540
OY	3541	TGATTGGCAACTCAATTAAACCAAGACAAATAGAATGGAAACAGAGCTAAACATAGAG	3600
Db	3541	TGATTGGCAACTCAATTAAACCAAGACAAATAGAATGGAAACAGAGCTAAACATAGAG	3600
OY	3601	GTTTGTCCCTTAACGAGACGACGACCTGGCAGATTACTCATATGTGTGCCATAAGATC	3660
Db	3601	GTTTGTCCCTTAACGAGACGACGACCTGGCAGATTACTCATATGTGTGCCATAAGATC	3660
OY	3661	GACCAATTCAGGACGAGACCCACAAAGGAGGCGCGACGATGAGGCGCAGAGGAAGC	3720
Db	3661	GACCAATTCAGGACGAGACCCACAAAGGAGGCGCGACGATGAGGCGCAGAGGAAGC	3720
OY	3721	GCGACGCCACGACGAGGAGATTAGGTCTCCACGAGAACTGACGACGAGGCGCATATCG	3780
Db	3721	GCGACGCCACGACGAGGAGATTAGGTCTCCACGAGAACTGACGACGAGGCGCATATCG	3780
OY	3781	AGGAGGGCCCGCTCGACGGTATCATATTATCATGCAACGACGAGATATCTCGATG	3840
Db	3781	AGGAGGGCCCGCTCGACGGTATCATATTATCATGCAACGACGAGATATCTCGATG	3840
OY	3841	AATATCCAGCTGATTTGCTGCCCCGAGTTGTAATAAGAAATTCGATCTTAAGCCGCTG	3900
Db	3841	AATATCCAGCTGATTTGCTGCCCCGAGTTGTAATAAGAAATTCGATCTTAAGCCGCTG	3900
OY	3901	ACGATGACTCGCGCTTCTGGCAGAGATGGGCAATTTACGACTGAAACTTTTCAATTA	3960
Db	3901	ACGATGACTCGCGCTTCTGGCAGAGATGGGCAATTTACGACTGAAACTTTTCAATTA	3960
OY	3961	TTGAAATTAATATTTTGAACAGCTGTATATCATATATTTAATGATAGTACGCTT	4020
Db	3961	TTGAAATTAATATTTTGAACAGCTGTATATCATATATTTAATGATAGTACGCTT	4020
OY	4021	TGGCAATTAAGAAATGACATCTGCCACAAAGCCATCTCAGAGATTTTATTAATTA	4080
Db	4021	TGGCAATTAAGAAATGACATCTGCCACAAAGCCATCTCAGAGATTTTATTAATTA	4080
OY	4081	TGGACAGAAATTTACGGTTATATCTTCTTGGAAATGTATCAAGTGTGGCGCTCG	4140
Db	4081	TGGACAGAAATTTACGGTTATATCTTCTTGGAAATGTATCAAGTGTGGCGCTCG	4140
OY	4141	GCTTCAAAAGTATCTTCAACCAACGGGTGTGTGGCTCGATTTGCTGATGTAT	4200
Db	4141	GCTTCAAAAGTATCTTCAACCAACGGGTGTGTGGCTCGATTTGCTGATGTAT	4200
OY	4201	CGCTTATCAACTTGGTGTCTTCACTTGTGTGAAGCTGTGTGATTCAGACCTTCAAGATA	4260
Db	4201	CGCTTATCAACTTGGTGTCTTCACTTGTGTGAAGCTGTGTGATTCAGACCTTCAAGATA	4260
OY	4261	TGCGAAGCTTAAGACACTGAGACCACTACGAGCAATGCCGATGAGAGGGCATGAGGG	4320
Db	4261	TGCGAAGCTTAAGACACTGAGACCACTACGAGCAATGCCGATGAGAGGGCATGAGGG	4320
OY	4321	TGCTGTTAATGCGCTGGTACAAAGCTATACGTCATCTTCAATGTGTATTTGGTGTCT	4380
Db	4321	TGCTGTTAATGCGCTGGTACAAAGCTATACGTCATCTTCAATGTGTATTTGGTGTCT	4380
OY	4381	TAAATTTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGGCTGGAATAATTTTA	4440
Db	4381	TAAATTTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGGCTGGAATAATTTTA	4440
OY	4441	AGTGGAGAGCAATGATGGCAAGAGCTCAGCAGAGATATACCAATGCGCAATGCT	4500
Db	4441	AGTGGAGAGCAATGATGGCAAGAGCTCAGCAGAGATATACCAATGCGCAATGCT	4500
OY	4501	GCGAAGCGAGAACTACAGTGGGTGAATTCAGCAATGAATTTGATCATGTAGTACG	4560

Db	4501	GGGAGGCGAACACTCACGCGGGGGAATTAAGCAATGAATTCGATCATGTAGTAACG	4560
QY	4561	CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAAGCTGGATCAAAATCATGAACGATG	4620
Db	4561	CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAAGCTGGATCAAAATCATGAACGATG	4620
QY	4621	CTATCGATTCCAGAGAGTGGACAGAACCAATTCGTAAAGCAACATCTACATGTAAT	4680
Db	4621	CTATCGATTCCAGAGAGTGGACAGAACCAATTCGTAAAGCAACATCTACATGTAAT	4680
QY	4661	TATATTTGATATTCCTCAATATTTGGATTCCTTTTCAACCTGAATCTGTTCATTTGGTG	4740
Db	4661	TATATTTGATATTCCTCAATATTTGGATTCCTTTTCAACCTGAATCTGTTCATTTGGTG	4740
QY	4741	TTATCATGTGATTAATTTTAAATAGCAAAAAGAAAAGAGGATGATCATTTGAATATGTTCA	4800
Db	4741	TTATCATGTGATTAATTTTAAATAGCAAAAAGAAAAGAGGATGATCATTTGAATATGTTCA	4800
QY	4801	TGACAGAAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACAT	4860
Db	4801	TGACAGAAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACAT	4860
QY	4861	TAAAAAGCATTCCAAGACCAAGGTGGGACCAACAGCAATATGTCTTTGAAATAGTAACCG	4920
Db	4861	TAAAAAGCATTCCAAGACCAAGGTGGGACCAACAGCAATATGTCTTTGAAATAGTAACCG	4920
QY	4921	ATTAAGAAATTCGATATATATCATTAATGTTATTCATTGGCTGTAACATGTTCCACATGACC	4980
Db	4921	ATTAAGAAATTCGATATATATCATTAATGTTATTCATTGGCTGTAACATGTTCCACATGACC	4980
QY	4961	TGATTCGTTACGATGCGTCGACACAGTAAACGGCGTCTTAAGACTATCTCAATGCGATAT	5040
Db	4961	TGATTCGTTACGATGCGTCGACACAGTAAACGGCGTCTTAAGACTATCTCAATGCGATAT	5040
QY	5041	TGCGTATTTATTTTCAAGTTCGCAATGTCTATTAATAATTTTGGCTTTACGATATCACTAAT	5100
Db	5041	TGCGTATTTATTTTCAAGTTCGCAATGTCTATTAATAATTTTGGCTTTACGATATCACTAAT	5100
QY	5101	TTATTTAGCCATGGAATTTTATTTATGATAGTAGTGTCAATTTATCCATCTTAGAGTCTTG	5160
Db	5101	TTATTTAGCCATGGAATTTTATTTATGATAGTAGTGTGTCAATTTATCCATCTTAGAGTCTTG	5160
QY	5161	TACTTAGCGATATTTATGAGAAAGTACTGCTGTCGCGACCTTCGTCGAGTGGTGCGTG	5220
Db	5161	TACTTAGCGATATTTATGAGAAAGTACTGCTGTCGCGACCTTCGTCGAGTGGTGCGTG	5220
QY	5221	TGGCGAAAGTGGGCGGTGCTCTTGCAGCTGGTGAAAGGAGCCAAAGGGCATTCGCAACATGCG	5280
Db	5221	TGGCGAAAGTGGGCGGTGCTCTTGCAGCTGGTGAAAGGAGCCAAAGGGCATTCGCAACATGCG	5280
QY	5281	TCTTCGCGTTGGCCATGTCGCTGCGCGGCCCTGTTCACATCTGCGCTGCTGTCTCCGCG	5340
Db	5281	TCTTCGCGTTGGCCATGTCGCTGCGCGGCCCTGTTCACATCTGCGCTGCTGTCTCCGCG	5340
QY	5341	TCATGTTCACTTTTGCATTTTCCGCAATGTGCTTTCATGCACTGAAGAGAGAGAACGCG	5400
Db	5341	TCATGTTCACTTTTGCATTTTCCGCAATGTGCTTTCATGCACTGAAGAGAGAGAACGCG	5400
QY	5401	GCATTTAAGCAGCTACAACTTCAAGACTTTTGGCCAGAGCATGATCTGTCTTTTCAGA	5460
Db	5401	GCATTTAAGCAGCTACAACTTCAAGACTTTTGGCCAGAGCATGATCTGTCTTTTCAGA	5460
QY	5461	TGTTCGAGCTCAGCCGGTGGATGTGTATCTGACGCGCATTTATCTAAAGAGAACATGCG	5520
Db	5461	TGTTCGAGCTCAGCCGGTGGATGTGTATCTGACGCGCATTTATCTAAAGAGAACATGCG	5520
QY	5521	ATTCACCCGACAGCGCAAAAGGCTATCCGGGCAATTTGGTTCAGCAGCAGTGGATTA	5580
Db	5521	ATTCACCCGACAGCGCAAAAGGCTATCCGGGCAATTTGGTTCAGCAGCAGTGGATTA	5580
QY	5581	CGTTTCTCTCTCAACCTAGTTAAAGCTTTTGTATGATTTAATATATGTAACATTCGTG	5640



Db 529 TGTGATCTGATCATTTCAATCCGATACGTCGTCGATTTCACTTCTAGTCATC 588  
Qy 481 CATTATTTTCCCTATTTCATCATCACACAAATTCGTCAACTCATCTGATGATATGC 540  
Db 589 CATTATTTTCCCTATTTCATCATCACACAAATTCGTCAACTCATCTGATGATATGC 648  
Qy 541 CGAACAACCCCAACGGTTAGTCCACTGAGGATATTTCAACGGATCTTACATTTGANT 600  
Db 649 CGAACAACCCCAACGGTTAGTCCACTGAGGATATTTCAACGGATCTTACATTTGANT 708  
Qy 601 CAGCTGTAAAGTAGTGACACGAGGTTCAATTTATGCCCCGTTTACGATCTTAGAGATG 660  
Db 709 CAGCTGTAAAGTAGTGACACGAGGTTCAATTTATGCCCCGTTTACGATCTTAGAGATG 768  
Qy 661 CATGGAATTTGCTGACCTTCGTAGTAATAGCTTTAGTTATGTGACCAATGGGTATAGAT 720  
Db 769 CATGGAATTTGCTGACCTTCGTAGTAATAGCTTTAGTTATGTGACCAATGGGTATAGAT 828  
Qy 721 TAGGTAATCTAGACACCTTCGGAAGTTTAGGTCCTGAGCCGTTTAAACCGTAGCA 780  
Db 829 TAGGTAATCTAGACACCTTCGGAAGTTTAGGTCCTGAGCCGTTTAAACCGTAGCA 888  
Qy 781 TTGTGACAGGCTTGAAAGCAATCGTCGGGCGCTCATCGAATCGGTGAAGAATCTGGCG 840  
Db 889 TTGTGACAGGCTTGAAAGCAATCGTCGGGCGCTCATCGAATCGGTGAAGAATCTGGCG 948  
Qy 841 ATGTGATTAATCTGACCAATGTTCTCCGTGCGTTCGCTGATGATGAGGCCCTTACAGATCT 900  
Db 949 ATGTGATTAATCTGACCAATGTTCTCCGTGCGTTCGCTGATGATGAGGCCCTTACAGATCT 1008  
Qy 901 ATATGAGGCGTGTCCACCGAAGATGATCAAGAATTTCCCGTGAACGTTCTTGGGCA 960  
Db 1009 ATATGAGGCGTGTCCACCGAAGATGATCAAGAATTTCCCGTGAACGTTCTTGGGCA 1068  
Qy 961 ATCTGACCGAGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTTGATTCGAGG 1020  
Db 1069 ATCTGACCGAGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTTGATTCGAGG 1128  
Qy 1021 ACGAGGGGATCTCATTTCCGTTATGCGGCAATATATCCGTCGCGGAGCAATGCGAGCG 1080  
Db 1129 ACGAGGGGATCTCATTTCCGTTATGCGGCAATATATCCGTCGCGGAGCAATGCGAGCG 1188  
Qy 1081 ATTACGTGTGCTGAGAGGGGTTTGGTCCGAATCCGAATTTAGGCTTACACAGCTTCGATT 1140  
Db 1189 ATTACGTGTGCTGAGAGGGGTTTGGTCCGAATCCGAATTTAGGCTTACACAGCTTCGATT 1248  
Qy 1141 CGTTCGGAATGGGCTTTCCTGTCCGCTTCGCGGCTGATGACACAGGACTTCTGGAGAGATC 1200  
Db 1249 CGTTCGGAATGGGCTTTCCTGTCCGCTTCGCGGCTGATGACACAGGACTTCTGGAGAGATC 1308  
Qy 1201 TGTACCAAGCTGTGTGCGCGCCGCGGACCAATGACATGCTGTTCTTTATAGTCATCA 1260  
Db 1309 TGTACCAAGCTGTGTGCGCGCCGCGGACCAATGACATGCTGTTCTTTATAGTCATCA 1368  
Qy 1261 TCTTCTAGGTTTCATTTCTATCTTGGAATTTGATTTTGGCCATTTGTGCTATGCTATG 1320  
Db 1369 TCTTCTAGGTTTCATTTCTATCTTGGAATTTGATTTTGGCCATTTGTGCTATGCTATG 1428  
Qy 1321 ACGAATTCGAAGAAGGCGGAGGAAGAAGGCTCGGAGAAGAGGCGATAGCTGAG 1380  
Db 1429 ACGAATTCGAAGAAGGCGGAGGAAGAAGGCTCGGAGAAGAGGCGATAGCTGAG 1488  
Qy 1381 CGGAAGAAGCTGCGCGCCGCAAAAGCGCCCAAGCTGGAAGAGCGGCGCAATGCGAGGCTC 1440  
Db 1489 CGGAAGAAGCTGCGCGCCGCAAAAGCGCCCAAGCTGGAAGAGCGGCGCAATGCGAGGCTC 1548  
Qy 1441 AGGCAAGCGGATGCGGCTGCGCGCAAGAGGCTGCACTGATCTCGGAATTTGCGCAAGA 1500  
Db 1549 AGGCAAGCGGATGCGGCTGCGCGCAAGAGGCTGCACTGATCTCGGAATTTGCGCAAGA 1608  
Qy 1501 GTCCGAGCTATTTCTGATGAGCTATGAGCTATTTGTTGGCGGCGAAGAAGGCGAATG 1560

Db 1609 GTCCGAGCTATTTCTTGATGAGTATGAGCTATTTGTTGGGCGGAGGAAGGCGAATG 1668  
Qy 1561 ACAAACAAGAGAGATGTTCATTTGGAGCGTGGAGTGAAGTGGAGTGGAGCG 1620  
Db 1669 ACAAACAAGAGAGATGTTCATTTGGAGCGTGGAGTGAAGTGGAGTGGAGCG 1728  
Qy 1621 TTATTAAGAAGCAACGACACTTACACAGACCAAGCTACCAAGTTGTTGAAGTGA 1680  
Db 1729 TTATTAAGAAGCAACGACACTTACACAGACCAAGCTACCAAGTTGTTGAAGTGA 1788  
Qy 1681 GCACGACATCTTTATCTTTACCTGATCCGTTTAAATATACGAGGAGATCAAGTATT 1740  
Db 1789 GCACGACATCTTTATCTTTACCTGATCCGTTTAAATATACGAGGAGATCAAGTATT 1848  
Qy 1741 CTCACAGTACACGATACGGAACGGAAGTGGCCGTTTGGTATACCCGTTAGCGATGTA 1800  
Db 1849 CTCACAGTACACGATACGGAACGGAAGTGGCCGTTTGGTATACCCGTTAGCGATGTA 1908  
Qy 1801 AGCAATGTATTTGCAACATATCAGAGATGCCCCAGACACTTGGCCCTATGCCGAGACT 1860  
Db 1909 AGCAATGTATTTGCAACATATCAGAGATGCCCCAGACACTTGGCCCTATGCCGAGACT 1968  
Qy 1861 CGAATGCCGTACCCCGATGTCCGAAGAAGATGGGSCCATATAGTCCCGTATCTATG 1920  
Db 1969 CGAATGCCGTACCCCGATGTCCGAAGAAGATGGGSCCATATAGTCCCGTATCTATG 2028  
Qy 1921 GCAATTTAGGCTCCGACACTCATGTATATCTTCGATCAATGCCGAATATCTATCTT 1980  
Db 2029 GCAATTTAGGCTCCGACACTCATGTATATCTTCGATCAATGCCGAATATCTATCTT 2088  
Qy 1981 CACATGGGATCTTCTGCGCGGCAAGTCCGTCATGAGGCGTCAAGCAATGACCAAGGAGA 2040  
Db 2089 CACATGGGATCTTCTGCGCGGCAAGTCCGTCATGAGGCGTCAAGCAATGACCAAGGAGA 2148  
Qy 2041 GCAATTTGCGCAACGCAACACGCAATCATATGATGAGGCGCAACCAATGGCGGCAACA 2100  
Db 2149 GCAATTTGCGCAACGCAACACGCAATCATATGATGAGGCGGCAACCAATGGCGGCAACA 2208  
Qy 2101 CTTGTCTGACACCAATCATCAAGCTCGATCATCGGACTATGAAATTTGGCTGAGTGA 2160  
Db 2209 CTTGTCTGACACCAATCATCAAGCTCGATCATCGGACTATGAAATTTGGCTGAGTGA 2268  
Qy 2161 CGGAGGAAGCTGGGAAGTTAAATCATCATGCAATCTTTATGAGGCGGTCGACAGC 2220  
Db 2269 CGGAGGAAGCTGGGAAGTTAAATCATCATGCAATCTTTATGAGGCGGTCGACAGC 2328  
Qy 2221 AAACGCTGTGATGATGAAGATGATGATGCTGAATGATGATGATGATGATGATGATG 2280  
Db 2329 AAACGCTGTGATGATGAAGATGATGATGCTGAATGATGATGATGATGATGATGATG 2388  
Qy 2281 GTGCGCACATGCGGCAAGCGATGCGGCTGCTCCGTTTACTATTTCCCAACAGAGAGC 2340  
Db 2389 GTGCGCACATGCGGCAAGCGATGCGGCTGCTCCGTTTACTATTTCCCAACAGAGAGC 2448  
Qy 2341 ATGACGAGATGGGCGGACGTTCAAGAAGCAAGGCACTCGAAGTATCTTCAAAAGGCAATG 2400  
Db 2449 ATGACGAGATGGGCGGACGTTCAAGAAGCAAGGCACTCGAAGTATCTTCAAAAGGCAATG 2508  
Qy 2401 ATGTGTTTGTGTGGGACTGTGCTGGGTTTGGTGAATTTCAAGAGTGGGATGCTG 2460  
Db 2509 ATGTGTTTGTGTGGGACTGTGCTGGGTTTGGTGAATTTCAAGAGTGGGATGCTG 2568  
Qy 2461 TCATGCTTTCGATCCCTTCGTGAGCTTTCATCAACGCTGTGATTTGCTCAACAGCA 2520  
Db 2569 TCATGCTTTCGATCCCTTCGTGAGCTTTCATCAACGCTGTGATTTGCTCAACAGCA 2628  
Qy 2521 TGTTCATGCGAATGAGTACCAAGATATGAAACAAGAGATGGAACGCGTGTCAAGAGTG 2580  
Db 2629 TGTTCATGCGAATGAGTACCAAGATATGAAACAAGAGATGGAACGCGTGTCAAGAGTG 2688  
Qy 2581 GCAACTATTTCTTACCGGCACTTTTGCATCGAGGCAACCATGATGATGAGCTATG 2640  
Db 2689 GCAACTATTTCTTACCGGCACTTTTGCATCGAGGCAACCATGATGATGAGCTATG 2748



[illegible]

Db	5914	TACCCATCTGTGCGCGTGAACCTCATTGTAATCTGCGTCGACATCTCTCGACGCCCTTAGAAAG	5973
Qy	5911	ACTTCTTTTGGCGGAAAGGGCAATCCGATAGAGAGACGGGTGAGATTGGTAGATAGACGG	5970
Db	5974	ACTTCTTTTGGCGGAAAGGGCAATCCGATAGAGAGACGGGTGAGATTGGTAGATAGACGG	6033
Qy	5971	CCCCGCCGGATACGGAAGGGCTTACGAGCCCGCTCATCAACGCTGTGGGTCAAGGTGAG	6030
Db	6034	CCCCGCCGGATACGGAAGGGCTTACGAGCCCGCTCATCAACGCTGTGGGTCAAGGTGAG	6093
Qy	6031	AGTACTGCGCCCGGCTAATCCAGACCGCTGCGGAAAGCAAGGCGCGCGGAGAG	6090
Db	6094	AGTACTGCGCCCGGCTAATCCAGACCGCTTGGCGAAAGCAAGGCGCGCGGAGAG	6153
Qy	6091	GTGGGTCTTTTGAAGCCGGATACGATCATGCGATGCGGATGATCCGGATGCGGGAGCC	6150
Db	6154	GTGGGTCTTTTGAAGCCGGATACGATCATGCGATGCGGATGATCCGGATGCGGGAGCC	6213
Qy	6151	CGGCGCCCGGATGAAAGCAACGGAACGGCGATGCGCCCGCTGGTGGAGATGGTAGTGAACG	6210
Db	6214	CGGCGCCCGGATGAAAGCAACGGAACGGCGATGCGCCCGCTGGTGGAGATGGTAGTGAACG	6273
Qy	6211	GTACTGCGAAGAGAGCTGCGCATGCGCATGAGAGTAATGTAAATAGTCCGGGTGAGATG	6270
Db	6274	GTACTGCGAAGAGAGCTGCGCATGCGCATGAGAGTAATGTAAATAGTCCGGGTGAGATG	6333
Qy	6271	CAGCGCGCGCGCGGACGACGACGACGACGCGCGCGCGGACGACGACGCGCGGAA	6330
Db	6334	CAGCGCGCGCGCGGACGACGACGACGACGCGCGCGCGGACGACGACGCGCGGAA	6392
Qy	6331	GTCCCGGAGCGGGTACGCGCCCGGCGACAGACCGCCGTTCTCTGTGAGAGCGACGGGTTCCG	6390
Db	6394	GTCCCGGAGCGGGTACGCGCCCGGCGACAGACCGCCGTTCTCTGTGAGAGCGACGGGTTCCG	6453
Qy	6391	TGACGAGAAAGCGGCAACAGGTGTGATCATCTCGCATTCGCGGAGCATCAGTCCGCGCA	6450
Db	6454	TGACGAGAAAGCGGCAACAGGTGTGATCATCTCGCATTCGCGGAGCATCAGTCCGCGCA	6513
Qy	6451	CGGCGGATGTCTGA 6464	
Db	6514	CGGCGGATGTCTGA 6527	
RESULT 4			
AAV82500			
ID	AAV82500 standard; cDNA; 6519 BP.		
XX	AAV82500;		
AC	18-MAR-1999 (first entry)		
XX			
DT			
XX			
DE	Calcium permeable voltage sensitive sodium channel encoding #3.		
XX			
KW	Calcium permeable; voltage sensitive sodium channel; VSSC; insect;		
KW	calcium transport; insecticide; pesticide; insect control; vertebrate;		
KW	intracellular calcium concentration; calcium-chelating fluorescent dye;		
XX	calcium-binding bioluminescent protein; ss.		
OS	Drosophila melanogaster.		
XX			
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
XX	1..6303		
XX	/*tag= a		
XX			
FN	US5858713-A.		
XX			
PD	12-JAN-1999.		
XX			
PF	28-FEB-1997; 97US-00808793.		
XX			
PR	01-MAR-1996; 96US-0012649P.		
PR	24-DEC-1996; 96US-0034361P.		
XX			

PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Ingles PJ, Soderlund DM;  
 XX  
 DR WPI, 1999-119877/10.  
 XX P-PSDB; AAW89579.  
 PT  
 PT Calcium permeable sodium channels - obtained by expression of insect  
 PT nucleic acid encoding a sodium channel, that includes a mutation which  
 PT renders the channel permeable to calcium.  
 PS  
 PS Claim 16; Col 71-78; 48pp; English.  
 XX  
 XX The present sequence encodes a voltage sensitive sodium channel (VSSC)  
 CC isolated from an insect, that has a mutation which renders the sodium  
 CC channel permeable to calcium. The VSSC can be used as a screening agent  
 CC to detect the ability to modify sodium channel function (i.e. to render  
 CC it permeable to calcium), by monitoring calcium transport through it.  
 CC Transformed cells, that include the calcium permeable VSSC, can be  
 CC exposed to various potential insecticides and pesticides, and evaluated  
 CC for their susceptibility to them. This will facilitate the development  
 CC and identification of insect control agents, that will not cause adverse  
 CC effects to vertebrate species. The VSSC can also be used for the  
 CC production of antibodies. The calcium permeable VSSC can be sensitively  
 CC monitored for changes in intracellular calcium concentrations, using  
 CC either: calcium-chelating fluorescent dyes, or calcium-binding  
 CC bioluminescent proteins  
 CC  
 SQ Sequence 6519 BP; 1707 A; 1544 C; 1698 G; 1570 T; 0 U; 0 Other;  
 Query Match 94.6%; Score 6163.8; DB 2; Length 6519;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 6339; Conservative 0; Mismatches 12; Indels 138; Gaps 3;

QY 624 GGTTCATTTTATGCCCCGTTTACGATCTCTAGAGATGCAATGGAATTGGCTGGACTTTCGA 683  
 DB 601 GGTTCATTTTATGCCCCGTTTACGATCTCTAGAGATGCAATGGAATTGGCTGGACTTTCGA 660  
 QY 684 GTAATAGCTTTAGCTTATGTCACATGAGGTATAGATTTAGTAATCTAGACAGCCCTGCGA 743  
 DB 661 GTAATAGCTTTAGCTTATGTCACATGAGGTATAGATTTAGTAATCTAGACAGCCCTGCGA 720  
 QY 744 ACGTTTAGGCTCTCGAGCGCTTAAACCGTAGCCATTGTGCGAGCTTGAAGCCATC 803  
 DB 721 ACGTTTAGGCTCTCGAGCGCTTAAACCGTAGCCATTGTGCGAGCTTGAAGCCATC 780  
 QY 804 GTGCGCGCCGTCATGAAATCCGTTGAAGATCCGCGCATGTATCTCTGACATGTTTC 863  
 DB 781 GTGCGCGCCGTCATGAAATCCGTTGAAGATCCGCGCATGTATCTCTGACATGTTTC 840  
 QY 864 TCCCTGTGCGTGTGCGCTTGAATGAGGCTTACAGATCTATATGAGGCGTGTCTCACAGAGA 923  
 DB 841 TCCCTGTGCGTGTGCGCTTGAATGAGGCTTACAGATCTATATGAGGCGTGTCTCACAGAGA 900  
 QY 924 TGCATCAGAGAGTTCCCGCTGACCGTTCTCTGGGCAATCTGACCGAGAACTGGGAC 983  
 DB 901 TGCATCAGAGAGTTCCCGCTGACCGTTCTCTGGGCAATCTGACCGAGAACTGGGAC 960  
 QY 984 TATCACAATCGCAATAGCTCCAAATGATGTTTCCGAGAGAGAGGCAATCTCATTTCCGTTA 1043  
 DB 961 TATCACAATCGCAATAGCTCCAAATGATGTTTCCGAGAGAGAGGCAATCTCATTTCCGTTA 1020  
 QY 1044 TCGGCAATATATCCGCTGCGGCGCAATGCGACAGAGATTAATGCTGTCGAGAGGCTT 1103  
 DB 1021 TCGGCAATATATCCGCTGCGGCGCAATGCGACAGAGATTAATGCTGTCGAGAGGCTT 1080  
 QY 1104 GGTTCGAATCCGAATTTATGCTTACACCACTTCTGATTCCTTGGAGAGGCTTCCGTGTC 1163  
 DB 1081 GGTTCGAATCCGAATTTATGCTTACACCACTTCTGATTCCTTGGAGAGGCTTCCGTGTC 1140  
 QY 1164 GCCTTCGCGGTGATGACACAGAGCTTCTGAGAGATCTTACAGAGTGTGTTGCGGCGC 1223  
 DB 1141 GCCTTCGCGGTGATGACACAGAGCTTCTGAGAGATCTTACAGAGTGTGTTGCGGCGC 1200  
 QY 1224 GCGGACCAATGACATGCTGTTCTTTATATGATCATCTTCTAGTCTTATCTTATCTT 1283  
 DB 1201 GCGGACCAATGACATGCTGTTCTTTATATGATCATCTTCTAGTCTTATCTTATCTT 1260  
 QY 1284 GTGAATTTGATTTTGGCCATGTTTGGCATGCTGTAAGAGAAATTTGAAAGGAGCGGA 1343  
 DB 1261 GTGAATTTGATTTTGGCCATGTTTGGCATGCTGTAAGAGAAATTTGAAAGGAGCGGA 1320  
 QY 1344 GAGAGAGGCTCCGAAAGAGAGGCGATACGTGAAGCGGAAGAGCTGCGCGCCAAA 1403  
 DB 1321 GAGAGAGGCTCCGAAAGAGAGGCGATACGTGAAGCGGAAGAGCTGCGCGCCAAA 1380  
 QY 1404 GCGGCCAAGCTGAGAGAGCGGCGCAATGCGAGGCTTCAAGCAGCAGATGCGGCTGCC 1463  
 DB 1381 GCGGCCAAGCTGAGAGAGCGGCGCAATGCGAGGCTTCAAGCAGCAGATGCGGCTGCC 1440  
 QY 1464 GCGGAAGGCTCACATGCAATCCGGAATGCGCAAGTCCGAGATTTCTTGCATCAGC 1523  
 DB 1441 GCGGAAGGCTCACATGCAATCCGGAATGCGCAAGTCCGAGATTTCTTGCATCAGC 1500  
 QY 1524 TATAGCTATTTTGTGGCGGCGAAGAGGCGCAAGATGACAAACAAGAGAAAGATGTC 1583  
 DB 1501 TATAGCTATTTTGTGGCGGCGAAGAGGCGCAAGATGACAAACAAGAGAAAGATGTC 1560  
 QY 1584 ATTGAGAGCTGAGAGGTGAGTGGAGTCCGTGAGGCTTATACAAAGCAACAAGACACT 1643  
 DB 1561 ATTGAGAGCTGAGAGGTGAGTGGAGTCCGTGAGGCTTATACAAAGCAACAAGACACT 1620  
 QY 1644 ACCAGAGCAACAAGATCCAAAGTTCTTAAAGTGAAGCAGCATCTTATCTTACTT 1703  
 DB 1621 ACCAGAGCAACAAGATCCAAAGTTCTTAAAGTGAAGCAGCATCTTATCTTACTT 1680

QY 1704 GGTTCACCGTTAACTATAGGAGGGGATCAAGTACTCTCAAACTAGACGATAGGAGAC 1763  
DB 1681 GGTTCACCGTTAACTATAGGAGGGGATCAAGTACTCTCAAACTAGACGATAGGAGAC 1740  
QY 1764 GGAGGTGGCCGCTTTGGTATACCCGGTGGAGCATCTAGAGCATTTGGTATGGACATAT 1823  
DB 1741 GGAGGTGGCCGCTTTGGTATACCCGGTGGAGCATCTAGAGCATTTGGTATGGACATAT 1800  
QY 1824 CAGAGTGGCCAGAGCACTTGCCCTTATGCGGACGATCTGAAATGCCGTACCCCGATGCC 1883  
DB 1801 CAGAGTGGCCAGAGCACTTGCCCTTATGCGGACGATCTGAAATGCCGTACCCCGATGCC 1860  
QY 1884 GAGAGATGGGGCCATATAGTGGCCGCTTATGCGGACGATCTGAAATGCCGTACCCCGATGCC 1943  
DB 1861 GAGAGATGGGGCCATATAGTGGCCGCTTATGCGGACGATCTGAAATGCCGTACCCCGATGCC 1920  
QY 1944 TCGATATCTGCAATCACTCCGAAATATCTGATACCTGACATGGCGATCTACTCGGCGGC 2003  
DB 1921 TCGATATCTGCAATCACTCCGAAATATCTGATACCTGACATGGCGATCTACTCGGCGGC 1980  
QY 2004 ATGGCCGTATGGGCGTCAAGCAATGACCAAGAGAGCAAAATGGCGAACCGCAACA 2063  
DB 1981 ATGGCCGTATGGGCGTCAAGCAATGACCAAGAGAGCAAAATGGCGAACCGCAACA 2040  
QY 2064 CGCAATCAATAGTGGGCGCAACCAATGGCGGACCACTGCTGGAGACCAATACAG 2123  
DB 2041 CGCAATCAATAGTGGGCGCAACCAATGGCGGACCACTGCTGGAGACCAATACAG 2100  
QY 2124 CTCGATCATCGGCACTAGAAATGGCTGAGTGCAGAGCAAGCTGGCAAGATTAA 2183  
DB 2101 CTCGATCATCGGCACTAGAAATGGCTGAGTGCAGAGCAAGCTGGCAAGATTAA 2160  
QY 2184 CATCATGCAATCTTTTATGAGCCGCTCAAGACAAACGCTGGTATGTAAGAT 2243  
DB 2161 CATCATGCAATCTTTTATGAGCCGCTCAAGACAAACGCTGGTATGTAAGAT 2220  
QY 2244 GTATGGCTGTAATGATCATGATGAAAGGCGCGTGGTGGGCAAGTGGGCAAGCAT 2303  
DB 2221 GTATGGCTGTAATGATCATGATGAAAGGCGCGTGGTGGGCAAGTGGGCAAGCAT 2280  
QY 2304 CGCGGTGTCCTGTTACTATTTCCCAAGAGAGATGAGATGGGCGGCGTTC 2363  
DB 2281 CGCGGT-----GAGAGCATGAGAGATGGGCGGCGTTC 2316  
QY 2364 AAAGACAAGGCACTCGAAAGTATCTCAAGGCAATGATGTTGTGTGGAGCTGT 2423  
DB 2317 AAAGACAAGGCACTCGAAAGTATCTCAAGGCAATGATGTTGTGTGGAGCTGT 2376  
QY 2424 TGCTGGGTTGGTGAATTTCAAGAGTGGTATCGCTCATCGCTTTCGATCCCTTCGTC 2483  
DB 2377 TGCTGGGTTGGTGAATTTCAAGAGTGGTATCGCTCATCGCTTTCGATCCCTTCGTC 2436  
QY 2484 GAGCTCTTCATCAGCTGTGATTTGGTCAACAGATGTCATGGCAATGATCAAC 2543  
DB 2437 GAGCTCTTCATCAGCTGTGATTTGGTCAACAGATGTCATGGCAATGATCAAC 2496  
QY 2544 GATATGAACAAGAGATGGAACGCGTGTCAAGAGTGGCAATATTTCTTCAACGCGCAC 2603  
DB 2497 GATATGAACAAGAGATGGAACGCGTGTCAAGAGTGGCAATATTTCTTCAACGCGCAC 2556  
QY 2604 TTTCGCAATCGAGGCAACATGATGTAATGGCCATGAGCCCAAGTACTATTTCAAGAG 2663  
DB 2557 TTTCGCAATCGAGGCAACATGATGTAATGGCCATGAGCCCAAGTACTATTTCAAGAG 2616  
QY 2664 GGCTGGAACATCTTCACTTATCGTGGCCCTATGCTATTTGAATGGGACTCGAG 2723  
DB 2617 GGCTGGAACATCTTCACTTATCGTGGCCCTATGCTATTTGAATGGGACTCGAG 2676  
QY 2724 GGTGTCCAGGGTCTGTCCGTAATGGCTCTTTGATTTGCTGGTATTTCAAACTGGCC 2783  
DB 2677 GGTGTCCAGGGTCTGTCCGTAATGGCTCTTTGATTTGCTGGTATTTCAAACTGGCC 2736  
QY 2784 AAGCTTGGGCCACCTTAATTAATTAATGATTTGATTTAGGAGCGACCATGGGCGCTTTG 2843

DB 2737 AAGCTTGGGCCACCTTAATTAATTAATGATTTGATTTAGGAGCGACCATGGGCGCTTTG 2796  
QY 2844 GGTATCTGACATTTGATCTTTGATTAATCTTTCATCTTTGGCGTATGGGATGCA 2903  
DB 2797 GGTATCTGACATTTGATCTTTGATTAATCTTTCATCTTTGGCGTATGGGATGCA 2856  
QY 2904 CTGTTGGAAAGATTAATCATGATCAAGAGACCGCTTTCCGATGGGACTGCGCGC 2963  
DB 2857 CTGTTGGAAAGATTAATCATGATCAAGAGACCGCTTTCCGATGGGACTGCGCGC 2916  
QY 2964 TGGAACTTACCGGCTTTATGACAGCTTCAATGATCGGTTCCGGGTCCTGGGAGAA 3023  
DB 2917 TGGAACTTACCGGCTTTATGACAGCTTCAATGATCGGTTCCGGGTCCTGGGAGAA 2976  
QY 3024 TGGATCGAGTCAATGGGAGCTGATGATCGTGGCGCATGCTGCTGATTCCTTCTTC 3083  
DB 2977 TGGATCGAGTCAATGGGAGCTGATGATCGTGGCGCATGCTGCTGATTCCTTCTTC 3036  
QY 3084 TTGGCCACCGTTGATCGGCAATCTTGTGATCTTAACTTTTCTTACCTTGTTC 3143  
DB 3037 TTGGCCACCGTTGATCGGCAATCTTGTGATCTTAACTTTTCTTACCTTGTTC 3096  
QY 3144 TCCAAATTTGGCTCATGATGATTAAGCGCGGCACTGCGGATTAAGATTAAGATTA 3203  
DB 3097 TCCAAATTTGGCTCATGATGATTAAGCGCGGCACTGCGGATTAAGATTAAGATTA 3156  
QY 3204 GCCGAGGCTTCAATTCGAATGGCGGATTTAAAGTTGGTAAAGCTTATTTCTGAT 3263  
DB 3157 GCCGAGGCTTCAATTCGAATGGCGGATTTAAAGTTGGTAAAGCTTATTTCTGAT 3216  
QY 3264 TGTTCGAATTAATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 3323  
DB 3217 TGTTCGAATTAATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 3269  
QY 3324 AGAGCAACAGATCAATGATTTGGAGGAGAGATGGTGAACACGAACTGGAGCTG 3383  
DB 3270 -----AAGAGTGGTGAACACGAACTGGAGCTG 3297  
QY 3384 GGCCAGACGAGATCTTCGCGGACGGCTCTATCAAGAGGGGATCAAGAGCAGACGCA 3443  
DB 3298 GGCCAGACGAGATCTTCGCGGACGGCTCTATCAAGAGGGGATCAAGAGCAGACGCA 3357  
QY 3444 CTGAGGTGGCTATCGGAGATCGATGATTAACAGATTAACGCGGACATGAAGAAC 3503  
DB 3358 CTGAGGTGGCTATCGGAGATCGATGATTAACAGATTAACGCGGACATGAAGAAC 3417  
QY 3504 AAGCGAAGAAATCAATTAATCTAAATTAAGCAAGATGATGGCACTCAATTAACAC 3563  
DB 3418 AAGCGAAGAAATCAATTAATCTAAATTAAGCAAGATGATGGCACTCAATTAACAC 3452  
QY 3564 CAAGACAATGATCGAAGACAGAGCTAAACATGAGGTTGTCTTCAAGAGCAGACGAC 3623  
DB 3453 -----GAGAGCAGAC 3462  
QY 3624 ACTGCCAGCATTAATCTATATGTAAGCAATTAAGATGACCATTTCAAGAGCAGACGAC 3683  
DB 3463 ACTGCCAGCATTAATCTATATGTAAGCAATTAAGATGACCATTTCAAGAGCAGACGAC 3522  
QY 3684 AAGGGACGCGCGAGAGATGAGAGGGGAGAGAGAGGCGACGACAGAGAGAGATTTA 3743  
DB 3523 AAGGGACGCGCGAGAGATGAGAGGGGAGAGAGAGGCGACGACAGAGAGAGATTTA 3582  
QY 3744 GGTCTCGACAGAGAACTGAGCAGAGAGGGGATGCGAGAGGGGCGCTCGACGCTGAT 3803  
DB 3583 GGTCTCGACAGAGAACTGAGCAGAGAGGGGATGCGAGAGGGGCGCTCGACGCTGAT 3642  
QY 3804 ATCATTTATGATGACAGCAGAGATTAATCTGATGATTAATCAAGCTGATTTGCTGCC 3863  
DB 3643 ATCATTTATGATGACAGCAGAGATTAATCTGATGATTAATCAAGCTGATTTGCTGCC 3702  
QY 3864 GATTCGATTAATGAATTTCCGATCTTACCGGCTGACGATGCTGCGGTTGCGCAA 3923

Db 3703 GATTGCTACTATAAGAAATTTCCGATCTTAGCCGGTGAAGATGACTCGCCGTTCTGGCAA 3762  
Qy 3924 GGATGGGGCAATTTAGACTGAACCTTTTCATTAATTAATTAATTAATTTGAAACA 3983  
Db 3763 GGATGGGGCAATTTAGACTGAACCTTTTCATTAATTAATTAATTTGAAACA 3822  
Qy 3984 GCTGTATATCACTATGATTTTAAATAGTAGTACCTTTGGCATTTAGAGATGATACATCTG 4043  
Db 3823 GCTGTATATCACTATGATTTTAAATAGTAGTACCTTTGGCATTTAGAGATGATACATCTG 3882  
Qy 4044 CCAAAAGACCCATCTGACGATTTTATTAATTAATTAATTAATTTAGAGATTTTACGTTAA 4103  
Db 3883 CCAAAAGACCCATCTGACGATTTTATTAATTAATTAATTTAGAGATTTTACGTTAA 3942  
Qy 4104 TTCTCTCTGGAATTTGTTAATCAAGTGGTGGCGCTGAGCTTCAAGTGTACTTCAACCAAC 4163  
Db 3943 TTCTCTCTGGAATTTGTTAATCAAGTGGTGGCGCTGAGCTTCAAGTGTACTTCAACCAAC 4002  
Qy 4164 GCGTGTGTGTGGCTCGATTTTCGTATTTGTCATGGTATCGCTTATCAACTTCTGTTGCTTCA 4223  
Db 4003 GCGTGTGTGTGGCTCGATTTTCGTATTTGTCATGGTATCGCTTATCAACTTCTGTTGCTTCA 4062  
Qy 4224 CTGTGTGTGTGGCTCGATTTTCGTATTTGTCATGGTATCGCTTATCAACTTCTGTTGCTTCA 4283  
Db 4063 CTGTGTGTGTGGCTCGATTTTCGTATTTGTCATGGTATCGCTTATCAACTTCTGTTGCTTCA 4122  
Qy 4284 CCACTACGTGCAATGTCCCGTATGCAAGGATGAGGATCGTGTAAATGCGTGTGTAACA 4343  
Db 4123 CCACTACGTGCAATGTCCCGTATGCAAGGATGAGGATCGTGTGTAAATGCGTGTGTAACA 4182  
Qy 4344 GCTATACCGTTCATCTTCAATGTGTCTATTTGTGTGTCTAATTTTGGCTAATTTTGGC 4403  
Db 4183 GCTATACCGTTCATCTTCAATGTGTCTATTTGTGTGTCTAATTTTGGCTAATTTTGGC 4242  
Qy 4404 ATATAGGTGTACAGCTTTTGTGTGTAATTTTAAAGTCCGAGACATGAATGAGCAGC 4463  
Db 4243 ATATAGGTGTACAGCTTTTGTGTGTAATTTTAAAGTCCGAGACATGAATGAGCAGC 4302  
Qy 4464 AAGCTCAGCCAGATCATTAACAATTCGCAATGCTGCGAGACGAGAACTACACGTGG 4523  
Db 4303 AAGCTCAGCCAGATCATTAACAATTCGCAATGCTGCGAGACGAGAACTACACGTGG 4362  
Qy 4524 GTGATTCAGCAATGATTTTGATCATGATAGTAAACGGTATCTGTGCTTTTCCAAATG 4583  
Db 4363 GTGATTCAGCAATGATTTTGATCATGATAGTAAACGGTATCTGTGCTTTTCCAAATG 4422  
Qy 4584 GCAACCTTCAAAAGGTGATCAATCATGAAGATGCTATGATTCAGACGAGAGTGGAC 4643  
Db 4423 GCAACCTTCAAAAGGTGATCAATCATGAAGATGCTATGATTCAGACGAGAGTGGAC 4482  
Qy 4644 AAGCAACCAATTCGTGAAGCAACATCTACATGATTTTAAATTTTCTTCAATCATTA 4703  
Db 4483 AAGCAACCAATTCGTGAAGCAACATCTACATGATTTTAAATTTTCTTCAATCATTA 4542  
Qy 4704 TTTGGATCTTTTCACTCACTCAATCTGTCATGTTGTTTCAATGATTTTAAATGAG 4763  
Db 4543 TTTGGATCTTTTCACTCACTCAATCTGTCATGTTGTTTCAATGATTTTAAATGAG 4602  
Qy 4764 CAAAAGAAAAAGCAGTGTATCATTAAGAAATGTTTATGACAGAGATCAGAAAAAGTAC 4823  
Db 4603 CAAAAGAAAAAGCAGTGTATCATTAAGAAATGTTTATGACAGAGATCAGAAAAAGTAC 4662  
Qy 4824 TATTAATGCTATGAATAAGTGGCTCTTAAAAAAGCAATTAAGCAATTCAGAACCAAG 4883  
Db 4663 TATTAATGCTATGAATAAGTGGCTCTTAAAAAAGCAATTAAGCAATTCAGAACCAAG 4722  
Qy 4884 TGGGACACCAAGCAATGCTTTGAAATAGTAAACCAATTAAGAAATTTGATATATCATT 4943  
Db 4723 TGGGACACCAAGCAATGCTTTGAAATAGTAAACCAATTAAGAAATTTGATATATCATT 4782  
Qy 4944 ATGTTATTCATTTGCTGTAACATGTTTCAATGATCCTGATGCTTAAAGTGGTGGAC 5003  
Db 4783 ATGTTATTCATTTGCTGTAACATGTTTCAATGATCCTGATGCTTAAAGTGGTGGAC 4842

Qy 5004 ACGTAAACGGGCTCTGACATCTCAATGCGATATTCAGTATTTTCCGAA 5063  
Db 4843 ACGTAAACGGGCTCTGACATCTCAATGCGATATTCAGTATTTTCCGAA 4902  
Qy 5064 TGTCTATTAATAATTTGCGTTTACAGATATCAATTTTATTTAGCCATGAAATTTATTT 5123  
Db 4903 TGTCTATTAATAATTTGCGTTTACAGATATCAATTTTATTTAGCCATGAAATTTATTT 4962  
Qy 5124 GATGTAGTATGTTGATTTTATTCATCTTAAAGTCTTGTATCTTAAAGATTTATCGAAG 5183  
Db 4963 GATGTAGTATGTTGATTTTATTCATCTTAAAGTCTTGTATCTTAAAGATTTATCGAAG 5022  
Qy 5184 TACTTGTGTGGCCGACCTTGTCCGATGTTGGTGGGGAAGTGGGCGGTCTCTT 5243  
Db 5023 TACTTGTGTGGCCGACCTTGTCCGATGTTGGTGGGGAAGTGGGCGGTCTCTT 5082  
Qy 5244 CGACTGTGTAAGGAGCCAAAGGCAATTCGACACTGCTCTTTCGCTTGGCAATGTGCTG 5303  
Db 5083 CGACTGTGTAAGGAGCCAAAGGCAATTCGACACTGCTCTTTCGCTTGGCAATGTGCTG 5142  
Qy 5304 CCGGCGCTGTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5363  
Db 5143 CCGGCGCTGTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5202  
Qy 5364 GCGATGTGCTTCTTCAATGACGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5423  
Db 5203 GCGATGTGCTTCTTCAATGACGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5262  
Qy 5424 AAGACCTTTTGGCCAGACATGATCTGCTTTCAGATGTGACGTCAGCCGCTTGGGAT 5483  
Db 5263 AAGACCTTTTGGCCAGACATGATCTGCTTTCAGATGTGACGTCAGCCGCTTGGGAT 5322  
Qy 5484 GGTGTCTGAGCGCCATTTATCAATGAGGAAGATGATGCAACCCGACAGCAAGAGGC 5543  
Db 5323 GGTGTCTGAGCGCCATTTATCAATGAGGAAGATGATGCAACCCGACAGCAAGAGGC 5382  
Qy 5544 TATCCGGGCAATTTGTGTGTCAGGACCGTGTGAATTAACCTTCTCTCATACCTAGTT 5603  
Db 5383 TATCCGGGCAATTTGTGTGTCAGGACCGTGTGAATTAACCTTCTCTCATACCTAGTT 5442  
Qy 5604 ATAAAGCTTTTGTATGTTATTAATTAATGATCATTTGCTGTCAATTTCTGAGAACTATGTCAG 5663  
Db 5443 ATAAAGCTTTTGTATGTTATTAATTAATGATCATTTGCTGTCAATTTCTGAGAACTATGTCAG 5502  
Qy 5664 GCAACCGAGAGCCTGGAAGAGGCTTAAACCGACGACGACGACGACGACGACGACGACGAC 5723  
Db 5503 GCAACCGAGAGCCTGGAAGAGGCTTAAACCGACGACGACGACGACGACGACGACGACGAC 5562  
Qy 5724 TGGCAGCAATTCGATCCGAGGAGCCACCAATGATCATGATGATGATGATGATGATGATGAT 5783  
Db 5563 TGGCAGCAATTCGATCCGAGGAGCCACCAATGATCATGATGATGATGATGATGATGATGAT 5622  
Qy 5784 CTGAGCACTGAGACCCCGCTGCGATGATCAACCAACCAACCAACCAACCAACCAACCAAC 5843  
Db 5623 CTGAGCACTGAGACCCCGCTGCGATGATCAACCAACCAACCAACCAACCAACCAACCAAC 5682  
Qy 5844 ATGAGCACTACCAATGCTGCGGATGATCTGATGATCTGATGATCTGATGATCTGATGAT 5903  
Db 5683 ATGAGCACTACCAATGCTGCGGATGATCTGATGATCTGATGATCTGATGATCTGATGAT 5742  
Qy 5904 ACGAAAGACTTCTTGTGCGGAAAGGCAATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 5963  
Db 5743 ACGAAAGACTTCTTGTGCGGAAAGGCAATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 5802  
Qy 5964 ATAGCCGCCCGCCGATTAAGAGAGGCTAAGAGCCGCTCAACCAAGCTGTGAGCTGAG 6023  
Db 5803 ATAGCCGCCCGCCGATTAAGAGAGGCTAAGAGCCGCTCAACCAAGCTGTGAGCTGAG 5862  
Qy 6024 CGTGAAGATATGCGCCCGCTAATCCAGACGCTTGGGAAAGCAAGAGGCGCGGCGC 6083  
Db 5863 CGTGAAGATATGCGCCCGCTAATCCAGACGCTTGGGAAAGCAAGAGGCGCGGCGC 5922



Db	748	GTGGTGTCTGTCAATGAATCTGTAAAAAATCTAGCGCATGTGAATATTTGACATGT	807
OY	864	TCCTGTTCGGTGTTCGGGTGATGGGCTTACAGATCTATATGGCGGTCTCACCGAGA	923
Db	808	TCCCTGTTCGGTGTTCGGGTGATGGGCTTACAGATCTATATGGGTGTCTTACACAAAG	867
OY	924	TGCATCAAGAAGTTCGCGTGTGAAGGTTTCCGAGGCAATCTGACCGACGAAATCGGAC	983
Db	868	TGCATTAACGATTCCTCCCTGAGCGCAGTTGGGGCAATCTGACCGAATCGAATCTG	927
OY	984	TATCACAATCGCAATAGCTCCATTTGGTATTCGAGGACGAGGGCATCTCATTTCCG	1043
Db	928	CTACACAATAGCAACAGTTCCAAATGGTTTACGAGAAACGATGCGCATATCTCCG	987
OY	1044	TGCGGCAATATATCCGGTGGGGGCAATGCGACGACATTAACGTGTCTGACAGGG	1103
Db	988	TGCGGCAATATATCCGGTGGGGGCAATGCGACGACATTAACGTGTCTGACAGGG	1047
OY	1104	GGTCCGAATCCGAATTAATGCTTACACGACGCTCATTTGTTCCGAGTGGGCTTCT	1163
Db	1048	GGCCCATATCCCATCTAGACCTAACACAGTTTGCATTTCCGTTGGGCTTCTGTG	1107
OY	1164	GCCTTCCGGCTGATGACACAGGACTTCTGGAGGATCTTATCCAGCTGTGTTCGG	1223
Db	1108	GCCTTCCGGCTGATGACACAGGACTTCTGGAGGATCTTATCCAGCTGTGTTCGA	1167
OY	1224	GCCGGACATGGGACATGCTGTCTTTATATGATCATCTTCCAGGTTCATTTATCT	1283
Db	1168	GCTGGACCTGGCAATGTGTCTTTATATGATCATCTTCCAGGTTCATTTATCT	1227
OY	1284	GTGAATTTGATTTTGGCCATTTGTTCCATGTCTATGACGAAATTCGAAAGAGCC	1343
Db	1228	GTGAATTTGATTTTGGCCATTTGTTCCATGTCTTATGACGAAATTCGAAAGAGCC	1287
OY	1344	GAAAGAGGCTGGCCGAAAGAGAGGCGCATAGTAAAGGAAAGAGCTGCCGCCAAA	1403
Db	1288	GAAAGAGGCTGGCCGAAAGAGAGGCGCATAGTAAAGGAAAGAGCTGCCGCCAAG	1347
OY	1404	GCGGCAAGCTGAGAGAGCGGGCCCATGCGAGGCTCAGGCAAGCGGATGCGGCTGC	1463
Db	1348	GCGGCAAGCTGAGAGAGCGGGCCCATGTCAGGCTCAGGATGCGGATGCGGAT	1407
OY	1464	GCCGAAAGGCTGACATGCAATCCGGAATATGCGCAAGAGTCCGAGGTATCTTGATCAG	1523
Db	1408	GCCGCTGGGCAAGCTGCAATCCGGAATATGCGCAAGAGTCCGAGGTATCTTGATCAG	1467
OY	1524	TATGAGCTATTTGTTGGCGGAGAGAGGCAACATGACCAACAAAGAAAGATGTC	1583
Db	1468	TATGAGCTATTTGTTGGCGGAGAGAGGCAACATGACCAACAAAGAAAGATGTC	1527
OY	1584	ATTGGAGCGTGCAGGTGGAAGTCCGAGTCCGTTAGCTTATACAAAGCAACGACACT	1643
Db	1528	ATTGGAGCGTGCAGGTGGAAGTCCGAGTCCGTTAGCTTATACAAAGCAACGACACT	1587
OY	1644	ACCAAGACACCAAGCTACCAAGTTGTAAAGTACAGACGATCCTTATCTTACT	1703
Db	1588	ACCAAGACACCC--GCTACTAAAGTCCGTAAAGTACAGACTTCTTATCTTACT	1644
OY	1704	GGTTCAACCGTTTAACTACCGCGGGGATCAAGTATTCACACAAGTACACAATACGAAT	1764
Db	1648	GGTTCAACCGTTTAACTACCGCGGGGATCAAGTATTCACACAAGTACACAATACGAAT	1704
OY	1764	GGAGCTGCGCTTTGTGTATACCGGTAGCGATGTAGCCATTTGTATTTGTCAACATAT	1823
Db	1708	GGAGCTGCGCTTTGTGTATACCGGTAGCGATGTAGCCATTTGTATTTGTCAACATAT	1764
OY	1824	CAGGATGCGCAGACGCTTGCCCTATGCGACGACTGAAATGCGTCAACCCGATGTCC	1883
Db	1768	CAGGATGCGCAGACGCTTGCCCTATGCGACGACTGAAATGCGTCAACCAATGTCC	1824
OY	1884	GAAAGAAATGGGCGCATATATGTCGCTGTATCTATGGCAATCTTAGCTCCGACCTCA	1943
Db	1828	GAAAGAAATGGGCGCATATATGTCACACCTATATTTAATTTAGTTCTTAGACATCT	1884

QY	1944	TCGTAATCCCTGGCATGATGTCGCCAATATCGTATACCTGATAGTGCATGACGATCCGCGGGC	2003
QY	1944	TCGTAATCCCTGGCATGATGTCGCCAATATCGTATACCTGATAGTGCATGACGATCCGCGGGC	2003
Db	1985	TCATATACCTCGCATCATCAAGAAATCGTATACATCATATGCTGATTTATTTGGGTGGC	1944
QY	2004	ATGAGCCCTCATGAGGCGCTGACGACAAATGACCCAGAGAGNCAAAATTTGGCAACCGCAACACA	2063
Db	1945	ATGGCGGCGCATGGGTGCGACGACAAATGACCAAAAGAGGCAAAATTTGGCACTGCCAACACA	2004
QY	2064	CGCAATCAATCAGTGGGCGCCACCAATGGGGGACCACTGTCTGCACACCAATTCACAG	2123
Db	2005	CGCAATCAATCAATCGGTGCTGCACCAATGATGGGCGATGATACGCTGTGGTGGCTAT	2064
QY	2124	CTGCAAT-----CATCGGCACTACGAAATTTGGCTGGAGTCCACGACGAA	2168
Db	2065	CCGATCCCAATCACAAGAAACAAAGGATTTATGAATTTGGGTGACAGATTTATACAGACGA	2124
QY	2169	GCTGGCAGATTTAAACATCATGACAAATCTTTATCGAGCGCTCCAGACACAAACGGTG	2228
Db	2125	GCTGGCAAAATTAACACCGACGACAAATCTTTATCGAGCGCTCCAAATCTCAACAGTG	2184
QY	2229	GTTGATATGAAAAGATGATGATGATCTCTGAATGACATCTGAAACAGCGCGGTGGTGGCAC	2288
Db	2185	GTAACACATGAAAGATGTTATGATCTTTAAATGATATCATGAACAGCGCTGGTGGCAT	2244
QY	2289	AGTGGGCAAGCGATCCGCGGTGCTCCGTTACTATTTCCCAACAGAGACGATGACGAG	2348
Db	2245	AGTGTGCTGATGAACGAGT-----GAGGACGATGACGAA	2280
QY	2349	GATGGGCGGACGTTCAAAAGACAGGACCTCGAAGTATCTCTCAAAGGACATGATGCTT	2408
Db	2281	GATGTGCCCATTTCAAGGACATGCGCTCGAATACATCTTAAAGGACATCGAAATCTTT	2340
QY	2409	TGTGTGTGGGACTGTGCTGGTGTGGTTGAAATTTGAGAGATGGGATGCGCTATCGTC	2468
Db	2341	TGTGTATGGGACTGTGTTGGGTGTGTTAAATTTGAGGAATGGGTGCTCTTTATTTGTG	2400
QY	2469	TTGATCCCTTGTGAGCTCTTTCATCAGCGCTGCAATTGTGTCAACACGATGTTATG	2528
Db	2401	TTCCATCCATTCGGGAGCTCTTTCATACCTCGTGTATTTGTGTCAATTAAGATGTTATG	2460
QY	2529	GCATGATATCCACGATATGAAACAAAGATGGAACGCGTGCACAGATGCGCACTAT	2588
Db	2461	GCCATGATATCACGACATGAATCCGGAATTAGAGAAAGTGTGAAAAATGTGATAT	2520
QY	2589	TTCTTTCACCGCACCTTTGCCATCGAGGCGCACCATGAAGCTAATGGCATGAGCCCCAG	2648
Db	2521	TTCTTTCACCGGCACTTTTGCATATGAAGCCAGCATGAATGCGCATGAGGCCAGAG	2580
QY	2649	TACTATTTTCCAGAGGCGTGGAAACATCTTGACCTTCACTTATCGGGCCATATGCTATG	2708
Db	2581	TACTACTTCCAGAGGCGTGGAAACATTTTGATTTCACTATTTGGGCGCTTGTCTCTGTG	2640
QY	2709	GAACTGGGACTCGAGGGTGTCCAGGGTCTGTCCGTAATTTGGCTCTCTTCGATATGCTGGT	2768
Db	2641	GAAATTTGGGCGCTGGAGGGTGTCCAGGGCTGTCCGTTGTGAAGATTTTCGTTGCTTGT	2700
QY	2769	GTATTTCAAATCTGSCCAAGTCTTGGCCACACTTAATTTACTCATTTGATTTATGGAGCGC	2828
Db	2701	GTATTTCAAATTTGGCAAAATCATGTGCCACACTCAATTTACTCATTTGATTTATGGGCGG	2760
QY	2829	ACCAATGGGCGCTTTGGGTAATCTGACATTTTGATCTTTGCAATATATCATCTTCATTTTGGC	2888
Db	2761	ACCAATGGGCGCTTTGGGTAATCTGACATTTTGATCTTTGCAATATATCATCTTCATTTTGGC	2820
QY	2889	GTGATGGGAATGCAACTGTTCCGAAAGAAATTTATCATGATCAACAAGACCGCTTCCGGAT	2948
Db	2821	GTGATGGGAATGCAACTTTTTCGAAAGAACTATATGACACACAGATGCGCTTCMAAGAC	2880
QY	2949	GGCGACTGCGCGCGCTGGAATCTTACCGGACTTTATGCAAGCTTCATGATCGTGTTCGG	3008
Db	2861	CATGAATTTACCGCGCTGGAATCTTACCGGACTTATGCAAGCTTCATGATGTTGTTCGGA	2940



Db 5062 AGGACATCATTTGAGAAGTATTTGATGCGCGACACTGCTCGTGTGTGAGAGTGGCC 5121  
 Qy 5226 AAATGGCCCGTGTCTTGTGACTGTGGAAGGAGCCAAAGGCACTTGGACACTGCTCTTC 5285  
 Db 5122 AAAGTGGGTGTGTCTGTGGTGTAGTCAAGGGGTGCAAGGGTATCCGAGCTGTGTGTC 5181  
 Qy 5286 GGGTTGGCAATGTGCGTGGCGGCGCTGTTCACATCTGCTGCTGTCTGTCTGTCTGT 5345  
 Db 5182 GCGTTAGCCATGTGTGCTGCTGCTTATTCACATTTGTCTGTGTGTGTGTGTGTGT 5241  
 Qy 5346 TTGATCTTGGCAATTTTGGCAATGTGTCTTATGCACTGAAGAGAGAGAGGGGAT 5405  
 Db 5242 TTGATCTTGGCAATTTTGGCAATGTGTCTTATGCACTGAAGAGAGAGAGGGGAT 5301  
 Qy 5406 AAGAGCTTACACTTCAAGACTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5465  
 Db 5302 AATGCTGTGTATTAATTTTAAAGACTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAG 5361  
 Qy 5466 ACGTCAAGCCGTTGGAGTGTGTAGTGAAGCCATTAATCAATAGAGAGAGAGAGAG 5525  
 Db 5362 ACGTCAAGCCGTTGGAGTGTGTAGTGAAGCCATTAATCAATAGAGAGAGAGAGAG 5421  
 Qy 5526 CCGGACAGCCGCAAAAGGCTATCCGGGCAATTTGTGTGACGACCGCTTGAATAAGGTT 5585  
 Db 5422 CCGGACAGCCGCAAAAGGCTATCCGGGCAATTTGTGTGACGACCGCTTGAATAAG 5481  
 Qy 5586 CTGCTCTCATACCTAGTTATTAAGCTTTTGTATTAATTAATTAATTAATTAATTA 5645  
 Db 5482 CTGCTCTCATACCTAGTTATTAAGCTTTTGTATTAATTAATTAATTAATTAATTA 5541  
 Qy 5646 CTGAGAACTATTAAGTGAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5705  
 Db 5542 CTGAGAACTATTAAGTGAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5601  
 Qy 5706 GACATGATATTAAGTGAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5765  
 Db 5602 GATATGATATTAAGTGAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5661  
 Qy 5766 GATCAGCTGTCCGATTTCTTGAAGCTTCTGAGGCGCCGCTGAGATCCAAACGCAAC 5825  
 Db 5662 GACAGCTGTCCGATTTCTTGAAGCTTCTGAGGCGCCGCTGAGATCCAAACGCAAC 5721  
 Qy 5826 AAGTACAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5885  
 Db 5722 AAGTACAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATG 5781  
 Qy 5886 GACATCTCGAGCGCCCTTACGAAAGACTTCTTGGCGGAGAGAGAGAGAGAGAGAG 5945  
 Db 5782 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5841  
 Qy 5946 ACGGCTGAGATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 Db 5842 ACGGCTGAGATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 Qy 6006 TCAACGCTGTGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6065  
 Db 5902 TCAACGCTGTGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5961  
 Qy 6066 AAGCAAGAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6125  
 Db 5962 CGTTTCAAGAGATGGC-----CCACCAGAGAGAGAGAGAGAGAGAGAGAGAG 5994  
 Qy 6126 GCGGCTGATCCGATGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6185  
 Db 5995 GAGGCGCGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6054  
 Qy 6186 GGT 6245  
 Db 6055 GCGGCGCGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6114  
 Qy 6246 AATGTAAATATGTCCGGGTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6305  
 Db 6115 ACATCACCT-----CAGATCCAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 6159

Qy 6306 GCGGCGCGAG 6365  
 Db 6160 GTCGCGCGAG 6219  
 Qy 6366 GTTCTGT 6425  
 Db 6220 GTACTGT 6279  
 Qy 6426 CGATGCGCGAG 6484  
 Db 6280 AGATGCGCGAG 6318  
 RESULT 6  
 AAV82498  
 ID AAV82498 standard; cDNA; 6318 BP.  
 AC AAV82498;  
 AC 18-MAR-1999 (first entry)  
 DE Calcium permeable voltage sensitive sodium channel encoding cDNA #1.  
 DE Calcium permeable; voltage sensitive sodium channel; VSSC; insect;  
 KW calcium transport; insecticide; pesticide; insect control; vertebrate;  
 KW intracellular calcium concentration; calcium-chelating fluorescent dye;  
 KW calcium-binding bioluminescent protein; ss.  
 OS Musca domestica.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 1..6218  
 FT /tag= a  
 PN US5858713-A.  
 PD 12-JUN-1999.  
 PP 28-FEB-1997; 97US-00808793.  
 PR 01-MAR-1996; 96US-0012649P.  
 PR 24-DEC-1996; 96US-0034361P.  
 PR  
 PA (CORR ) CORNELL RES POUND INC.  
 XX  
 XX Ingles PJ, Soderlund DM;  
 XX WPI; 1999-119877/10.  
 DR P-PSDB; AAW89577.  
 XX  
 PT Calcium permeable sodium channels - obtained by expression of insect  
 PT nucleic acid encoding a sodium channel, that includes a mutation which  
 PT renders the channel permeable to calcium;  
 PS  
 PS Claim 13; COL 23-28; 48pp; English.  
 XX  
 XX The present sequence encodes a voltage sensitive sodium channel (VSSC)  
 CC isolated from an insect, that has a mutation which renders the sodium  
 CC channel permeable to calcium. The VSSC can be used as a screening agent  
 CC to detect the ability to modify sodium channel function (i.e. to render  
 CC it permeable to calcium), by monitoring calcium transport through it.  
 CC Transformed cells, that include the calcium permeable VSSC, can be  
 CC exposed to various potential insecticides and pesticides, and evaluated  
 CC for their susceptibility to them. This will facilitate the development  
 CC and identification of insect control agents, that will not cause adverse  
 CC effects to vertebrate species. The VSSC can also be used for the  
 CC production of antibodies. The calcium permeable VSSC can be sensitively  
 CC monitored for changes in intracellular calcium concentrations, using  
 CC either: calcium-chelating fluorescent dyes, or calcium-binding  
 CC bioluminescent proteins  
 CC  
 CC Sequence 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 U; 0 Other;

Query Match 68.3%; Score 4447.8; DB 2; Length 6318;  
Best Local Similarity 82.0%; Pred. No. 0;  
Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

```
QY 24 ATGACAGAAAGATTCGACATCTGATATCTGAGAGAAACGAGTTTCTTCGCTCCCTTAC 83
DB 1 ATGACAGAAAGATTCGACATCTGATATCTGAGAGAAACGAGTTTCTTCGCTCCCTTAC 60
QY 84 CGCGAATCATTTGGTGCAGAAATGCAACACGCAATTCGCGTGAACATGAAAGCAGAGAG 143
DB 61 CGCGAATCATTTGGTGCAGAAATGCAACACGCAATTCGCGTGAACATGAAAGCAGAGAG 117
QY 144 CTGGAAGAAAGAGAGCGGAGAGAGAGTCCGCAATATGATCGAGAGAGAGAGAGAGAG 203
DB 118 CTGGAAGAAAGAGAGCGGAGAGAGAGTCCGCAATATGATCGAGAGAGAGAGAGAGAG 148
QY 204 GAAATCCGATATGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 263
DB 149 -AGATACGATATGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 207
QY 264 CAGGCTGCGCAATACCTGTTGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAG 323
DB 208 CAGGCTGCGCAATACCTGTTGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAG 267
QY 324 CCTCTGAGATATGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 383
DB 268 CCTCTGAGATATGATGAGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 327
QY 384 GAAAGAGATATTTTTCGCTTTCTGATCAAAAGAGATGAGATGAGATGAGATGAGATGAG 443
DB 328 GAAAGAGATATTTTTCGCTTTCTGATCAAAAGAGATGAGATGAGATGAGATGAGATGAG 387
QY 444 CGGATACGCTGCTGAGCAATTTACATCTGATGATGATGATGATGATGATGATGATGATG 503
DB 388 CGGATACGCTGCTGAGCAATTTACATCTGATGATGATGATGATGATGATGATGATGATG 447
QY 504 ACCACAAATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
DB 448 ACCACAAATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
QY 564 ACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
DB 508 ACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567
QY 624 GGTTCATTTTATGCGCGTTTACGATCTTACGATGATGATGATGATGATGATGATGATG 683
DB 568 GGTTCATTTTATGCGCGTTTACGATCTTACGATGATGATGATGATGATGATGATGATG 627
QY 684 GTATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743
DB 628 GTATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
QY 744 ACGTTTAGGCTGCTGAGCGCTTAAACCGTAGCATTGTCGAGCTTGAAGACATC 803
DB 688 ACGTTTAGGCTGCTGAGCGCTTAAACCGTAGCATTGTCGAGCTTGAAGACATC 747
QY 804 GTGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
DB 748 GTGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
QY 864 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
DB 808 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
QY 924 TGCAATCAAGAGTTCCGCTGAGCGCTTCTGAGGCAATGATGAGAGAGAGAGAGAGAGAG 983
DB 868 TGCAATCAAGAGTTCCGCTGAGCGCTTCTGAGGCAATGATGAGAGAGAGAGAGAGAGAG 927
QY 984 TATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1043
DB 928 TATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
```

```
QY 1044 TGCGCAATATATTCGCGGAGCGGCAATGCGAGCAATTAAGTGTGCTGACGAGGCTTT 1103
DB 988 TGCGCAATATATTCGCGGAGCGGCAATGCGAGCAATTAAGTGTGCTGACGAGGCTTT 1047
QY 1104 GGTCCGAATCCGAATTAATGCTAGACACAGCTTGTGATGCTGATGAGAGGCTTTCCTGTC 1163
DB 1048 GGTCCGAATCCGAATTAATGCTAGACACAGCTTGTGATGCTGATGAGAGGCTTTCCTGTC 1107
QY 1164 GCTTTCGCGCTGATGACACAGAGCTTGTGAGAGATGCTGATGACAGCTGCTGCTGCTG 1223
DB 1108 GCTTTCGCTGATGACACAGAGATTTGAGAGATGCTGATGACAGCTGCTGCTGCA 1167
QY 1224 GCGGACCAATGCGCATGCTGCTTATAGTCAATCTTCTAGGCTTATGATGCTT 1283
DB 1168 GCTGACCTGCGCATGCTGCTTATAGTCAATCTTCTAGGCTTATGATGCTT 1227
QY 1284 GTGAATTTGATTTTGCCATTTGCTGATGCTGATGAGAGATGAGAGAGAGAGAGAGAG 1343
DB 1228 GTGAATTTGATTTTGCCATTTGCTGATGCTGATGAGAGATGAGAGAGAGAGAGAGAG 1287
QY 1344 GAGAGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
DB 1288 GAGAGAGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347
QY 1404 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
DB 1348 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1407
QY 1464 GCGGCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
DB 1408 GCGGCAAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1467
QY 1524 TATGAGATTTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
DB 1468 TATGAGATTTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527
QY 1584 ATTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
DB 1528 ATTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587
QY 1644 ACCACAGACACAAAGCTTACCAAGTTCTGTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1703
DB 1588 ACCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1644
QY 1704 GGTTCACCTTTTAACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
DB 1648 GGTTCACCTTTTAACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1704
QY 1764 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823
DB 1708 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1764
QY 1824 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
DB 1768 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1824
QY 1884 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1943
DB 1828 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
QY 1944 TCGATATCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2003
DB 1888 TCGATATCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1944
QY 2004 ATGCGCGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
DB 1948 ATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2004
QY 2064 CGCAATCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2123
DB 2008 CGCAATCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2064
QY 2124 CTGAT-----CATGCGAGCTAGAGAAATTTGGCTGAGAGTGAAGAGAGAGAG 2168
```

Db 2065 CCCGATGCCAATCAAGGAACTTAATGGAATGGCTGACGATTATACAGCGAA 2124  
 Qy 2169 GCGGCAAGATTAAACATCATGACAACTTTATGAGCCCGTCCAGACAAACGCTG 2228  
 Db 2125 GCTGGCAAAATTAACACACGCAATCTTTATGAGCCCGTCCAAATCTCAACAGTG 2184  
 Qy 2229 GTTGATATGAAGATGATGATGCTCTGAATGACATCATGAAACGCGCTGCTGGCAC 2288  
 Db 2185 GTAGACATGAAGATGATGATGCTTAATGATATCATGAAACGCGCTGCTGGCAC 2244  
 Qy 2289 AGTCGGCAAGCATGCGCTGCTCTCCGTTACTATTTCCCAACAGAGACGATGACGAG 2348  
 Db 2245 AGTCGTCGTAAGTAAACGAGT-----GAGACGATGACGAA 2280  
 Qy 2349 GATGGGCGGACGTTCAAAAGCAAGCACTGAAAGTATCCTCAAGGACATCGATGCTT 2408  
 Db 2281 GATGTCGCCATTCAGAGACATCGCCCTCGAATACCTTAAGGACATCGAAATCTTT 2340  
 Qy 2409 TGTGTGGGACCTGTGCTGGGTTTGTTGAATTTCAAGAGTGGGTATCGCTCATCGTC 2468  
 Db 2341 TGTGTAGGAGACTGTTGTGGGTGTGTTAAATTTCAAGAAATGGGTGTCTTTATTTG 2400  
 Qy 2469 TTGGATCCCTGCTGCAAGCTCTTCATGACGCTGATGCTGGTCAACAGATGTCATG 2528  
 Db 2401 TTGATCCATTCGTGAGCTCTTCATTTACCTGTGATGCTGATGATGATGATGATG 2460  
 Qy 2529 GCAATGATCAACGATATGAACAAAGAGATGAACGCGTCTCAAGAGTGCATAT 2588  
 Db 2461 GCATGATCATCAACGATGAATCCGGAATAGAGAGTGTCTGAAATGTTAACTAT 2520  
 Qy 2589 TTCTTCACCGCCACTTTGCTCATGAGCCACATGAAGTAAATGGCAATGAGACCCCA 2648  
 Db 2521 TTCTTCACCGCCACTTTGCTCATGAGCCACATGAAGTAAATGGCAATGAGACCCCA 2580  
 Qy 2649 TACTATTCCAGAGGCTGGAACATCTTGATCTTATCTGATGAGCTGATGCTATTTG 2708  
 Db 2581 TACTACTCCAGAGGCTGGAACATCTTGATCTTATCTGATGAGCTGATGCTATTTG 2640  
 Qy 2709 GAACTGGAGCTGAGGCTGTCCAGAGTCTGTCCGATGTGCTGCTTTCATGCTGCT 2768  
 Db 2641 GAATGGGCTGAGGCTGTCCAGAGTCTGTCCGATGTGCTGCTTTCATGCTGCTGCT 2700  
 Qy 2769 GTATTCAACTGCGCAAGCTTGGCCCACTTAATTTACTCATTTGATGATGATGAGAG 2828  
 Db 2701 GTATTCAAAATGCGAAATATGAGCCCACTCAATTTACTCATTTGATGATGATGAGAG 2760  
 Qy 2829 ACCATGGGCGCTTGGGTAATCTGACATTTGATCTTTCATTTATCATCTTTCATCTT 2888  
 Db 2761 ACAATGGGCTGATGGGTAATCTGACATTTGATCTTTCATTTATCATCTTTCATCTT 2820  
 Qy 2889 GTGATGGGAATGCACTGTTCGGAAGAAATTAATCATGATCAAGAGACCGCTTCCGAT 2948  
 Db 2821 GTGATGGGAATGCACTGTTCGGAAGAAATTAATCATGATCAAGAGACCGCTTCCGAT 2880  
 Qy 2949 GCGGACCTGCGCGCTGGAATCTTCAACGATTTATGACAGCTTCAAGATGATGATGAT 3008  
 Db 2881 CATTAATTAACGCGCTGGAATCTTCAACGATTTATGACAGCTTCAAGATGATGATGAT 2940  
 Qy 3009 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3068  
 Db 2941 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
 Qy 3069 TGCATTCCTTCTTCTTGGCCACCGTGTATCGGCAATCTTGGTACTTAACTTTTC 3128  
 Db 3001 TGTATACCTTCTTCTTGGCCACCGTGTATGATGATGATGATGATGATGATGATGAT 3060  
 Qy 3129 TTACCTTCTTCTTCTTGGCCACCGTGTATGATGATGATGATGATGATGATGATGAT 3188  
 Db 3061 TTACCTTCTTCTTCTTGGCCACCGTGTATGATGATGATGATGATGATGATGATGAT 3120  
 Qy 3189 GATACGATTAATAATGCGAGGCTTCAATGCAATGGCCGATTTAAAGTTGGGTTAAG 3248

Db 3121 GATACCAATTAATAATGACAGGCTTCAATGCTGATTTGCTTTTAAAGACTGGTGAA 3180  
 Qy 3249 CGTAATATTGCTGATTTGTTTCAAGTTAATAGCTAACAAATTAAGTAT 3308  
 Db 3181 CGTAATATTGCTGATTTGTTTCAAGTTAATAGCTAACAAATTAAGTAT 3240  
 Qy 3309 CAACCATAGGTGAGAGGACCAACAGATGATGATTTGAGGCAAGAGCATGATGAT 3368  
 Db 3241 CAACCATG-----AGACATGGCGAT 3261  
 Qy 3369 AAGCAATGAGCTGGGCGACGACGAGATCTCGCGACGCGCTCATCAAGAGGATC 3428  
 Db 3262 AATGAATGAGTGGGTGATGACGAATCATGGGCGATGCTGATCAAAAAGGATATG 3321  
 Qy 3429 AAGGACGAGCGCACTGAGGTGGCTATCGGGATTCGATGGAATTCACGATACAGGC 3488  
 Db 3322 AAGGCGGAGACCCAGTGGAGGTGCTATGCGATGCGATGAGAGTTCAAGTACATGGC 3381  
 Qy 3489 GACATGAGAGACAAAGCCGGAAGAAATCCAATATCTTAATTAAGCAACGATGATGGC 3548  
 Db 3382 GATATGAAAAAACAAGCCGAGAAATCAATTCATGACAAACAGATGATGGA 3441  
 Qy 3549 AACTCAATTAACCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 3608  
 Db 3442 AACTCAATTAACCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 3501  
 Qy 3609 TTAACGAGAGAGACATGCGCCGATTAATGATGATGATGATGATGATGATGATGATG 3668  
 Db 3502 ATACAGAGAGAGACATGCGCCGATTAATGATGATGATGATGATGATGATGATGATG 3561  
 Qy 3669 AAGGACGAGAGACCAAGGCGAGCGGAGAGATGAGAGGCGAGAGAGCGGACGCGC 3728  
 Db 3562 AAGGACGAGAGACCAAGGCGAGCGGAGAGATGAGAGGCGAGAGAGCGGACGCGC 3621  
 Qy 3729 AGCAAGAGAGATTTAGGTCTCGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAG 3788  
 Db 3622 AGCAAGAGAGACCTCGGCTCGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAG 3681  
 Qy 3789 CGGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3845  
 Db 3682 CAGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3741  
 Qy 3846 CCAGCTGATTTGCTGCGCCGATTTGATTAAGAAATTTGATTTTACCGGTCGAT 3905  
 Db 3742 CCGGCGAGCTGTTTCCCGATCTGTACTCAAGAAATTTCCGATCTTGGCCGCGAC 3801  
 Qy 3906 GACTCGCGCTTCTGCAAGAGATGAGGCAATTTACGATGATGATGATGATGATGAT 3965  
 Db 3802 GACTCGCGCTTCTGCAAGAGATGAGGCAATTTACGATGATGATGATGATGATGAT 3861  
 Qy 3966 AATTAATTTTGAACAGCTGTTATCAATGATTTTATGATGATGATGATGATGAT 4025  
 Db 3862 AATTAATTTTGAACAGCTGTTATCAATGATTTTATGATGATGATGATGATGAT 3921  
 Qy 4026 TTAAGAGATGATCATGTCGCAAAAGACCAATCTGAGAGATTTTATTAATGATGAT 4085  
 Db 3922 TTAAGAGATGATCATGTCGCAAAAGACCAATCTGAGAGATTTTATTAATGATGAT 3981  
 Qy 4086 AGAATTTTACGCTTATTTCTTCTGGAATGATGATGATGATGATGATGATGATGAT 4145  
 Db 3982 AGAATTTTACGCTTATTTCTTCTGGAATGATGATGATGATGATGATGATGATGAT 4041  
 Qy 4146 AAGGTGATCTTCAACCAAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 4205  
 Db 4042 AAGGTGATCTTCAACCAAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 4101  
 Qy 4206 ATCACTTCTGCTTCACTTGTGAGAGCTGTGATTTCAAGCTTCAAGATGATGATGAT 4265  
 Db 4102 ATCACTTCTGCTTCTGCTTGTGAGAGCTGTGATTTCAAGCTTCAAGATGATGATGAT 4161  
 Qy 4266 ACCTTAAGAGACATGAGACCAATGAGGCAATGATGATGATGATGATGATGATGATGAT 4325  
 Db 4162 ACATGCGCGCTTAAGGCGATGCTGCTCTTAAGATGAGAGGATGATGATGATGATGAT 4221

QY 4326 GTTAATGGCTGGTCAAGCTATACGCTCCATCTTCAATGCTATGCTGTCTTATA 4385  
Db 4222 GTGAATGGCTGGTCAAGCTATACGCTCCATCTTCAATGCTATGCTGTCTGATA 4281  
QY 4386 TTTTGGCTAATTTTGGCATTAATGGGTGTAACAGCTTTTGTGTAATAATTTAAGTGC 4445  
Db 4282 TTTTGGCTAATTTTGGCATTAATGGGTGTAACAGCTTTTGTGTAATAATTTAAGTGC 4341  
QY 4446 GAGCATGATGAGCAAGAGCTCAGCCAGAGATCATACCAATTCGAATGCTTCGAG 4505  
Db 4342 AAAGATGATTAATGACATGCTGCTGAGCATGAATCATACCGAATCGTAATGCTCGAAA 4401  
QY 4506 AGCGGAATCTACAGTGGGTGAATTCAGCAATGAATTTGATCAGTAGTAGTACCGTAT 4565  
Db 4402 AGTGAATCTACAGTGGGTGAATTCAGCAATGAATTTGATCAGTAGTAGTACCGTAT 4461  
QY 4566 CTGTGCTTTTCCAGTGGTCCACTTCAAAAGGCTGATACAAATCATGTAAGTGTATC 4625  
Db 4462 CTGTGCTTTTCCAGTGGTCCACTTCAAAAGGCTGATACAAATCATGTAAGTGTATC 4521  
QY 4626 GATTACGAGAGGTGAGCAAGCAACCAATTCGTGAAGCAATCTACATGTAATTAAT 4685  
Db 4522 GATTACGAGAGGTGAGCAAGCAACCAATTCGTGAAGCAATCTACATGTAATTAAT 4581  
QY 4686 TTCCGATCTTCTCATATATTGATGATCTTTTCACTCAATCTGTTCATTTGCTATC 4745  
Db 4582 TTCCGATCTTCTCATATATTGATGATCTTTTCACTCAATCTGTTCATTTGCTATC 4641  
QY 4746 ATTGATTAATTTAATGACAAAGAAAGAGAGGTGATCTAGAAATGTTCAAGCA 4805  
Db 4642 ATTGATTAATTTAATGACAAAGAAAGAGAGGTGATCTAGAAATGTTCAAGCA 4701  
QY 4806 GAAATTCAGAAAAGTACTATATATGCTATGAAAAAGATGGGCTTAAAAAACATTA 4865  
Db 4702 GAAATTCAGAAAAGTACTATATATGCTATGAAAAAGATGGGCTTAAAAAACATTA 4761  
QY 4866 GCCATTTCCAAAGCCAGGTGGGACCAAGCAATGCTTTGAATGATGTAACGATAG 4925  
Db 4762 GCCATTTCCAAAGCCAGGTGGGACCAAGCAATGCTTTGAATGATGTAACGATAG 4821  
QY 4926 AAATTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4985  
Db 4822 AAATTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4881  
QY 4986 CGTTACGATGCTGCGACAGCTAATACCGGCTCTAGACATCTCAATGCGATATCTGA 5045  
Db 4882 CGTTACGATGCTGCGACAGCTAATACCGGCTCTAGACATCTCAATGCGATATCTGA 4941  
QY 5046 GTTATTTTCAAGTTCGGAATGCTATTAATAAATATTCGCTTACGATATCAATTTTAT 5105  
Db 4942 GTTATTTTCAAGTTCGGAATGCTATTAATAAATATTCGCTTACGATATCAATTTTAA 5001  
QY 5106 GAGCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
Db 5002 GAGCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
QY 5166 AGCGATTAATCGAAGATTAATTCGCTGCGACAGCTTCGAGTGGTGGTGGCG 5225  
Db 5062 AGCGATTAATCGAAGATTAATTCGCTGCGACAGCTTCGAGTGGTGGTGGCG 5121  
QY 5226 AAAATGGGCGCTGCTTCGACGTGTAAGGAGCGAAGGCAATTCGACATGCTCTTC 5285  
Db 5122 AAAATGGGCGCTGCTTCGACGTGTAAGGAGCGAAGGCAATTCGACATGCTCTTC 5181  
QY 5286 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5345  
Db 5182 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5241  
QY 5346 TTTCATCTTTGCAATTTTGGCAATGCTGTTCTTCAATGACGTAAGAGAGAGCGGCA 5405  
Db 5242 TTTCATCTTTGCAATTTTGGCAATGCTGTTCTTCAATGACGTAAGAGAGAGCGGCA 5301

QY 5406 AACGAGCTCTAACATTCAGACCTTTGGCCAGAGCATATCTCTTCAAGATGCTG 5465  
Db 5302 AATGCTGTGATTAATTTTAAGCATTTGGCCAAAGTATGATATGCTGTTCAAGATGCT 5361  
QY 5466 AGCTACGCGGTGGGATGCTGATCTGACCGCATTTAATCAATGAGAGCATGCGATCA 5525  
Db 5362 AACTACGCGGTGGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 5421  
QY 5526 CCCGACGAGCAAAAGGCTATCCGGGCAATTTGGTTCAGGACCGCTTGAATACGTTT 5585  
Db 5422 CCCGACGAGCAAAAGGCTATCCGGGCAATTTGGTTCAGGACCGCTTGAATACGTTT 5481  
QY 5586 CTCTCTCATATCTAGTATTAAGCTTTTGAATGATTAATGATATGATATGCTGCTAT 5645  
Db 5482 CTCTCTCATATCTAGTATTAAGCTTTTGAATGATTAATGATATGATATGCTGCTAT 5541  
QY 5646 CTTCGAACTATTAATGACAGCCAGAGACCTGCAAGAGGCTTCAACGAGACGATAC 5705  
Db 5542 CTTCGAACTATTAATGACAGCCAGAGACCTGCAAGAGGCTTCAACGAGACGATAC 5601  
QY 5706 GACATGATCTATGAGATCTGCAAGCAATTCGATCCGAGGCAATCCAGTATACGCTAT 5765  
Db 5602 GACATGATCTATGAGATCTGCAAGCAATTCGATCCGAGGCAATCCAGTATACGCTAT 5661  
QY 5766 GATCAGCTGCTCGAATTCCTGAGCTGATGAGGCCCCGCTGCAAGATCAGAAACGCA 5825  
Db 5662 GATCAGCTGCTCGAATTCCTGAGCTGATGAGGCCCCGCTGCAAGATCAGAAACGCA 5721  
QY 5826 AAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
Db 5722 AAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
QY 5886 GACATCTGACGCGCTTACGAAAGATCTTTTGGGCGGAAAGGCAATCCATGATGAGAG 5945  
Db 5782 GATATATTGATGATGCTGACCAAGAGATCTTTTGGGCGGAAAGGCAATCCATGAGAG 5841  
QY 5946 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
Db 5842 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
QY 6006 TCAACGCTGTGGCTGACGCTGAGAGATGATGATGATGATGATGATGATGATGATGAT 6065  
Db 5902 TCAACGCTGTGGCTGACGCTGAGAGATGATGATGATGATGATGATGATGATGATGAT 5961  
QY 6066 AAGCAAAAGCGCGCGGAGAGAGTGGGCTTTGAGCCGATACGATATGCGAT 6125  
Db 5962 CGTTACAAAGATGGC-----CCAGCCAGAGAGGATGAT 5994  
QY 6126 GCGGCTATCCGATGCGGAGACCGGCGCCGATGAAGCAAGGAGCGGATGCGGCC 6185  
Db 5995 GAGGCGGAGGCGGCTGGTGGGAGATGCTGAAGGCGGATGAGGAGGAGGAGG 6054  
QY 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
Db 6055 GCGGCGGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6114  
QY 6246 AATGTAATTAATGCTCGGATGAGATGACAGGCGCGGAGAGAGAGAGAGAGAGG 6305  
Db 6115 AATGTAATTAATGCTCGGATGAGATGACAGGCGCGGAGAGAGAGAGAGAGAGG 6159  
QY 6306 GCGGCGGAG 6365  
Db 6160 GCGGCGGAG 6219  
QY 6366 GTTCTGAG 6425  
Db 6220 GTTCTGAG 6279  
QY 6426 CGATGCGGAGATCAGTGGCGAGCGGAGGATGCTGA 6464  
Db 6280 AGATGCGGAGATCAGTGGCGAGCGGAGGATGCTGA 6318



QY 1344 GAAAGAGGCTGCCGAGAGAGAGGCGCATACGTGAGCGGAAGAGTCCCGCGCCAAA 1403  
Db 1288 GAAAGAGGCTGCCGAGAGAGAGGCGCATACGTGAGCGGAAGAGTCCCGCGCCAAA 1347  
QY 1404 GCGGCCAAGCTGAGAGAGCGGGCCCAATGCGAGGCTCAGGAGCAGCGGATGCGGCTGC 1463  
Db 1348 GCGGCCAAGCTGAGAGAGCGGGCCCAATGAGAGCTCAGGAGCAGCGGATGCGGCGAT 1407  
QY 1464 GCGGAGAGGCTGCACTGCAATCCGGAATGCGCAAGAGTCCGAGCTATTTTCATCAGC 1523  
Db 1408 GCGCGTGGGAGGCTGCAATCCGGAATGCGCAAGAGTCCGAGCTATTTTCATCAGC 1467  
QY 1524 TATGAGCATTTGTTGGCGGAGAGAGGCGCAACGATGACCAACAAAGAGAGTGGCC 1583  
Db 1468 TATGAGCATTTGTTGGCGGAGAGAGGCGCAACGATGACCAACAAAGAGAGTGGCG 1527  
QY 1584 ATTGAGAGGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1643  
Db 1528 ATAGGAGAGGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1587  
QY 1644 ACCAGAGCAGCAGAGCTACCAAGTTCGTAAGTGGAGCAGCAGCAGTCTTATCTTACCT 1703  
Db 1588 ACCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1644  
QY 1704 GGTTCACCGTTTAACTATCGCAGAGGAGTACAGTATCTCACAAGTACAGATAGGAGAC 1763  
Db 1645 GGTTCACCGTTTAACTATCGCAGAGGAGTACAGTATCTCACAAGTACAGATAGGAGAT 1704  
QY 1764 GAGAGTGGCGCTTTGGTATACCGGATGAGCGATGAGAGCAGTGGATGAGTGGATGAG 1823  
Db 1705 GAGAGTGGCGCTTTGGTATACCGGATGAGCGATGAGAGCAGTGGATGAGTGGATGAG 1764  
QY 1824 CAGAGTGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1883  
Db 1765 CAGAGTGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1824  
QY 1884 GAAAGAGAGGAGGAGTATAGTGGCGGATGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1943  
Db 1825 GAAAGAGAGGAGTATAGTGGCGGATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1884  
QY 1944 TCGATATACCTGCGATAGTCCGGAATATGATATGATATGATATGATATGATATGATAT 2003  
Db 1885 TCGATATACCTGCGATAGTCCGGAATATGATATGATATGATATGATATGATATGATAT 1944  
QY 2004 ATGCGCGTATGCGCGTCAAGCAATGACCAAGAGAGCAAAATGCGCAACCGCAACA 2063  
Db 1945 ATGCGCGTATGCGCGTCAAGCAATGACCAAGAGAGCAAAATGCGCAACCGCAACA 2004  
QY 2064 CGCAATCAATAGTGGGCGCCCAATGAGCGGCGCACACTGTCTGAGACCAATCAAG 2123  
Db 2005 CGCAATCAATAGTGGGCGCGCAACCAATGAGTGGCGCGCGGCGGCGGCGGCGGCGAT 2064  
QY 2124 CTCGAT-----CATCGCGATACGAAATTTGGCTGAGTGGAGCGGAGCGAA 2168  
Db 2065 CCGCATGCGCATCAAGAGAGCAAAAGGATTTGAAATGGGTGAGGATTTATACAGAGAA 2124  
QY 2169 GCTGGCAAGATTAAACATCATGACCAATCTTTTATGAGCGCGTCCAGACCAACCGGTG 2228  
Db 2125 GCTGGCAAGATTAAACATCAAGCAATCTTTTATGAGCGCGTCCAGACCAACAGGTG 2164  
QY 2229 GTTATATGAAAGATGATGCTCTGATATGATCATGCAAGCGCGCTGCTGGGAGC 2288  
Db 2185 GTTATATGAAAGATGATGCTCTGATATGATCATGCAAGCGCGCTGCTGGGAGC 2244  
QY 2289 AGTGGGCAAGCGATGCGGCTGTCTCGTTTACTATTTCCAAAGAGAGAGATGAGCGAG 2348  
Db 2245 AGTGGTGTATGAAAGAGT-----GAGGAGAGTGAAGAA 2280  
QY 2349 GATGGGCGAGCGTTCAAGAGAGAGCACTGAGAGTATCTCAAGAGCGATGATGTTT 2408  
Db 2281 GATGGTCCCAATTCAGAGAGATGCGCTCGATATATCTTAAAGAGGATGAAATCTTT 2340

QY 2409 TGTGTGGGAGCTGTGCTGGGCTTTGTTGTAATTTTACAGAGTGGATATGCTATGCTC 2468  
Db 2341 TGTGTATGGAGCTGTGCTGGGCTTTGTTGTAATTTTACAGAGTGGATATGCTATGCTC 2400  
QY 2469 TTGATCCCTTCTGTCAGAGCTCTTATCATCAGCTGTGATGTTGTGTCAACAGATGTTCA 2528  
Db 2401 TTGATCCCTTCTGTCAGAGCTCTTATCATCAGCTGTGATGTTGTGTCAACAGATGTTCA 2460  
QY 2529 GCATGATTCACCAAGATATGAACAGAGATGAGACCGTGTCTCAAGAGTGGCACTAT 2588  
Db 2461 GCATGATTCACCAAGATATGAACAGAGATGAGACCGTGTCTCAAGAGTGGCACTAT 2520  
QY 2589 TTCTTACCGGCTGCTGATGAGAGCGCAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 2648  
Db 2521 TTCTTACCGGCTGCTGATGAGAGCGCAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 2580  
QY 2649 TACTATTTCCAGAGAGGCTGAGACATCTTCACTTATATGATGAGCGCTATGCTATG 2708  
Db 2581 TACTATTTCCAGAGAGGCTGAGACATTTTGAATTTATGATGAGCGCTATGCTATGCTG 2640  
QY 2709 GAATGGGAGCTGAGAGGCTGTCAGAGGCTGTCCGATTTGCGTCTTTCATGCTGCTG 2768  
Db 2641 GAATGGGAGCTGAGAGGCTGTCAGAGGCTGTCCGATTTGAGAGTTCGTTTTCGTTGCT 2700  
QY 2769 GTATTTCAAACTGGCCAGGCTGGGCGCACCTTAAATTTACTCATTTGATGATGAGAGC 2828  
Db 2701 GTATTTCAAACTGGCCAGGCTGGGCGCACCTTAAATTTACTCATTTGATGATGAGAGC 2760  
QY 2829 ACCATGGGCGCTTTGGGATATCTGATATGATGATGATGATGATGATGATGATGATGATG 2888  
Db 2761 ACCATGGGCGCTTTGGGATATCTGATATGATGATGATGATGATGATGATGATGATGATG 2820  
QY 2889 GTGATGGAGATGCACTGTTGCGAAAGATATATCATGATCAAGAGCCGCTTTCCGAT 2948  
Db 2821 GTGATGGAGATGCACTGTTGCGAAAGATATATATCAACAGAGTCCGTTCAAGAGC 2880  
QY 2949 GCGAGCTGGCGGCTGGGAACTTCAACGAGCTTATGACAGCTCATGATGATGATGATG 3008  
Db 2881 CATGATTTACCGGCTGGGAACTTCAACGAGCTTATGACAGCTCATGATGATGATGATG 2940  
QY 3009 GTGCTTGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3068  
Db 2941 GTGCTTGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000  
QY 3069 TGCATTCCTTCTTCTTGGCCACCGTGTGATGCGCAATCTTGTGTGATCTTAACTTTTC 3128  
Db 3001 TGCATTCCTTCTTCTTGGCCACCGTGTGATGCGCAATCTTGTGTGATCTTAACTTTTC 3060  
QY 3129 TTAGCTTGTGTTGTCGAATTTTGGCTCATCTGATGATGATGATGATGATGATGATGATG 3188  
Db 3061 TTAGCTTGTGTTGTCGAATTTTGGCTCATCTGATGATGATGATGATGATGATGATGATG 3120  
QY 3189 GATACGATTAATATAGCGGAGGCTTCAATGATGATGATGATGATGATGATGATGATGATG 3248  
Db 3121 GATACGATTAATATAGCGGAGGCTTCAATGATGATGATGATGATGATGATGATGATGATG 3180  
QY 3249 CGTAAATATGCTGATGTTGTTCAAGTAAATGATGATGATGATGATGATGATGATGATGAT 3308  
Db 3181 CGTAAATATGCTGATGTTGTTCAAGTAAATGATGATGATGATGATGATGATGATGATGAT 3240  
QY 3309 CAACATCAGGTGAGAGCAACCAAGATCAGTTGATTTGAGAGCAAGAGATGATGAGC 3368  
Db 3241 CAACATC-----AGAGAGATGAGGAGT 3261  
QY 3369 AACGATGAGGCTGGGCGACAGAGATCTTCCGAGCGGCTCATACAGAGAGGAGTTC 3428  
Db 3262 AATGATCTGAGATGGGTGATGAGAGATCATGCGAGATGAGCTTGAATCAAAAGGATATG 3321  
QY 3429 AAGAGCAAGAGCACTGAGAGTGGCATGCGGATGAGATGATGATGATGATGATGATGATG 3488  
Db 3322 AAGGCGAGAGCCGAGTGGAGTGGCCATTTGGCGATGAGATGAGATGAGATGAGATGAG 3381  
QY 3489 GACATGAGAGCAACAGCGGAGAGATTCGAATATCTTAAATAGCAAGATGATGAGC 3548

```
Db 3382 GATATGAAAAACAAGCCCAAGAAATCAAAATCATTAACAAACAACGATGATGGA 3441
Qy 3549 AACTCAATTAACACCAAGACATAGCTGGAACAGAGCTAAACCATAGAGTTTGTCC 3608
Db 3442 AACTCAATTAACACCAAGACATAGCTGGAACAGAGCTAAACCATAGAGTTTGTCC 3501
Qy 3609 TTACAGACGACGACACTGCGACATTAATCTCATATGTTAGCCATAAGATCGACATTC 3668
Db 3502 ATACAGACGATGACCTGCGACATTAATCTCATATGTTAGCCATAAGATCGACATTC 3561
Qy 3669 AAGAGAGAGGACCAAGAGGACCGCCGAGACATGAGAGGCGAGAGGAGGAGGCGC 3728
Db 3562 AAGAGAGAGGACCAAGAGGACCGCCGAGACATGAGAGGCGAGAGGAGGAGGCGC 3621
Qy 3729 AGCAGAGAGATTTAGTCTCGACGAGAACTGAGAGAGGCGCATATGCGAGAGGCGC 3788
Db 3622 AGCAGAGAGATTTAGTCTCGACGAGAACTGAGAGAGGCGCATATGCGAGAGGCGC 3681
Qy 3789 CCGCTGACGCTGATATCATTTATTCATG--ACACGACGAGATATCTCATGATAT 3845
Db 3682 CAGCTGATGATGATCATCATTCATTCATGCCCCAAAGACGACGAGATATCGACATAT 3741
Qy 3846 CCGAGTATGCTGCCCCGATTTGCTATAGAAATTTCCGATTTAGCGGCTGAGAT 3905
Db 3742 CCGGCGACATGTTCCCGACCTGCTACTACAGAAAGTTTCGATCTTGCGCGGACGAG 3801
Qy 3906 GACTCGCGCTTCTGCGAGAGATGCGGCAATTTACGACTGAAAACTTTTCAATTAATGA 3965
Db 3802 GACTCGCGCTTCTGCGAGAGATGCGGCAATTTACGACTGAAAACTTTTCAATTAATGA 3861
Qy 3966 AATTAATATTTTGAACAGCTGTTATCATATGATTTTAAATGATAGCTTATGCGCA 4025
Db 3862 AATTAATATTTTGAACAGCTGTTATCATATGATTTTAAATGATAGCTTATGCGCC 3921
Qy 4026 TTGAGAGATGATCATCTGCAACAAGACCATATCTGAGATATTTATCTATATGAGC 4085
Db 3922 TTGAGAGATGATCATTTACCGCATGACCTGTCAATGAGATATCTGATCTATGAGAC 3981
Qy 4086 AGAATATTTACGTTATATTTCTTGTGAAATGTTAATCAAGTGTGCGCTTC 4145
Db 3982 AGAATATTTACGTTATATTTCTTGTGAAATGTTAATCAAGTGTGCGCTTC 4041
Qy 4146 AATGATATTTACCAACGCGTGTGTTGCTCATGATTTGATGATGATGATGCTT 4205
Db 4042 AATGATATTTACCAACGCGTGTGTTGCTCATGATTTGATGATGATGATGCTT 4101
Qy 4206 ATCAACTTCTGTTCTTCACTTGTGAGCTGTGTGATTCAGGCTTCAAGACTATGCGA 4265
Db 4102 ATCAACTTCTGTTCTTCACTTGTGAGCTGTGTGATTCAGGCTTCAAGACTATGCGC 4161
Qy 4266 ACGTTAAGACACTGAGACCACTAGCTGCAATGCTCCGATGACAGGAGATGAGGCTGTC 4325
Db 4162 ACGTTAAGACACTGAGACCACTAGCTGCAATGCTCCGATGAGGAGATGAGGCTGTC 4221
Qy 4326 GTTATGCGCTGATCAAGATATACCGTCACTTCAATGATGATGATGATGATGAT 4385
Db 4222 GTTATGCGCTGATCAAGATATACCGTCACTTCAATGATGATGATGATGATGAT 4281
Qy 4386 TTTTGGCTAATTTTGGCATATGAGTGTATACAGCTTTTGTGAAAAATATTTAAGTGC 4445
Db 4282 TTTTGGCTAATTTTGGCATATGAGTGTATACAGCTTTTGTGAAAAATATTTAAGTGT 4341
Qy 4446 GAGAGCATGATGAGACGAGAGCTAGCCACGAGATCATATCCAAATGCGATGCGAGAG 4505
Db 4342 AAGAGATGATGACACTGTGCTAGGCTATGAATCATATCCGAATCGTAATGCTGCAAA 4401
Qy 4506 AGCAGAGATCACTAGTGGGTGAATTCAGCATGATGATGATGATGATGATGATGAT 4565
Db 4402 AGTGAATCACTAGTGGGTGAATTCAGCATGATGATGATGATGATGATGATGAT 4461
Qy 4566 CTGTGCTTTTCAAGTGGCACCTTCAAGGCTGATATCAAAATCATGAAGATGATATC 4625
Db 4462 CTGTGCTTTTCAAGTGGCACCTTCAAGGCTGATATCAAAATCATGAAGATGATATC 4521
Qy 4626 GATTCAGAGAGGTGAGACAGAACCAATTTGTGAAGAGAACATCTATATATATAT 4685
Db 4522 GATTCAGAGAGGTGAGACAGAACCAATTTGTGAAGAGAACATCTATATATATAT 4581
Qy 4686 TTGATATCTTCAATATTTTGAATCCCTTTTCACTCAATCTGTTCATGTTATC 4745
Db 4582 TTGATATCTTCAATATTTTGAATCCCTTTTCACTCAATCTGTTCATGTTATC 4641
Qy 4746 ATTGAATATTTTATGACAAAAGAAAAAGACGATGATCATTAAGAAATGTTATGACA 4805
Db 4642 ATTGAATATTTTATGACAAAAGAAAAAGACGATGATCATTAAGAAATGTTATGACA 4701
Qy 4806 GAAATTCAGAAAAAGTACTATATATGCTATGAAAAAGATGGGCTCTAAAAAACTATAA 4865
Db 4702 GAAATTCAGAAAAAGTACTATATATGCTATGAAAAAGATGGGCTCTAAAAAACTATAA 4761
Qy 4866 GCCATTCAGAACCAAGGTGGACCAACAGCAATAGCTTTTGAATATGTAACGATAG 4925
Db 4762 GCCATTCAGAACCAAGGTGGACCAACAGCAATAGCTTTTGAATATGTAACGATAG 4821
Qy 4926 AATTCGATATATATATATATATATATATATATATATATATATATATATATATAT 4985
Db 4822 AATTCGATATATATATATATATATATATATATATATATATATATATATATATAT 4881
Qy 4986 CCGTACGATGCTCGGACACCGTATACCGGCTAGACTATCTCATGCGATTCGTA 5045
Db 4882 CCGTACGATGCTCGGACACCGTATACCGGCTAGACTATCTCATGCGATTCGTA 4941
Qy 5046 GTTATATTTTCACTTCCGAATGCTATTAATAAATATGCTTTAATCATATATATAT 5105
Db 4942 GTTATATTTTCACTTCCGAATGCTATTAATAAATATGCTTTAATCATATATATAT 5001
Qy 5106 GAGCAGATGATATATATATATATATATATATATATATATATATATATATATAT 5165
Db 5002 GAGCAGATGATATATATATATATATATATATATATATATATATATATATATAT 5061
Qy 5166 AGGATATATATATATATATATATATATATATATATATATATATATATATATAT 5225
Db 5062 AGGATATATATATATATATATATATATATATATATATATATATATATATATAT 5121
Qy 5226 AAAATGAGGCGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5285
Db 5122 AAAATGAGGCGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5181
Qy 5286 GCGTGGCCATATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5345
Db 5182 GCGTGGCCATATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5241
Qy 5346 TTCACTTTGCGATTTTCCGCAATGCTGCTTCTATGACAGTGAAGAGAGCGGAT 5405
Db 5242 TTCACTTTGCGATTTTCCGCAATGCTGCTTCTATGACAGTGAAGAGAGCGGAT 5301
Qy 5406 AACGACGCTCAACTTCAAGACCTTGGCCAGAGCATATCTGCTCTTCAAGATGCG 5465
Db 5302 AATGCTGTATATATATATATATATATATATATATATATATATATATATATAT 5361
Qy 5466 ACGTACGCGGCTGGAGTGTATGAGAGCGCATATCAATGAGAGAGCATGCGATCA 5525
Db 5362 ACGTACGCGGCTGGAGTGTATGAGAGCGCATATCAATGAGAGAGCATGCGATCA 5421
Qy 5526 CCCGACAGGACAAAGGCTATCCGAGCAATGCTGTTACGCAACGTTGATATACGTT 5585
Db 5422 CCCGACAGGACAAAGGCTATCCGAGCAATGCTGTTACGCAACGTTGATATACGTT 5481
Qy 5586 CTCTCTCATATCTATATATATATATATATATATATATATATATATATATATAT 5645
Db 5482 CTCTCTCATATCTATATATATATATATATATATATATATATATATATATATAT 5541
Qy 5646 CTGAGAGATATATGAGGACCGAGAGAGTGCAGAGAGGCTATACAGAGCACTATC 5705
Db 5542 CTGAGAGATATATGAGGACCGAGAGAGTGCAGAGAGGCTATACAGAGCACTATC 5601
```

```

OY 5706 GACATGCTATAGATCTGGAGCAATTCGATCCGGAGGAGCAACCAATGACTATACGCTAT 5765
DB 5602 GATATGTAATAGCAATTTGGCAACAATTCGAGAGGGTAACTCAGATCAATGAAGATAC 5661
OY 5766 GATCAGCTGTCCGAATTCCTGGACGTAATGAGCCCGCTCAGATCCACAACCGCAAC 5825
DB 5662 GACCAAGCTGTCCGAATTCCTGGACGTAATGAGCCCGCTCAGATCCACAACCGCAAC 5721
OY 5826 AAGTACAAAGATCAATATGATGAGCAATACCATCTGTCCGGGTGACCTCATGTAAGCTG 5885
DB 5722 AAGTACAAATCAATATGATGAGCAATACCATCTGTCCGGGTGACCTCATGTAAGCTG 5781
OY 5886 GACATCCCTGAGACCCCTTACGAAACATCTTTGGCCGAGAGGCAATCCGATTAAGAG 5945
DB 5782 GATATATGATGATGCTGACCAAGAGATCTTTGGCCGAGAGGATATCCGATTCAGAG 5841
OY 5946 ACGGCTGAGATTTGATGATAGCGGCGCCGAGATTAAGAGGCTACGAGCCGCTCA 6005
DB 5842 ACGGCTGAAATTTGATGATAGCGGCGCCGAGATTAAGAGGCTACGAGCCGCTCA 5901
OY 6006 TCAACGCTGTGGCGTACGATGAGAGTATGCGCCGCTAATCCAGACGCTGGCGA 6065
DB 5902 TCGACACTGTGGCGCGCAGCTGAGAGTATGCGCCAGCTGATACAGAACTCGTGGCG 5961
OY 6066 AAGCAACAGCGCGCGCGGAGAGAGTGGGTCTTTGAGCCGGAATACGATATGCGCAT 6125
DB 5962 CGTTACAAAGATGCG----- 5976
OY 6126 GCGCGTGTATCCGATGCGCGGAGACCGGCGCCGATGAAGCAACGAGCGCGATCGGCC 6185
DB 5977 CCACCCGAGAGGGTATGAGAGGCGAGCGCGTGTGGCGAGAGATGTGTGAAGCGCGT 6036
OY 6186 GCTGTGAGATGTATGTATTAACGCTACTGCAAGAGAGCTCCGATGCCGATGAGT 6245
DB 6037 GAGGCTGAAGCGCGGAGCGCGCGCGGCGGATGATGATGTGTGTGCTCAGCGCGCGG 6096
OY 6246 AATGTAATATGCTCCGGGTGAGATGCAAGCGCGCGGAGAGCGAGCGAGCGAGCGG 6305
DB 6097 GAGGCAATATCAATCAACAGATTCAGATGCGCGGAGAGAGATGTGTGCAAGCGCGCAT 6156
OY 6306 GCGCGCGGAGCAACGAGCGCGGAGATCCCGGAGCGGATGAGCGCGGAGAGCGCGC 6365
DB 6157 GGTGCGCGGCGCCCTTATGCTCGGCGCTGTGTATGCGCGGAGATGAGCGCGCAACCGCC 6216
OY 6366 GTTCTCGTGAAGAGCGAGGCTTCTGACGAGAAAGCGCGCAAGGTGATCCACTCG 6425
DB 6217 GTACTGTGCGAAGGAGATGTTTGTTCATAAAGCGGTCAATGATGATATACACTCG 6276
OY 6426 CGATGCGCGGAGATCACTGCGCGCAGCGCGGATGTTCTGA 6464
DB 6277 AGATCGCGAGCATTAATCCAGAGCGGAGAGATGTTCTGA 6315

```

## RESULT 8

AAV82499 standard; cDNA, 6315 BP.

AAV82499;

18-MAR-1999 (first entry)

Calcium permeable voltage sensitive sodium channel encoding cDNA #2.

Calcium permeable; voltage sensitive sodium channel; VSSC; insect;

calcium transport; insecticide; pesticide; insect control; vertebrate;

intracellular calcium concentration; calcium-chelating fluorescent dye;

calcium-binding bioluminescent protein; ss.

Musca domestica.

Musca domestica.

Musca domestica.

```

FT  /tag= a
XX  US5858713-A.
XX  12-JAN-1999.
XX  28-FEB-1997; 97US-00808793.
XX  01-MAR-1996; 96US-0012649P.
XX  24-DEC-1996; 96US-0034361P.
XX  (CORR ) CORNELL RES FOUND INC.
XX  Ingles PJ, Soderlund DM;
XX  WPI; 1999-119877/10.
XX  P-Psdb; AAM89578.
XX  Calcium permeable sodium channels - obtained by expression of insect
XX  nucleic acid encoding a sodium channel, that includes a mutation which
XX  renders the channel permeable to calcium.
XX  Claim 13; Col 29-34; 48pp; English.
XX  The present sequence encodes a voltage sensitive sodium channel (VSSC)
XX  isolated from an insect, that has a mutation which renders the sodium
XX  channel permeable to calcium. The VSSC can be used as a screening agent
XX  to detect the ability to modify sodium channel function (i.e. to render
XX  it permeable to calcium), by monitoring calcium transport through it.
XX  Transformed cells, that include the calcium permeable VSSC, can be
XX  exposed to various potential insecticides and pesticides, and evaluated
XX  for their susceptibility to them. This will facilitate the development
XX  and identification of insect control agents, that will not cause adverse
XX  effects to vertebrate species. The VSSC can also be used for the
XX  production of antibodies. The calcium permeable VSSC can be sensitively
XX  monitored for changes in intracellular calcium concentrations, using
XX  either: calcium-chelating fluorescent dyes, or calcium-binding
XX  bioluminescent proteins
XX  Sequence 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 U; 0 Other;
XX  Query Match 68.1%; Score 4434.2; DB 2; Length 6315;
XX  Best Local Similarity 81.8%; Pred. No. 0; Mismatches 1013; Indels 162; Gaps 8;
XX  Matches 5284; Conservative 0;
OY 24 ATGACAGAAAGATTCGATCTGATATCTGAGGAGAGACGAGTTTGTTCCTTTCACC 83
DB 1 ATGACAGAAAGATTCGATCTGATATCTGAGGAGAGACGAGTTTGTTCCTTTCACC 60
OY 84 CGCGATCATTTGGTGAATGAAACACGATTTGCCGCTGAACATGATAAGAGAGAG 143
DB 61 CGCGATCATTTGGTGAATGAAACACGATTTGCCGCTGAACATGATAAGAGAGAG 117
OY 144 CTGGAAGAAGAGAGCGGAGAGAGTGGCGGATATGATGCGAAGAAAAAACAATA 203
DB 118 CTGGAAGAAGAGAGCGGAGAGAGTGGCGGATATGATGCGAAGAAAAAACAATA 148
OY 204 GAAATCCGATATGATGAGAGAGAGATGAAGGTCCACAAACCGATCTTACCTTGA 263
DB 149 -AGATAGATATGATGAGAGAGAGATGAAGGTCCACAAACCGATCTTACCTTGA 207
OY 264 CAGGCTGTCCCAATCTGTTTGAATGAGAGGCGAGCTTCCCGCGGAATTTGGCTTCACT 323
DB 208 CAGGCTGTCCCAATCTGTTTGAATGAGAGGCGAGCTTCCCGCGGAATTTGGCTTCACT 267
OY 324 CCTCTCGAGATATGATCTCTTACAGCAATGATGATGATGATGATGATGATGATGATGAT 383
DB 268 CCTCTCGAGATATGATCTCTTACAGCAATGATGATGATGATGATGATGATGATGATGAT 327
OY 384 GAAAAGATATTTTTCGCTTTTCTGATCAAAAGCAATGATGATGATGATGATGATGAT 443
DB 328 GAAAAGATATTTTTCGCTTTTCTGATCAAAAGCAATGATGATGATGATGATGATGAT 387

```

444 CCGATACGTGCTGAGCAATTTACATTCATGTCATCCATTAATTTTCCCTATTCATC 503  
388 CCGATAGCTGTAGCAATTTATTTATGTCATCCCTGTTTCTGTTATTCATTAATC 447  
504 ACCAACAATTCGTCTCACTGCAATCCGATGATTAATGCCCAACAGCCACCGTTAGTCC 563  
448 ACCAATTAATCTAACTAAATTTATTTATGATTAATGCCCAACAGCCACCGTTAGTCC 507  
564 ACTAGAGTATTTACCACTGCAATCTACACATTTGAATCAGCTGTTAAAGTATGACGA 623  
508 ACAGAGTATTTACCACTGCAATCTACACATTTGAATCAGCTGTTAAAGTATGACGA 567  
624 GGTTCATTTTATGCTGCTGTTAATGATCTTAAGATGATGAAATTTGCTGATCTGTA 683  
568 GGTTCATTTTATGCTGCTGTTAATGATCTTAAGATGATGAAATTTGCTGATCTGTA 627  
684 GTATAGCTTTTACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
628 GTATAGCTTTTACCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
744 AGCTTTAGGCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCTGCT 803  
688 ACATTTAGGCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCTGCT 747  
804 GTGCGCGCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 863  
748 GTGCGCGCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 807  
864 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923  
808 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867  
924 TGCATCAAGAAATTCCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCT 983  
868 TGCATCAAGAAATTCCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCT 927  
984 TATCAATAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043  
928 TATCAATAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987  
1044 TGCATCAAGAAATTCCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCT 1103  
988 TGCATCAAGAAATTCCTGCTGCAAGCGCTTAAACCGTATGCTGCTGCTGCTGCTGCTGCT 1047  
1104 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163  
1048 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107  
1164 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1223  
1108 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167  
1224 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283  
1168 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227  
1284 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343  
1228 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287  
1344 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403  
1288 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1347  
1404 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1463  
1348 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1407  
1464 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1523  
1408 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1467  
1524 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1583

1468 TATGAACGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1527  
1584 ATTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1643  
1528 ATACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1587  
1644 ACCACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1703  
1588 ACCACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1644  
1704 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1763  
1645 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704  
1764 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1823  
1705 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1764  
1824 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1883  
1765 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1824  
1884 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1943  
1825 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884  
1944 TCGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2003  
1885 TCGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1944  
2004 ATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2063  
1945 ATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2004  
2064 CCGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2123  
2005 CCGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2064  
2124 CCGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124  
2065 CCGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124  
2169 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2228  
2125 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2184  
2229 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2288  
2185 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2244  
2289 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2348  
2245 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
2349 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2408  
2281 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
2409 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2468  
2341 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
2469 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2528  
2401 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
2529 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2588  
2461 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520  
2589 GGTTCATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2648

Dh 2521 TTCTTCAGGCGCACTTTTGCAATTGAGGCGAGCATGAACTGATGGCCATGAGCCCGAAG 2580  
Qy 2649 TACTATTTCAGAGAGGCTGGAAACATCTTCCACTTATATATGTGGCCCTATGCTATATG 2708  
Db 2581 TACTACTTCAGAGAGGCTGGAAACATCTTCCACTTATATATGTGGCCCTATGCTATATG 2640  
Qy 2709 GAACCTGGAGCTCGAGGAGTGTCCAGGAGTGTCCGTAATGTCCGTTCCCTTTCGATGTGCGGT 2768  
Db 2641 GAATTTGGGCTGGAGGAGTGTCCAGGAGCTGTCCGTTGAGAGAGTTTGTGTGTTCTGCT 2700  
Qy 2769 GTATTCAAACTGGCCAGTCTTGGCCCACTTAAATTTACTATTTTCATTTGAGAGAGC 2828  
Db 2701 GTATTCAAAATTTGGCAAAATTCATGCGCCCACTGAATTTACTCATTTTCATTTAGGCGCG 2760  
Qy 2829 ACCATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGATATATCATCTTCACTCTTGG 2888  
Db 2761 ACAATGGGTGATGGGTAACTGACATTTGTACTTTGATATATCATCTTCACTCTTGGCC 2820  
Qy 2889 GTGATGGGAAATGCACTGTTGGGAAAGATTATCATGATCAACAAGACCGGCTTCCGGAT 2948  
Db 2821 GTGATGGGAAATGCACTTTGGGAAAGATTATATGACACACAGAGATGCTTCAAGAGAC 2880  
Qy 2949 GAGCACTGCGCGCTGGAACTTCAACGACTTTATGCAAGCTTTCATGATGCTGTCCGG 3008  
Db 2881 CATGAATTAACCGCGCTGGAAATTTCAACGACTTTCATGCAAGCTTTCATGATGCTGTCCGA 2940  
Qy 3009 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3068  
Db 2941 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
Qy 3069 TGCAATCCCTCTTCTTGGGCAACGCTGTCATCGGCAATCTTGGGTAATTAACTTTTC 3128  
Db 3001 TGTAATCCCTCTTCTTGGGCAACGCTGTCATCGGCAATTTTGGGTAATTAACTTTTC 3060  
Qy 3129 TTGACCTTCTTCTTGGGCAACGCTGTCATCGGCAATTTTGGGTAATTAACTTTTC 3188  
Db 3061 TTGACCTTCTTCTTGGGCAACGCTGTCATCGGCAATTTTGGGTAATTAACTTTTC 3120  
Qy 3189 GATACGAATAAATAGCCGAGGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 3248  
Db 3121 GATACGAATAAATAGCCGAGGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 3180  
Qy 3249 CGTATATTTGCGATGTTTCAAGTTAAATGAGTAAACAATGCAATCAATTAAGTAT 3308  
Db 3181 CGTATATTTGCGATGTTTCAAGTTAAATGAGTAAACAATGCAATCAATTAAGTAT 3240  
Qy 3309 CAACCATCAGGTGAGAGGACCAACGATCAGTTGATTTGAGCGAGAGCATGTGATC 3368  
Db 3241 CAACCATC-----AGAACATGTGCGAT 3261  
Qy 3369 AACGAATGAGCTGGGCGACGAGCATCTTCCGCGAGCGCTTCATCAAGAGGGAGTC 3428  
Db 3262 AATGAATGAGCTGGGCGACGAGCATCTTCCGCGAGCGCTTCATCAAGAGGGAGTC 3321  
Qy 3429 AAGGAGGAGGAGCACTGGAGGTGGCATTCGGGAGATGCGGATTTACATACACAGCGC 3488  
Db 3322 AAGGAGGAGGAGCACTGGAGGTGGCATTCGGGAGATGCGGATTTACATACACAGCGC 3381  
Qy 3489 GACATGAGAGCAACAAGCCGAGAAATCAAAATTTCAAAATTAACGACAGATGTTGGC 3548  
Db 3382 GATATGAGAGCAACAAGCCGAGAAATCAAAATTTCAAAATTAACGACAGATGTTGGC 3441  
Qy 3549 AACTCAATTAACGACAGCAATGACTGGAACGAGCTTAAACATTAAGAGTTTGTCC 3608  
Db 3442 AACTCAATTAACGACAGCAATGACTGGAACGAGCTTAAACATTAAGAGTTTGTCC 3501  
Qy 3609 TTACAGAGGAGCACTGCGAGCAATTAATCATATGTTAGCAATTAAGATCGACATTC 3668  
Db 3502 ATACAGAGGAGCACTGCGAGCAATTAATCATATGTTAGCAATTAAGATCGACATTC 3561  
Qy 3669 AAGGAGGAGGAGCACTGCGAGCAATTAATCATATGTTAGCAATTAAGATCGACATTC 3728  
Db 3562 AAGGAGGAGGAGCACTGCGAGCAATTAATCATATGTTAGCAATTAAGATCGACATTC 3621

Qy 3729 AGCAAGAGGATTTAGTCTCGACGAGCACTGACACGAGAGGCGCAATTCGAGAGGCGC 3788  
Db 3622 AGCAAGAGGAGCTTCGCGCTCGACGAGCACTGACGAGAGGCGCGAGGCGGATAGGCGC 3681  
Qy 3789 CGGCTCGAGGAGGATATCATTTATTCATGCG---ACACGAGGAGGATATCTCGATGATAT 3845  
Db 3682 CAGCTGAGGAGGATATCATTTATTCATGCG---ACACGAGGAGGATATCTCGATGATAT 3741  
Qy 3846 CAGCTGAGGAGGATATCATTTATTCATGCG---ACACGAGGAGGATATCTCGATGATAT 3905  
Db 3742 CCGGCGAGCTGTTCCCGGCTCGACGAGCAATTAAGAGGATTTCCGATCTTGGCGCGAGCAG 3801  
Qy 3906 GACTCGCGCTTTCGCAAGAGATGGGCAATTTAGCACTGAAATCTTTCAATTAATGAA 3965  
Db 3802 GACTCGCGCTTTCGCAAGAGATGGGCAATTTAGCACTGAAATCTTTCAATTAATGAA 3861  
Qy 3966 AATAAATATTTGAAAGAGCTGTTATCATGATGATTTAATGAGTATGAGCTTATGAGCA 4025  
Db 3862 AATAAATATTTGAAAGAGCTGTTATCATGATGATTTAATGAGTATGAGCTTATGAGCA 3921  
Qy 4026 TTGAGAGATGACATCTGCGCAAAAGACCATCTGACAGATATTTATTAATGAGAC 4085  
Db 3922 TTGAGAGATGACATTTATCCGATCGACCTGTCATGAGATATATCTGATACATGAGAC 3981  
Qy 4086 AGAATATTTAGGTTATATTTCTTGGAAATGTTATCAAGTGTGTGGCGCTGCGCTTC 4145  
Db 3982 AGAATATTTAGGTTATATTTCTTGGAAATGTTATCAAGTGTGTGGCGCTGCGCTTC 4041  
Qy 4146 AAGATGATCTCACCAAGCGGAGGAGTGTGAGTGTGATGATGATGATGATGATGATGATGAT 4205  
Db 4042 AAGATGATCTCACCAAGCGGAGGAGTGTGAGTGTGATGATGATGATGATGATGATGATGAT 4101  
Qy 4206 ATCAATCTGTTGCTTCACTTGTGAGAGCTGAGTATCAAGCTTTCAGACATATGCGA 4265  
Db 4102 ATCAATCTGTTGCTTCACTTGTGAGAGCTGAGTATCAAGCTTTCAGACATATGCGA 4161  
Qy 4266 ACCTTAAAGAGCATGAGACCACTAGCTGAGATGTCGCTATGAGAGGAGTAAAGGCTGC 4325  
Db 4162 ACCTTAAAGAGCATGAGACCACTAGCTGAGATGTCGCTATGAGAGGAGTAAAGGCTGC 4221  
Qy 4326 GTTATGAGGCTGATCAAGAGCTATACCGGATCTTCAATGATGATGATGATGATGATGATGAT 4385  
Db 4222 GTTATGAGGCTGATCAAGAGCTATACCGGATCTTCAATGATGATGATGATGATGATGATGAT 4281  
Qy 4386 TTTTGGCTAATTTTGGCATATGAGGAGTATCAAGCTTTCGAGAAATATTTTAAAGTC 4445  
Db 4282 TTTTGGCTAATTTTGGCATATGAGGAGTATCAAGCTTTCGAGAAATATTTTAAAGTC 4341  
Qy 4446 GAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4505  
Db 4342 GAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4401  
Qy 4506 AGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4565  
Db 4402 AGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4461  
Qy 4566 CTGTCCTTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4625  
Db 4462 CTGTCCTTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4521  
Qy 4626 GATTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4685  
Db 4522 GATTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4581  
Qy 4686 TTGCTATTTCTCATATTTGATTTGATTTTTCATCTGATCTGATCTGATCTGATCTGATCTGAT 4745  
Db 4582 TTGCTATTTCTCATATTTGATTTGATTTTTCATCTGATCTGATCTGATCTGATCTGATCTGAT 4641  
Qy 4746 ATTGATATTTTATGAGCAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4805  
Db 4642 ATTGATATTTTATGAGCAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4701

QY 4806 GAAATCAGAAAAAGTATATATGCTATGAAAAAGTGGGCTCTTAAAAACCATTTAAA 4865  
 DB 4702 GAAGATCAGAAAAAGTATATATGCTATGAAAAAGTGGGCTCTTAAAAACCATTTAAA 4761  
 QY 4866 GCCATTCAGAACAGAGTGGGCGACCAAGCAAGCAATGCTTTGAATPAGAACGATAAG 4925  
 DB 4762 GCCATTCAGAACAGAGTGGGCGACCAAGCAAGCAATGCTTTGAATPAGAACGATAAG 4821  
 QY 4926 AATATGAT 4985  
 DB 4822 AATATGAT 4881  
 QY 4986 CGTTAGATGCGTGGACAGTATTAACGCGCTCTTACATATCTCAATGAGATATTCGTA 5045  
 DB 4882 CGGTACACACCTCCGAGGCGTACCAACATGCTCTCAACAACTCAATGGAAATTCGTA 4941  
 QY 5046 GTTATTTTCCAGTCCGAAATGCTATTAATAATATGCTTTAGATATCAATATTTTAT 5105  
 DB 4942 GTTATTTTCCAGTCCGAAATGCTATTAATAATATGCTTTAGATATCAATATTTCAA 5001  
 QY 5106 GAGCATGAT 5165  
 DB 5002 GAGCATGAT 5061  
 QY 5166 AGCGATTTTCCAGAAATCTTGTGTGCGCCGACCTGCTCCGAGTGGCGGTGGCG 5225  
 DB 5062 AGCGACATCATTTGAGAAATTTTCGATCGCCGACATGCTCGGTGGTGAAGTGGCC 5121  
 QY 5226 AAGTGGGCGGTGCTTTCGACTGCTGAGAGGAGCCAAAGGCAATTCGAGACATGCTTTC 5285  
 DB 5122 AAGTGGGCTGTGCTGCTGCTTATAGTCAAGGATCCAAAGGATTCGGAAGTGTGCTTC 5181  
 QY 5286 GCGTGGGCGATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTG 5345  
 DB 5182 GCGTACCATGCTGTGCTGCTGCTTATCAACATTTGTGCTGCTGCTGCTGCTGCTG 5241  
 QY 5346 TTCAATCTTCCATTTCCGAGTGTGCTGCTCAATGAGTGAAGGAGAGGCGGCAAT 5405  
 DB 5242 TTCAATCTTCCATTTCCGAGTGTGCTGCTCAATGAGTGAAGGAGAGGCGGCAAT 5301  
 QY 5406 AACGACGCTTACACTTCAAGACCTTTGGCCAGACATGATCTGCTCTTCAAGATGCG 5465  
 DB 5302 AATGCTGTAT 5361  
 QY 5466 ACCTGACCGGCTGGAGTGTGCTGCTGCTTATCAATGAGGAGATTTGGATCCA 5525  
 DB 5362 ACCTGACCGGCTGGAGTGTGCTGCTGCTTATCAATGAGGAGATTTGGATCCA 5421  
 QY 5526 CCGGACGCGCAACAAAGGCTATCCGGGCAATTTGCTTCAAGGACGCTTGGAAATACGTT 5585  
 DB 5422 CCGGACGCGCAACAAAGGCTATCCGGGCAATTTGCTTCAAGGACGCTTGGAAATACGTT 5481  
 QY 5586 CTCTCTCATATCTTAT 5645  
 DB 5482 CTCTCTCATATCTTAT 5541  
 QY 5646 CTGAGAACTATATGTCAGGCGACCGAGGACGCTGCAAGAGGCTTAAACGAGATCAC 5705  
 DB 5542 CTGAGAACTATATGTCAGGCGACCGAGGATTTAAGAGGCTTCAACCGAGATCAT 5601  
 QY 5706 GACATGTCTATGATCTGGCAGCAATTCGATCCGAGGAGGACCCAGATACATACGCTAT 5765  
 DB 5602 GATATGTATCTAGATTTGGCAACATTCGATCCGAGGATACCCAGATACATACGCTAT 5661  
 QY 5766 GATCAGCTGTCCGATTTCTTGAAGCTTCTGAGGCGGCTGAGATTCACAAACCGAAC 5825  
 DB 5662 GATCAGCTGTCCGATTTCTTGAAGCTTCTGAGGCGGCTGAGATTCACAAACCGAAC 5721  
 QY 5826 AAGTACAAAGATCATATGATGAGCAATACCATCTGTGCGGCTGAGCTTCAATGATGCTC 5885  
 DB 5722 AAGTACAAAGATCATATGATGAGCAATGCTGTGCGGCTGAGCTTCAATGATGCTC 5781  
 QY 5886 GACATCTCTGAGGCGCTTACGAAAGACTTCTTGGCGGAGAGGCAATCCGATGAGAGAG 5945

DB 5782 GATATATTTGATGCTTACGCTTACGCAAGACCTTTCTTGGCGGAGAGGTAATCCGATCGAGAG 5841  
 QY 5946 ACGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 DB 5842 ACGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 QY 6006 TCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6065  
 DB 5902 TCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5961  
 QY 6066 AAGCAACAGGCGCGCGAGGAGGATGCTTCTTGAACCCGATACGATCATGCGCAT 6125  
 DB 5962 CATTACAGAAATGCG----- 5976  
 QY 6126 GCGGCTGATCCGATGCTCCGAGACCCGCGCCGATGAGACACGAGCGCATGCGCC 6185  
 DB 5977 CCACCCAGAGGATGATGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6036  
 QY 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
 DB 6037 GAGGCTGAGAGGCG 6096  
 QY 6246 AATGTAAATATGCTCCGCTGAGATGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 6305  
 DB 6097 GAGGCGCAATCAACCCACAGATCOAGATGCGCGGAGGAGGAGATGCTGCGCGCGCAAT 6156  
 QY 6306 GCGGCGGCGACGACGACGCGCGGGAATCCCGAGCGGCTGAGCGCGCGCGCGCGCGCG 6365  
 DB 6157 GGTGGCGGCG 6216  
 QY 6366 GTTCTGCTGAGAGGCGAGCGGCTTCTGAGCAAGAAACGCGCAAGAGTGTCTCACTCG 6425  
 DB 6217 GTTCTGCTGAGAGGCGAGCGGCTTCTGAGCAAGAAACGCGCAAGAGTGTCTCACTCG 6276  
 QY 6426 CGATGCGCGAGCATCACTGCGCGACGCGCGAGTGTCTGA 6464  
 DB 6277 AGATGCCGAGCATTAATCCAGAGCGCGAGATGTCTGA 6315

RESULT 9  
 AAV58423  
 ID AAV58423 standard; cDNA; 6586 BP.  
 XX  
 AC AAV58423;  
 XX  
 DT 01-DEC-1998 (first entry)  
 XX  
 DE PNA sodium channel clone variant.  
 XX  
 KW Tetrodotoxin-sensitive sodium channel; rat; PNA sodium channel; stroke;  
 KW nervous system disorder; epilepsy; brain injury; diabetic neuropathy;  
 KW AIDS-associated neuropathy; therapy; ss.  
 XX  
 OS Rattus sp.  
 XX  
 FT Key Location/Qualifiers  
 FT misc\_feature 2051..2080  
 FT /tag= a  
 FT /note= "insert sequence"  
 XX  
 PD WO9838302-A2.  
 XX  
 XX 03-SEP-1998.  
 XX  
 XX 20-FEB-1998; 98MO-EP000997.  
 XX  
 XX 26-FEB-1997; 97US-0039447P.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran J;

DR WPI; 1998-481204/41.

XX New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for  
PT detecting inhibitors which alleviate pain, and treating nervous system  
PT disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.

XX Claim 18; Page; 87pp; English.

CC This sequence represents the isolated rat PNA sodium channel cDNA clone  
CC of the invention. This sequence was isolated from a peripheral nerve from  
CC a rat dorsal ganglia. The PNA sodium channel sequences are tetrodotoxin-  
CC sensitive sodium channels. The protein is used in assays for detecting  
CC inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate  
CC pain. The probes can be used to detect and isolate the DNA or protein in  
CC tissues. The antibodies can also be used to isolate the protein. The  
CC protein is used as a therapeutic target for compounds to treat disorders  
CC of the nervous system, such as epilepsy, stroke and brain injury.  
CC diabetic neuropathy, and AIDS-associated neuropathy, etc. Note: This  
CC variant sequence was created by the indexer using the information given  
CC in the specification, and the sequence shown in AAV58419

SO Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;

Query Match 15.7%; Score 1021.4; DB 2; Length 6586;  
Best Local Similarity 52.5%; Pred. No. 2.3e-245;  
Matches 3125; Conservative 0; Mismatches 2486; Indels 342; Gaps 27;

QY 186 CGCAAGAAAAAACAAGAAATCCGATATGATGACGAGACGAGATGAAGTCCACAA 245  
DB 268 CTCAAGAAACCAACCAAGGCGATGACGACCGGAGACGATGAGAGACGACGAGCC 327  
QY 246 CCGATCTCTACCTGAAACAGGTGTGCAATCTGTCATGTGACGAGGACGCTTCCG 305  
DB 328 AAGCCAAACAGTACCTGAGGCTGGAAGATTTGCTTTCATCTACGAGGACATCCG 387  
QY 306 CCGAATTTGGCTCTCACTCTCTCGAGATATGATCCCTTACATGACGATGTACGACA 365  
DB 388 CAAGGCTGTGGCGGTTCCCTGAGAGACTTGACCTTACTATTTGACGAGAAAC 447  
QY 366 TTCTGATTTGAGCAAGAAAGATTTTTCCTTTCTGATCAAAACGAAATGTGG 425  
DB 448 TTTGTAGTATTTAAACAGAGGGAACCTCTTCATTTAGTGCACACCTGCTGTAC 507  
QY 426 ATGCTCATTCATTCATTCGATAGTGTGTGTCATTTATCTATGATGATCATTA 485  
DB 508 ATTTAAGCCCTTTTAACTGTATTAAGAAATGATTAATTAATTTGATACCTAGT 567  
QY 486 TTTTCCCTATTCATCATCAACCAATTCCTGCACTGATCTGATGATTAATGCGACA 545  
DB 568 TTGACGATGATCATATGACCACTCTGACCACTGTGTGATGACCTTTAGTAC 627  
QY 546 ACGCCACGCTTGAATCACTGAGGTG--ATATTCACCGAATCTACACATTTGAATCA 602  
DB 628 CTTCCAGATGAGTCCAAAGATGTGAGTACACATTCACAGGATTTTACATTTGATCA 687  
QY 603 GCTGTAAAGTATGAGCAGAGTTTCATTTATGCGCGTTTACGATCTTGAATGCA 662  
DB 688 CTAGGAAATATGTCAGAAAGGTTTTCATTAAGCGGCTTCACTTTCTGAGAACCG 747  
QY 663 TGGAAATGGCTGACCTTGTATGATTAAGCTTATGATGACCATGAGGTATTAATTA 722  
DB 748 TGGAACTGTTAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
QY 723 GGTATCTAGACGCTTGCAGAACTTTAGAGGTGTGCGAGCGCTTAAACCGTACCAT 782  
DB 808 GGCATATGCTCAGCGCTGAGAACTTCAAGGGTTTCTCCAGCTTTGAAAACTATCTGTA 867  
QY 783 GTGCAAGCTTGAACCATGCTGCGCGCTGATCGAATCGGTGAAGATTTGCGCAT 842  
DB 868 ATTCCAGGCTGGAACCAATGCTGGCGCTTAAATCCAGTCCGTGAAGAAAGTGTGAGC 927  
QY 843 GTGATATCTGACCATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902

DB 928 GTGATATCTGACAGTGTCTGCTGATGTTTTCGCTGATTTGGCTGACGCTTTC 987  
QY 903 ATGGCGTGTCTACCGAAGATGCAAT-----CAAGAGTTCCTGTCAGCGTTC 953  
DB 988 ATGGGAACTTTCGAAACAGATGTCTGTGTGCGCCATTAACCTTCAACGAGGCTTACCTG 1047  
QY 954 TGGGGCAATCTGACCGACGAGAACTGGGACTATCACAATCCGATATGCTCAATGTGTAT 1013  
DB 1048 GAGAACCGACACAGAGCTTTGATCTGGAGAGATATATCAACATTAACAACTTTTATC 1107  
QY 1014 TCCGAGACGAGGCGATCTCATTTTCCGTTATGCGCAATATATCCGCTGCGGCAATGTC 1073  
DB 1108 ATGTTTCCGAGATCTGAAACCTTGTCTGCGGAAACAGTTGATGCTGTGGCAATGTC 1167  
QY 1074 GACGACGATTAAGTGTCTGACAGGAGTTTGTGCGAATCCGATTAATGCTACACGAC 1133  
DB 1168 CCAGGAGGATTCATGATGATGAAG--CAGGAAGAAACCCCACTACGCTTACACGAC 1224  
QY 1134 TTGATGTTGTTGAGTGGGCTTTCTGTGCGCTTCCGCTGATGACACAGGACTTTCG 1193  
DB 1225 TTGACACCTTACGCTGGGCTTTCTGTGATTAATTCGCTTATACACGAGCTATTTGG 1284  
QY 1194 GAGATCTGTACCACTGTGTGTGCGCGCGCGGACCATGACATGACATGCTTCTTATA 1253  
DB 1285 GAGAACTTATACAGCTGACCTTACGAGCGCGTGGGAAACGATACATGATCTTCTTGTTC 1344  
QY 1254 GTCATATCTTCTAGTTCATTTCTTGTGAATTTGATTTGATTTGCGATTTGCGCATG 1313  
DB 1345 TTGATCATCTTGTGTGTTCTTTCTATCTGGAACCTTGTGCTGTGTGTGTGCTGATG 1404  
QY 1314 TGTATGACGATTTGCAAGAAAGGCGGCAAGAAAGAGGCTGCGGAAAGAGAGCGATTA 1373  
DB 1405 GCTTATGAGAA--CAAGAACGAGCACTGAGGAGGAGAGCAAAAGAGC--- 1457  
QY 1374 CGTGAAGGGAAGAGTGTGCGCGCGCAAGGCGCAAGCTGAGAGAGCGGCGCATGCG 1433  
DB 1458 CGAGTTCAAGGCAATGCTGAGCACTGAG--AGCAGACAGAGAGAGCAAGCT 1512  
QY 1434 CAGGCTCAGGACAGCGGATGCGGCTGCGCGGAGAGGCTGACCTGATCGGAATG 1493  
DB 1513 GCTGCAATGCGCACCTCAGCGGCACTGTCTGCAAGA--CGCATTTGAAGAAAGAG 1569  
QY 1494 GCAAGAGTCCGAGATATTTCTGATGACGATATGATGATTTGTTGGGCGGAGAAAGG 1553  
DB 1570 GAAATGAGGATGAGCTTCCGAGAGCTTCTGAACTGTCTAACTGATTTCAAGAGC 1629  
QY 1554 AACGATGACCAACCAAGAAAGATGTCAATTCGAGCGTGAAGTGAAGTGCAGTGC 1613  
DB 1630 GCGAAGAGCGCGGAGAA-----CGAGCGAAGAAAGAGAGCAAGAA 1673  
QY 1614 GTGAGCTTATTAACAAAGCAACAGCACCTTACACAGACCAACGATTAACAAAGTGT 1673  
DB 1674 GCTCTGTAAGGCGAGGAGAAAGGAGACCGGAGAGGATGTTTAA-----GT 1720  
QY 1674 AAAGTGAACAGATCTTATCTTATCTTACCTGTTCACCGTTTACATACAGAGGGATCA 1733  
DB 1721 CAGAGTCCGAAAGCGATATGAGAAAGGCTTCTGCGCTCCACAGCAACAGATAGGGA 1780  
QY 1734 GGTAGTTCTCAAGATACAGATACGGAACGAGCGCTTGTGATACCGGCTGAGC 1793  
DB 1781 GAAAGTTTTCATATGATATAGTGTGCTGCTGACATTCAGAGCTGCGCTTCTCTGCC 1840  
QY 1794 GATGTAAGCAATTTGATTTGTCAATATAGAGATGCTCAGACAGCACTTGCCTATGCC 1853  
DB 1841 GACATTAACAGCAAAAGCAGATCTTACGCTTCCGGGAGCCCG--GTGCTTCCGAGACCC 1899  
QY 1854 GACGATGATGCTGCTGACCCGATGTCGGAAGAGATGAGGAGCATATGATGCTGCTG 1913  
DB 1900 GCTCTGAGAAATG-----AGTTGCAAGCAATGAAACACAGACCGTGAAGAG 1947  
QY 1914 TACTATGCAATTTAGGCTCCGACACTCATCTGATACCTGCAATCAGTCCGATATG 1973  
DB 1948 AGCGAGGCGCGGCTGATGCTGCTCTTATCTCCGATCCGCGGCGGAGCGCGGAGC 2007

QY 1974 TATACCTCAGATGCGATCTACTGCGGCGATGCGCGTCAATGCGGCTGACCAATAGCC 2033  
DB 2008 TACAGTGGCTACAGCGGCTACAGCTCAGCTCAGCGGCTCGCTGCTGTAATAATAGAGC 2067  
QY 2034 AAGAGAGCAATATGCGCAACCGCAACACGCAATCAATCACTGCGCGCCCAATGGC 2093  
DB 2068 AGCTAGGGAAGGCGCATCTTCCAGCTGCGGCGGCGAGCTGGAAGCGCAACACAGCGTG 2127  
QY 2094 GGCACCACTCTGTGAGACCAATCAACACTGATCATGCGAGCTACGAAATGGCGTG 2153  
DB 2128 GACTGCAACGCGGAGTGTACTCATCTGCGGCGCTCAACAATCGGCGGCTCTGCTC 2187  
QY 2154 GAGTGCACGACGAAAGCTGCAAGATTAAATCATCATGCAATCTTTATGAGCCGCTC 2213  
DB 2188 GAGGCAACGACTAGGTGGAATTAAGAGAAAGCCCTGGAATCTTTATGTTTATG 2247  
QY 2214 CAGACAAACGCGTGTGATGTAAGAAAGATGTAGTGTCTGAAATGACATCATGAAAG 2273  
DB 2248 GACCAACTCGCTCTACGAGCGGAAGGA-----CAGATCAACAGCATTAATGAG 2297  
QY 2274 GCGCGTGTGCGGCACTGCGGCGAAGGATGCGGCTGCTCCGTTTACTATTTCCCAACA 2333  
DB 2298 CGTGTCAAAACGCTAGTGAAGAGCTGAAAGTCTCAGAGAA----- 2344  
QY 2334 GAGGACGATGACGAGATGGCGCGAGCTTCAGAACAGGCACTGAAATGATCTCAAA 2393  
DB 2345 -----AGTCCCAACGCTGCTGTATTAAGTTTGCACAACCTTCTCTCA-- 2386  
QY 2394 GGCATCATGTGTTTGTGTGTGGAAGCTGTGCGGCTGTTGTAATTCAGGAGTGG 2453  
DB 2387 -----TCTGGAAGTCAACCTTCACTGGAATAAATCGAAGAAATC 2427  
QY 2454 GTATGCTCATCTGCTTGTGATCCCTGCTGAGCTTTCATCAGCTGTGATGTGCTC 2513  
DB 2428 GTGAATTAATGCTATGAGACCTTTTGTAGACTTAAGCATCAATCTGATGCTGCTG 2487  
QY 2514 AACAAGATGTTCAATGCAATGATGATCAACGATTAAGAAAGAGATGAAACGCTGCTC 2573  
DB 2488 AATAGCTATTATTAAGCAATGAGACCATCCATGACACCAAGTTGAAACAGCTCTTG 2547  
QY 2574 AAGAGTGCACATATTTCTTCAACGCGCACTTTGCGATCGAGGCCACCATGAAGCTAATG 2633  
DB 2548 GCCGTGAATATCTGTGTTCACCGGATCTTCAAGCGGAAATGTTTCTGAAGCTATA 2607  
QY 2634 GCCATGACCCCACTATTTCTTCAAGAGGCGTGAACATCTTGAATCTTATATCTG 2693  
DB 2608 GCCATGACCCCTACTATTAATTTCAAGAGGCTGAACATTTTGAACGATTAATGTC 2667  
QY 2694 GCCCTATGCTATTTGAACTGGAGACTCGAGGCTTCAGGAGTCTGCTCGTATGCTTCC 2753  
DB 2668 TCCCTCACTTAATGAGAGTGAAGTCTCGAGATGAGAGGCGCTCTGAGTGTGCGTCT 2727  
QY 2754 TTTGATGCTGCTGATTAATCAACTGCGCAAGTCTTGCGCCCACTTAATTTACTACT 2813  
DB 2728 TTCCAGTGTCTCGAGTCTTCAAGTCTGCGCAAGTCTTGCGCCCACTGAACATGCTGATC 2787  
QY 2814 TCGATTATGAGACGACCATGCGCTTGGGTAATCTGACATTTGTACTTTGCTATATC 2873  
DB 2788 AAGATCATCGGAACTCCGTGAGTCCCTGCGCAACCTGACCTGAGTGTGCGCATATC 2847  
QY 2874 ATCTTCACTTTTGGCTGATGAGAAATGCACTGTTGCGAAAGAAATTAATCATGA--TCAAC 2930  
DB 2848 GTCTTCACTTTGCGCTGTGAGAGTGAAGTGTGTAAGAAAGTTTACAGAGTGGCTC 2907  
QY 2931 AAGGACCGCTTTCGGATGCGACCTGCGCGCTGGAACCTTCAACGACTTTATGACAGC 2990  
DB 2908 TGTAAATCAACAGAGATGCAAGTCCGCGCTGGCATGAGACGACTTCTTCACTCC 2967  
QY 2991 TTCTATGATGTGTTCCGGGTGCTCTGCGAGAAATGATGATGATGATGAGGAGCTGCAAG 3050  
DB 2968 TTCTCATGCTTCTCGAGTGTGTGTGAGAGTGAAGACCAATGTGGAGCTGCAAG 3027

QY 3051 TAGCTG---GGGATGTCTGCTGCTATCCCTTCTTTGGGCAACCGTGTGATCGGCAAT 3107  
DB 3028 GAGTGGCGCGGCGAGGCGCATGTGCTCATGTGCTTATGATGATGTATGTATGCGCAAC 3087  
QY 3108 CTTGTGATTAACCTTTTCTTACCTTGTGCTTTTGTCCAAATTTGGCTCATTAAGCTTA 3167  
DB 3088 CTGTGTGTCTGATCTTATCTTCTGCGCTTGTGCTTGTGAGCTCTTCAAGCGAGCAACCTG 3147  
QY 3168 TGAAGCGGAGCTGCGGATTAAGATTAAGAAATTAAGCCGAGGCTTCAATGAAATTTGGC 3227  
DB 3148 GCGGCAACAGACGAGCGGGAATGAACAA----- 3179  
QY 3228 CGATTTAAAGTTGGTTAAGGTAATATGCTGATGTTTCAAGTTAATAGTAACAA 3287  
DB 3180 ----- 3179  
QY 3288 TTGACAAATCAATTAAGTATCAACATCAAGTGAAGAGCAACCAAGATCACTTGAAT 3347  
DB 3180 -----CTGCGAGTCTCAGTGTATC 3198  
QY 3348 TGAAGCAAGACATGATGATCAACGAATGAGCTGGGCGCAAGAGATCTCGCGCAC 3407  
DB 3199 CGATCAAGAGGCGTGGCTTGACCAAAATGAAGTGAAGCTGCTTATGAGGCTCAC 3258  
QY 3408 GGCCTCATCAAGAGGAGATCAAGAGCAGCACTGAGGTGCCATCGGGATCGG 3467  
DB 3259 TTCAACAGCGGAGCGGATGAAGTGAACCTCTGACGACTGTATGAAGAAAGCGC 3318  
QY 3468 ATGAATTCACGATACACGCGCATGAAGAAACAGACCGAAGAAATCCAAATATCTA 3527  
DB 3319 ACTGATGCGCCACCAACGAGCGCTGTGATTCACCGAAGCGGCACTTCCAGAAAC 3378  
QY 3528 AATTAAGCAACGATGATGGAACCTCAATTAACCAAGCAACATGAATGAGAACAGAG 3587  
DB 3379 GGAAGCAACCAACGCGATCGCAGAGCTGGAAGATGATCATGACGAGAC 3438  
QY 3588 CTAACCATTAAGAGTTTGTCTTACAGAGCAGACGACATGCGACATTAATCATATGCT 3647  
DB 3439 CACG-----TGTCTTTCATTAACAC-----CCAACTCAACGCTCGGAT 3479  
QY 3648 AGCCATTAAGATGACCATTTCAAGAGCAGAGCAGCAAGAGGCGCGAGACGATGAG 3707  
DB 3480 GCCATTTGCTGTGGGAGTCT---TGACTTGAATCTTCAACAGAGATGTTAGC 3534  
QY 3708 GCGAGAGAAAGCGCGACGCGCAAGAGAGATTTAGTCTGACGAGAACTGACAGAG 3767  
DB 3535 AGCGAATCAACCTGAAAGGCAACAAATPA-----ACTGACATACCACTCTCA 3588  
QY 3768 GAGGCGAATGCAAGAGAGGCGCGCTGACAGTGAATCATTTATGATGACACAGAGAG 3827  
DB 3589 GAAGGAAGTACATGACATCAAGCTGAGGTGAAGAAAGTTCCGTGAGCAACTGAG 3648  
QY 3828 GATTAATCGATTAATTCAGCTGATGTGCTGCCCGATCTGATTAAGAAATTTCCG 3887  
DB 3649 GAATACTTGG-----ATCGAGAGCTGCTTTTACAGAGGTTGCGTCCAGCGTTCAAG 3702  
QY 3888 ATCTTACCGGATGACATGACTGCGCTTCTGCAAGATGAGGCAATTTACAGCTGAA 3947  
DB 3703 TGCTGCAAGCAACATCGAGAAAGACTAGGCAAGTGTGAGATCTTGGCGAAAC 3762  
QY 3948 ACTTTCAATTAATGAAATTAATTTTGAACAGCTGTATCACTATGATTTATG 4007  
DB 3763 TGCTTCTCATTTGAGCAACATTTGATTTGAGCTTCAATCATCTTCAATGATTTCTC 3822  
QY 4008 AGTAGCTTAGCTTGGCATTAAGATGATGATGCTGCAAGAACCAATCTGACAGAT 4067  
DB 3823 AGCAGTGGCGCTGCGCTTTGAGAGCATCTACATTAAGAGAGAGAACCATCCGAC 3882  
QY 4068 ATTTTATATTAATGACAGAAATTTAAGCTTATTTCTTTGGAATTTAATGAG 4127  
DB 3883 ATCTGAGATTAAGGACAAAGTCTTCACTTCACTTCACTTCCGAGATGTTGCTAAG 3942  
QY 4128 TGTGTTGGCTGCGCTTCAAGTGTACTTCAACAAAGCGTGTGTGATTTGCTGATTTGCTG 4187

Db 3943 TGGACGCTACGGCTTGTCAAGTCTTTCACCAATGCTGTGTGGATCTTCTC 4002  
Qy 4188 ATTGTATGATGATGCTTATCACTTGTGCTTCACTTGTGAGCTGTGTATTCAA 4247  
Db 4003 ATTGTGCTGTCTTGTAGTCAAGCTTATAGTATGCTGTGGGCTACCTGGAATAGT 4062  
Qy 4248 GCTTCAAGACTATGCGAAGTAAAGACCTGAGACCACTACGTGCAATGCCATG 4307  
Db 4063 GCGATTAAGTCCCTTAAGACCTTAAGACCTTGAACCTTAAAGCCTTATCAAGATT 4122  
Qy 4308 CAGGAGTGAAGGATGCTGTAATGCGTGTATCAAGTATACGCTTCACTTCAATG 4367  
Db 4123 GAAAGATGAGGATGCTGTGAATGCTTGTGGGCGGCACTCCCTCATATGATG 4182  
Qy 4368 CTATGTGTGTCTAATATTTTGGCTAATTTTGGCAATATGAGTGAACAGCTTTTCT 4427  
Db 4183 CTGCTGGTGTCTCATCTTGTGCTGATTTTCAAGCATATGAGATTAACCTGTTGCG 4242  
Qy 4428 GGAATATTTTAAAGTGC---GAGACATGATGACAGAAAGCTACGCCAGATCTTA 4484  
Db 4243 GGGAAATACCACTGCTTTAATGAGCTTCTGAATCCGATTCGAATGATATGTC 4302  
Qy 4485 CCAATGCAATGCTGTGCGAG-----AGGAGAACTACACGTGGG 4526  
Db 4303 AACATTAACGAGCTGTGAAGAGCTCATGAGGCAACAGCAGATCGATGAG 4362  
Qy 4527 AATTGACATGAATTTGATCATGTAGTAAAGGATGCTGTGCTTTTCCAGTGGCC 4586  
Db 4363 AATGTCAAGATCACTTGTGAATGTGAGACAGGATGCTGGCCCTTCAAGTGGCA 4422  
Qy 4587 ACCTTCAAGGCTGTATCAATCATGAAAGATGCTATGATTCACGAGAGTGAACAG 4646  
Db 4423 ACCTTCAAGGCTGTATGATCATGATGATGATGATGATGATGATGATGATGAT 4482  
Qy 4647 CAACCAATTCGTGAACGACATCTACATGATTTAATTTGATTTCTTCACTATTT 4706  
Db 4483 CAGCTGACTGAGAGGCAATCTACATGATCTATCTTGTGATCTTCACTATCTTC 4542  
Qy 4707 GGAATCTTTTCACTCACTCAATCTGTCATGATGATGATGATGATGATGATGATG 4766  
Db 4543 GGCCTCTTCTTCACTCACTCACTGTCATGATGATGATGATGATGATGATGATG 4602  
Qy 4767 AAGAAAAAGAGTGTGATTAAGAAATGTTATGATGATGATGATGATGATGATGATG 4826  
Db 4603 AAGAAAA---GTTGAGGTGAGACATCTTCAATGACAGAGAACAGAAAGTACTAC 4659  
Qy 4827 AATGCTATGAATAAGATGAGCTTAAATAACATTAAGCAATTCAGAACAGAGTGG 4886  
Db 4660 AATGCTATGAATAAGATGAGCTTAAATAACAGAAAGCAAGAGCCATCCCGACCTTGAAC 4719  
Qy 4887 CGACCAAGCAAGATGCTTGAATAAGTAAACGATTAAGAAATTCATATATCATATG 4946  
Db 4720 AATAATCAAGGATGCTTGAATTTGATGATGATGATGATGATGATGATGATGATG 4779  
Qy 4947 TTATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5006  
Db 4780 ATGCTCATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4839  
Qy 5007 TATAACGCGTCTAGACTATCTCAATGATGATGATGATGATGATGATGATGATGATG 5066  
Db 4840 ATGAGAAATCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 4899  
Qy 5067 CTATTAATAATATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 5126  
Db 4900 GTGCTCAAAATGTTGCTTGAACAATAATTTCACTATGCTGAGAACATCTTTGAC 4959  
Qy 5127 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5186  
Db 4960 TTTGTGTGTGTCTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATG 5019  
Qy 5187 TTGCTGTGCGGACCGCTGCTCCGAGTGTGCTGTGCGGAAAGTGGCCGTGCTTGA 5246

Db 5020 TTGCTTCCCAACCTTATCCAGTTATCCGATTTGGCCGCTATTTGGGCGATCTTGGCT 5079  
Qy 5247 CTGTGAAGGAGCCAAAGGCTATGCACTGCTCTTCCGCTTGGCCATGCTGCTGG 5306  
Db 5080 CTGATCAAGGCGCCAAAGGATCCGACCTGCTCTTGGCTTAAATGATGCTGCTGCC 5139  
Qy 5307 GCCCTTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5366  
Db 5140 GCGCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5199  
Qy 5367 ATGCTTCTTCACTGCACTGTAAGAGAAAGCGGCAATTAAGAGCTTCACTTCAAG 5426  
Db 5200 ATGTCAACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5259  
Qy 5427 ACCTTGGCCAGAGATGATGCTGCTCTTCAATGCTGATGATGATGATGATGATGATG 5486  
Db 5260 ACATTTGGCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5319  
Qy 5487 GFACTGAGCGCTTATCA-----TGAGGAAGATGCGATCCAGCAGGAGC 5537  
Db 5320 CTGCTGCTGCCAATCTGAAACCGCCCTGATGCTGAGCTTGAACAAAGACCCAGG 5379  
Qy 5538 AAAGCTATCCGAGCAATGCTTCAAGCAAGCTTGAATACGTTCTCTCTCATAC 5597  
Db 5380 AGTGGCTTCAAGGAGCTGTGGGAACCCCTGCTGGGCACTTCTTGTGAGTAC 5439  
Qy 5598 CTAGTTAAGCTTTTGTATGATTAATATGATGATGATGATGATGATGATGATGATG 5657  
Db 5440 ATCATCATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5499  
Qy 5658 AGTCAAGGCAACCGAGAGCTGCAAGAGGCTTACCGAGAGCTGATGATGATGATGATG 5717  
Db 5500 AGCTGCTCACCGAGAGAGCGCCGCTCTGATGATGATGATGATGATGATGATGATG 5559  
Qy 5718 GAGATCTGGAGCAATTCGATCCGAGAGGCAACCGATATACGCTATGATCAGCTGCC 5777  
Db 5560 GAGATCTGGAGAGTGTGATCCGAGAGGCAACCGATATACGCTATGATGATGATGATG 5619  
Qy 5778 GAATTCCTGAGCTGATGAGAGCCCGCTGATGATGATGATGATGATGATGATGATG 5837  
Db 5620 GACTTTCAGAGCGCTGAGAGAGCCGCTCGATGATGATGATGATGATGATGATGATG 5679  
Qy 5838 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5897  
Db 5680 ATGCTCATGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5739  
Qy 5898 GCCCTTCAAGAGCTTCTTTCGCGAGAGGCAATCCGATGATGATGATGATGATGATGATG 5957  
Db 5740 GCTTTCAGAGAGCTGCTGAGAGAGGCTGAGAGAGGCTGAGAGAGGCTGAGAGAGG 5799  
Qy 5958 GGTGAG-----ATAGCGCCCGCGGATGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 6011  
Db 5800 GAGAGAGGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5859  
Qy 6012 CTGTGAGGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6071  
Db 5860 CTGCGGCGCAAGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 5919  
Qy 6072 AAGCGCGCGCGG 6084  
Db 5920 TTGGCTAAGGCGG 5932

RESULT 10  
AAVS8421  
ID AAVS8421 standard; cDNA; 6007 BP.  
XX  
XX AAVS8421;  
AC  
XX  
XX 01-DEC-1998 (first entry)  
DT  
XX  
XX Tetradotoxin-sensitive sodium channel PN4a coding sequence.

KW Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;  
 nervous system disorder; epilepsy; brain injury; diabetic neuropathy;  
 AIDS-associated neuropathy; therapy; ss.

XX Rattus sp.

XX Key Location/Qualifiers  
 XX CDS 22..5988  
 XX /\*tag= a

XX MO9838302-A2.

XX 03-SEP-1998.

XX 20-FEB-1998; 98WO-EP000997.

XX 26-FEB-1997; 97US-0039447P.

XX (HOF) HOFFMANN LA ROCHE & CO AG F.

XX Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;

XX WPI: 1998-481204/41.

XX P-PDB; AAM69362.

XX New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for  
 PT detecting inhibitors which alleviate pain, and treating nervous system  
 PT disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.

XX Claim 19; Page 33-36; 87pp; English.

XX This sequence represents the isolated rat PN4 sodium channel cDNA clone  
 CC of the invention. This sequence was isolated from a peripheral nerve from  
 CC a rat dorsal ganglia. The PN4 sodium channel sequences are tetrodotoxin-  
 CC sensitive sodium channels. The protein is used in assays for detecting  
 CC inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate  
 CC pain. The probes can be used to detect and isolate the DNA or protein in  
 CC tissues. The antibodies can also be used to isolate the protein. The  
 CC protein is used as a therapeutic target for compounds to treat disorders  
 CC of the nervous system, such as epilepsy, stroke and brain injury,  
 CC diabetic neuropathy, and AIDS-associated neuropathy, etc

XX Sequence 6007 BF; 1490 A; 1559 C; 1609 G; 1349 T; 0 U; 0 Other;

XX Query Match 15.7%; Score 1019.4; DB 2; Length 6007;

XX Best Local Similarity 52.8%; Pred. No. 7e-245;

XX Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;

XX 186 CGAAGAAAAAAGAAAAAATCCGATATGATGACGAGACGAGATGAAGTCCAA 245

XX 121 CTCAGAAACCAACCAAGCGGATGCGACGCCGAGGAGCATGAACAGCAAGCCC 180

XX 246 CCGGATCTTACACTTGAACAGGGGTGCGCAATACCTGTCGATTCAGGGGAGCTTCCG 305

XX 181 AAGCAAAACAGTGAACCTGAGGCTGGGAAAGATTGCTTCATCTACGGGAGATCCG 240

XX 306 CCGGATTTGGCTCCTCCTCTGAGGATATCGATCCCTACTACAGCATATGACTGACA 365

XX 241 CAAAGCCCTGCTTGGCTTCCCTGAGGACCTTGAACCTTACCTTGAACGCAAAAAC 300

XX 366 TTCTGATTTGTAAGCAAAAGAAATATTTTTCCTTTTCTGCAACAAAGCAATGG 425

XX 301 TTGTGATTTAAGCAAGGAAACCTCTTCAGATTGACACACCTGCTTGAAC 360

XX 426 ATGCTGATTCATTCATTCGATTCGTCGTGGCCATTTCATTTCTAGTGCATCTTA 485

XX 361 ATTTTAAGCCCTTTTAACTGATTAAGAAATAGCTATTAATTTTGAATACCTCACTT 420

XX 486 TTTTCCCATTCATTCATTCATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 545

XX 421 TTACAGATGATCATGTCGACCAATCCGACCAACCTGTGTTTATACCTTTAGTAC 480

XX 546 ACGCCACAGGTTGATGCTGAGGTG--ATATTACCGGAATCTACATTGGAATCA 602

DB 481 CTCCAGATGATCCAAAGATGTGAGTACACATTCACAGGATTTACATTTGATCA 540

DB 603 GCTGTTAAAGTATGATGACAGAGTTTCAATTTATGCCCCGTTTACGATCTTAGAGTCA 662

DB 541 CTAGTAAATATCATGCAAGAGGTTTCTGCATAGACGCTTACCTTCTCGAGACCG 600

DB 663 TGGATTTGGCTGACCTTGGTATAGCTTATAGCTTATGATGACCATGGATATAGATT 722

DB 601 TGGAACTGGTATGACCTTCACTGATCATGATGACATATGACAGATTTGTGACCTG 660

DB 723 GGTAAATGACAGCCCTCGAAACGTTTAAAGGTGCTGCGAGGCTTAAACCGTACCAT 782

DB 661 GGCATATGTCAGCCCTGAGAAACATTCAGAGGTTCTCCAGCTTGAACATATCTCTTA 720

DB 783 GTCCAGAGCTTAAAGACCATGTCGCGCCCGTCATCGAATGCGTGAAGATTCGCGCAT 842

DB 721 ATTCCAGGCTTGAAACAAATCGTGGGCGCTTAATCGATCGTGAAGAGCTTGGCAGC 780

DB 843 GTGATTTATCTGACCATGTTCTCCCTGTCGAGTTCGCTGATGATGAGGCTTACAGAT 902

DB 781 GTGATGATCTTCAAGTGTCTGCTGAGTGTTCGCTGAGTGTTCGCTGAGTGTTCGCTG 840

DB 903 ATGGGCGTCTCAGCAGAGAGTGCAAT-----CAAGATTCCTCGTGAAGCTTCC 953

DB 841 ATGGGGAACCTTCGAAACAAAGTGTGCTGTCGCTGAGGCTTAACTTCAACGAGCTACCTG 900

DB 954 TGGGGAATCTGACCGACGAGAACTGGGACCTTCAATTCGCAATAGCTTCATTTGAT 1013

DB 901 GAGAACGACCAAGAGGCTTGAATGAGGAGATTTATTAACAAATTAACAACTTTTAC 960

DB 1014 TCCGAGAGCAGAGGCACTCATTTCCGTTATGCGCAATATATCCGTCGCGGCAATCC 1073

DB 961 ATGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

DB 1074 GACGACGATTAAGTGTGCTGCGAGGCTTGTGCTGCAATTCGCAATGCTTCAACCGC 1133

DB 1021 CCAGAGGATTTCCAGTGAAGAAAG---CAGAAAGAAACCACTACGTTTACCGAC 1077

DB 1134 TTGATTTGTTGAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1193

DB 1078 TTGATGACCTTCAAGCTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137

DB 1194 GAGATCTGATCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1253

DB 1138 GAGAACCTTATACAGCTGACCTTACAGAGCGCTGGGAAACGATATCTTCTTGTGTC 1197

DB 1254 GTGATCATCTTCTAGCTTCACTTATCTTGAATTTGATTTGCTGCTGCTGCTGCTGCTG 1313

DB 1198 TTGATCATCTTCTGAGTGTCTTCTATCTGATGATGATGATGATGATGATGATGATGAT 1257

DB 1314 TCGATGACGATTTGCAAAAGAGAGGCGCAAGAGAGGCTGCGCAAGAGAGGCGATTA 1373

DB 1258 GCTTTTGAAGAA---CAGAAACAGGCAACCTGAGAGAGGAGAGAGAGAGGAGC---- 1310

DB 1374 CGTGAACGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1433

DB 1311 CGAGTTCAAGGCAATGTGTGAGCACTCAAG---AAGAGAGAGAGAGAGAGAGAGGCT 1365

DB 1434 CAGGCTCAGGCAAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1493

DB 1366 GCTGCAATGCGACCTGAGCGGCACTGTTCGAAAG---CGCATTTGAAGAGAGAGG 1422

DB 1423 GAGATGAGGATGAGCTTCCAGAGAGCTTCTGAACTGCTTAACTCACTTCAAGAGC 1482

DB 1494 GCCAAGATCCGACGATTTCTTCACTAGCTATGATGATTTTGTGGCGGCAAGAGGC 1553

DB 1554 AAGCATGACAAACAAGAGAGAGATGCTCATTTGAGAGCTCGAGGTGAGTGGAGTGC 1613

DB 1483 GCGAAGAGAGCGGAGAA-----CGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1526

DB 1514 GTAGAGCTTTTAAAG 1673

Db 1527 GCTCTGTAAGGCGAGAGAAAGGGACCGGAGAGAGGTTAA-----GT 1573  
Qy 1674 AAAGTAGACAGACATCTTATCTTACCTGTTACCGTTTAAATACGAGGGGATCA 1733  
Db 1574 CAGAGTCGAGAGACGGTATGAGAGAGAGCCCTTCGCTGCGACAAACAGAGATAGGA 1633  
Qy 1734 CGTAGTTCTCAAGATACAGATACGAGAACGGACGTGGCCGCTTGGTATACCGGTAGC 1793  
Db 1634 GGAAGTTTTCATCATGATCATGATGCTGCTCAGATTCAGAGCTCGCCCTTCTCTCC 1693  
Qy 1794 GATCGTAAAGCCATTGGTATTTGCAATATCAGATGAGTCCGACAGACACTTGGCCCTTTC 1853  
Db 1694 GACATTAACAGAGAAAGACAGATCTTACAGCTTCGGGGACCGG-GTGGTTCGGGACCC 1752  
Qy 1854 GACGACTGATGCTCCGTACCCCGATGCTCCGAGAGAAATGGGGCCATATAGTCCGCTG 1913  
Db 1753 GGCCTGAGAAATG-----AGTTGCGAGAGATGAACAGACAGACCGTGAAGAG 1800  
Qy 1914 TACTATGGCAATCTTAGGCTCCCGACATCATGTATACCTGCGATCAGTCCGAAATATCG 1973  
Db 1801 AGCGAGGCGCGGCTGACTCGCTTCTTCAATCCGATCCGCGCCGCGAGCGCCGACGAC 1860  
Qy 1974 TATACCTCAATGCGGATCTACTCGGCGGATGCGCCGTCATGAGCGCTGACGACATGAC 2033  
Db 1861 TACAGTGGCTACAGCGGCTACAGCGAGCGAGCGCTGCGCGCATCTTCCCGACCTG 1920  
Qy 2034 AAGGAGCAAAATTCGCGAACCGGACACAGCAATCATATGAGGGCGCCACCATGGC 2093  
Db 1921 CGGGCGACCGTGAAGCGGACAGCA-----CGGTGACCTGCAACGCG 1962  
Qy 2094 GGCAACCACTGTCTGGAACCAATCAAGACTCGATCGGAGTACGAAATGGCCGTG 2153  
Db 1963 G-----TAGTCTCACTATCGGCGCCGCTCACATGCG 1997  
Qy 2154 GAGTGACGAGAGAGCTGCGAAGATTAACATCAATGACATGCAATCTTTATGAGCCGCTC 2213  
Db 1998 GCGGCTCTGCTGAGTGAATA-----GATTAAGGAGCTACGAGACGCGCA 2046  
Qy 2214 CAGACCAAAAGGTGTGATGATGAAAG---ATGTGATGTCTGATGATGATGATGAA 2270  
Db 2047 ACGACTGGTGAATTAAGAAAGAGAGAGCCCTGATCTCTTTAGTTTATGAGACAA 2106  
Qy 2271 CAGGCGGTGCTGCGACAGTCCGGGACAGCGATGCGGCTGCTCGTTTAACTATTTC 2330  
Db 2107 CTGCGCTCTCAAGAGAGAGACAGAAATCAACAGCAATATGAGCTGTGTCACAAACG 2166  
Qy 2331 ACAGAGACGATGACAGAGATGGGCGGACGTTCAAGACAAGGCACTGGAATGCTTC 2390  
Db 2167 CTAAGTGAAGAGCTGGAGAA-----GTCTCAGAGAAAGTCCACCGTGTGTA 2216  
Qy 2391 AAAGGATCATGTGTGTTGT-GTGTGGAGCTGTGTGGTGTGTGTAATTCAGGA 2449  
Db 2217 TAAAGTTGCGAAACCTTCTCATCTGGAGTGTCAACCCCTACGTGATTAACCTGAAGA 2276  
Qy 2450 GTGGGTATCGCTCATGCTTGCATCCCTGTGAGAGCTCTTCAATCAGCTGTGATGT 2509  
Db 2277 GATGTGAATTAATGCTATGAGACCTTTGTGTAACCTTAGCCATCACTGTGATGT 2336  
Qy 2510 GGTCAACAGATGTTTCATGAGATGATCACACGATATGAACAAGAGATGAAAGCGGT 2569  
Db 2337 TCTGAATACGCTATTTATGAGAGAGACCATCCATGACACAGAGTTGGAACAGT 2396  
Qy 2570 GCTCAAGATGGCACTATTTCTTCAACGCGCACTTTGCCATCGAGGCCACCATGAGCT 2629  
Db 2397 CTGGCCGTAGAAATCTGTGTTCACCGGATCTTCAACGCGGAAATGTTTCTGAACT 2456  
Qy 2630 AATGGCCATGAGCCCAAGTACTATTTTCAGAGAGGCGTGAACATCTTCACTTAT 2689  
Db 2457 CATAGCCATGAGACCCCTACTATTTATTTCCAAAGAGGCTGGAACATTTTGAACGATTTAT 2516  
Qy 2690 CGTGGCCCTATCGCTATTTGAACCTGGAAGCTGAGGGGTCTCAAGGCTGTCTGATTCG 2749  
Db 2517 TGTCTCCCTCAGTTTAAATGAGCTGAGTCTCGCAGATGTGAGAGGGGCTCTCAGTGTCTCG 2576

Qy 2750 TTCCCTTGATTTGCTGCTGATTAATCAAACTGGCCCAAGTCTTGGCCCACTTAATTTACT 2809  
Db 2577 GTCCTTCCGACTGCTCCAGTCTTCAAGCTGGCCCAAGTCCCGCCACCTGGAACATCT 2636  
Qy 2810 CATTTGATTAATGAGAGCAGCAACCATGAGCGCTTGGGTAAATGACATTTGTACTTTGAT 2869  
Db 2637 GATCAAGATCATGGGAAGTCTCGTGGTGGTCCCTGGGCACTGAGCCCTGTGTCCAT 2696  
Qy 2870 TATCATCTTCAATCTTGGGATGAGATGCAACTGTTGGAAGAAATATCATGA-- 2926  
Db 2697 CATGCTCTTCACTTCCCGGTGGGGATGACAGCTGTTTGAAGAGTTCAAGAGAGTGG 2756  
Qy 2927 TCACAGAGACCGCTTCCGATGAGCGACCTGCGCGCTGGAATTCACCGACTTATGCA 2986  
Db 2757 GGTCTGTAAGATCAACAGAGTGCAGAGTCCCGCGTGGACATGAACGACTTCTTCA 2816  
Qy 2987 CAGCTTCATGATCGTGTTCGCGGTCTCTGCGAGAAATGATGAGTCAATGTGGGACTG 3046  
Db 2817 CTCCTTCTCATCTGCTTCCGAGTGTGTGTGGGAGTGGATCGAGACATGTGGACTG 2876  
Qy 3047 CATGTACGTG--GGGATGTCTGTGCATTCCTTCTTGGCCACCGTTTCATCGG 3103  
Db 2877 CATGAGGTGGCCGCGACGACATGTGCTTATTTGCTTCAATGATGTTATGTCATGG 2936  
Qy 3104 CAATCTGTGTACTTAACTTTTCTTACCTTCTTGTTCGCAATTTGGCTCATG 3163  
Db 2937 CAACCTGTGTGTGATTAATCTTCTGCGCTTCTTGTGAGCTCTTCACGCGACAGCA 2996  
Qy 3164 CTATACGCGCGCATCGCCGATTAACGATACAAATTAATAAGCCAGGCTTCAATCGAAT 3223  
Db 2997 CTTGGCCGCGCACAGACAGACGAGGAAATGAACA----- 3032  
Qy 3224 TGCCGATTTAAAGTTGGTTAAGCGTAAATATGCTGATTTTCAAGTTAATGCTAA 3283  
Db 3033 ----- 3032  
Qy 3284 CAAATGCAAAATCAAAATAGTATCAACCATGAGTGAAGAGACCAACGATCAGTTG 3343  
Db 3033 -----CTGCAATCTCAGT 3047  
Qy 3344 GATTGAGCGAAGACATGATGACAAAGAACTGAGCTGGGCGACGACGATCTTGC 3403  
Db 3048 GATCCGATCAAGAGGCGGTGCTGAGCCAAAGTGAAGTGAACCGCTTCAATGACAGC 3107  
Qy 3404 CGACGCGCTCATCAAGAGGAGATCAAGAGCAGACCGCACTGAGGTGCTATCGGGA 3463  
Db 3108 TCATCTTCAAGAGGAGGAGGAGATGAAGTGAACCCCTGACGAGCTGTATGAAGAA 3167  
Qy 3464 TCGATGGAATTCAGATACCGGCGACATGAAAGAAACAAAGCCGAAATTCGAATA 3523  
Db 3168 GGGCAATGATTCGCAACCAACAGGCGGTGATATCCACCGAGAGCGGACTTCAGAA 3227  
Qy 3524 TCTAATTAAGCAACGATGATGGAATGCACTCAATTAACCAACCAATATAGCTGAACA 3583  
Db 3228 GAAAGGAGAGAGACACAGCGGATTCGAGAGAGGTGAAGATCATCATGACGA 3287  
Qy 3584 CGAGCTAAACCATAGAGTGTCTTACAGAGAGACGACACTGCAAGATTAACCTATA 3643  
Db 3288 GAGCACCA-----TGTCTTCAATTAAC-----CBAACCTGACCGTCC 3328  
Qy 3644 TGTAGGCAATTAAGATGACCATTCAGAGAGAGACCAAGGCGAGCGCGAGAGAT 3703  
Db 3329 GGGTGCATATGCTGTGGGCGAGTCT-----TGACTTGAAGAACTTCAACAGAGAGTGT 3383  
Qy 3704 GGAAGGCGAGAGAGAGCGCGACAGAGAGAGATTTAGTCTGACAGAGAACTGGA 3763  
Db 3384 TAGAGAGATCAACCCCTGAAGGCAAGAAATTA-----ATGAGACGATACAGCTC 3437  
Qy 3764 CGAGAGGCGAATGCAAGAGAGGCGCTGACGCTGATATCTTAATGACAGCA 3823  
Db 3438 CTCAGAGAGAAATCAATCAATCAAGCTGAGGTGAAGAGTCCCGTGGAGCAAC 3497

OY	3824	CGAGGATATCTCGATGAAATATCCAGTGAATTCGCGCCGATTCGGTACTATTAAGAAAT	3883
Db	3498	TGAGGAATACTGG-----ATCCGAGCGCTCTTTACAGAGGGTTGGCTCAGCGCGTT	3551
OY	3884	TCCGATCTTACCGGCTGACGATGACTGCGCGTTCTGGCAAGATGGGGCAATTTACACT	3943
Db	3552	CAAGTGTCCAGGTCAACATCGAGGAAGACTAAGCAAGTCCGTGGTGATCTTTGGCGAA	3611
OY	3944	GAAAACTTTCATTAATTTGAAAATAAATATTTTGAACAGCTGTATCACTATGATTTT	4003
Db	3612	AACTGCTCTCTCATGTGTGAGCAATTTGGTTGAACCTTCATCATCTTCATGATTTCT	3671
OY	4004	AATGATAGCTTACTTTGGATCTAGAAGATGTACATCTGCCAAGAACCCATCTGCA	4063
Db	3672	GCTCAGACATGGCGCCCTGGCTTTGAGACATCTCATATTGAGAGAGGAAGCAATCG	3731
OY	4064	GGATATTTTATCTATATATGACAGAAATATTTACGGTTATATCTTTCTTGGAAATGTTAAT	4123
Db	3732	CACCATCTCGAGATACGGGACAAGGCTTCACCTACATCTTCATCTCGAAGATGTTGCT	3791
OY	4124	CAATGTGTGGCGCTCGGCTTCAAAAGTACTTACCAACGCGCGGTGGTGGCTGCATTT	4183
Db	3792	CAAGGACACCTTACCGCTTTCGCAAGTTTTCACCAATGCCGTGGTGGTGTGACTT	3851
OY	4184	CGTATTTGTCAATGATTCGCTTATCAACTTCGTGCTTCACTTGTGGAGCTGTGTAT	4243
Db	3852	CCGATTTGTGCTGTCTTTTATGTCAGGCTTATGTCTAATGCCCTGGGCTATCGGAAT	3911
OY	4244	TCAAGCTTCAAGACTATGCGAAGGTTAAGGCACTGAGACACTAGTGCATGTCGCG	4303
Db	3912	AGGTGCCAATAAGTCCCTTAGAACCCCTTAAGGCTTTGAGACCTTAAGAGCTTATACG	3971
OY	4304	TATGACGGGCAATGAGGGTCTGTTAATGCGCTGTGTCAAGACTATACGCTCATCTTCAA	4363
Db	3972	ATTGGAAGGATGAGCGGTGTGGTGAATGCTTGTGGGCGCCATCCCTTCATCATGA	4031
OY	4364	TGTGCTATTTGGTGTCTAATATTTTGGCTAATTTTGCATATATGGTGTACAGCTTT	4423
Db	4032	TGTGCTGTGTGTGTCTCATCTTCTGCTAATTTGACGACATGGAGTTAACTGTT	4091
OY	4424	TGCTGGAATAATTTTAATGTC---GAGACATGATGGACGAAGCTCAGCCAGAT	4480
Db	4092	TGCGGGGAATACACACTGCTTTAAAGAGCTTGTGAATTCGGGTTCGAAATCGATAT	4151
OY	4481	CATACCAATCGCAATGCCCTGGAG-----AGCGAAGCTACACAGT	4522
Db	4152	TGTCAACAATATAAAGCGACTGTGAAGAGCTCATGAGGGCAACGACGAGATCGATG	4211
OY	4523	GGTGAATTCAGCAATGAAATTCGATCATGTAGTGAACCGATCTGTGCTCTTTCAAGT	4582
Db	4212	GAAAGATGTCAAGATCAACTTTGACAAATGTGAGACAGGGTACCTGGCTCTTTCAAGT	4271
OY	4583	GGCCACCTTCAAAAGCTGATACAATCATGAAAGATCTATCGATTCAGAGAGGTGA	4642
Db	4272	GGCAACTTCAAAAGCTGGATGACATGATGATCGGCTGTGAATCCGAAAGCCAGA	4331
OY	4643	CAGGAAACCAATTCGTGAAGAAGACATCTACATGATTAATTAATTTGATCTTCATCAT	4702
Db	4332	CGAGGACCTGTACATGAGGGCAACATCTACATGTACATCTTCTGTCTCATCTCATCAT	4391
OY	4703	ATTGTGATCTTTTCACTCACTCAATCTGCTCATGTTGTGTTATCATTTGAATTTAATGA	4762
Db	4392	CTTCGGCTCTTCTTCACTCACTCACTGTTCACTGTGTCACTCATCTGCAACTTCACCA	4451
OY	4763	GCAAAAGAAAAAGCAGGTGATCATTTAATAATGTTCAATGACAGAAAGTACGAAAAAGTA	4822
Db	4452	GCAAGAAAAA---GTTTGGAGTTCAGGACATCTTCATGACAGAGGAACGAGAAAGTA	4508
OY	4823	CTATATGCTATGAAAAAAGTGGGCTTAAAAAACCATTTAAAGCCATTCAGAGCAAG	4882
Db	4509	CTACATGTCAATGAAAAAAGTGGGCTTCAAGAAAGCAAGAGCCATCTCCCGACCTT	4568
OY	4883	GTGGCGACCAAGCAATATGCTTTTGAATACTAATCCGATTAAGAAATTCGATATATCAT	4944

Db	4569	GAA	CAAAATCC	AAGG	ATGTCTTTG	ATTTG	GCATCTCA	AAAG	CCCTTG	ACATTTG	ATG	4628
Qy	4943	T	ATTTATTC	ATG	GTCTGA	CAAC	ATGTC	CAAC	AGCC	TCGAT	TCGAT	5002
Db	4629	C	ATGATG	CTCAT	CTGG	CTTAA	CTGTGA	CAATGA	TGG	TGGAGA	CAGAC	4688
Qy	5003	C	ACGT	ATAAC	GCGG	TCT	AGACT	ATCT	CAAT	TGCGA	TATTT	5062
Db	4689	G	CAGAT	TGGAG	AAC	ATCTTT	ACT	AGATTA	T	CGCTT	GTCA	4748
Qy	5063	A	ATC	TAATA	AAAA	ATAT	TGCTT	ACGAT	ATCA	CTATTT	ATG	5122
Db	4749	G	TGT	GTCT	CAAA	ATGTTT	GCTT	GAG	CACTA	CTATTT	CA	4808
Qy	5123	T	GA	TGTA	GTG	ATTC	ATTTAT	TCAT	CTTAG	CTT	AG	5182
Db	4809	T	GACT	TTGT	GTG	ATC	CTCT	CTCA	ATG	TGG	AGAA	4868
Qy	5183	G	TAT	CTG	GTG	CCCG	CA	CCCTG	CCG	AGTGG	GGCG	5242
Db	4869	G	TAT	CTG	GTG	CCCG	CA	CCCTG	CCG	AGTGG	GGCG	4928
Qy	5243	T	CGA	CTG	TGA	AGG	AGCC	AAAGG	CA	TTCG	AG	5302
Db	4929	G	CGT	CTG	ATCA	AGG	GCG	CAAA	GGGAT	CCG	CA	4988
Qy	5303	G	CGG	CCG	CTG	TTAA	CA	CTG	CCG	CGT	CT	5362
Db	4989	G	CGG	CCG	CTG	TTAA	CA	CTG	CCG	CGT	CT	5048
Qy	5363	C	CG	ATG	TG	TTCTT	CA	TGAC	GTGA	AGAA	AG	5422
Db	5049	T	GG	ATG	TC	CA	ACTT	CG	ATAC	GTGA	AG	5108
Qy	5423	C	AA	AC	CTTT	GG	CA	AG	CA	TG	AT	5482
Db	5109	C	GA	AC	CTTT	GG	CA	AG	CA	TG	AT	5168
Qy	5483	T	GT	GT	AT	CTGA	CG	CA	TTAT	TCA	-----	5533
Db	5169	T	GG	CT	GT	GT	CA	TT	CTGA	CG	CA	5228
Qy	5534	C	GA	CA	AA	GG	CT	AT	CC	GG	CA	5593
Db	5229	A	GG	GA	TG	GG	CTT	CA	AA	GG	GA	5288
Qy	5594	A	T	A	CT	CTG	T	T	A	A	G	5653
Db	5289	C	T	A	C	T	A	C	T	A	C	5348
Qy	5654	C	T	A	T	A	G	T	C	A	G	5713
Db	5349	C	T	T	C	A	G	T	C	A	G	5408
Qy	5714	C	T	A	T	A	G	T	C	A	G	5773
Db	5409	C	T	A	T	A	G	T	C	A	G	5468
Qy	5774	G	T	C	C	A	T	T	C	T	G	5833
Db	5469	G	G	C	A	C	T	T	T	C	C	5528
Qy	5834	G	A	T	C	A	T	T	C	C	A	5893
Db	5529	G	C	T	A	T	C	C	A	T	T	5588
Qy	5884	C	G	A	C	C	C	T	T	A	G	5953
Db	5589	T	T	G	C	C	T	T	A	G	C	5648
Qy	5954	G	A	T	T	G	T	A	G	-----	-----	6007

DB 5649 GATGAGAGGCGGTTGTCGATCCATTCCTTCCAAAGTGTCTTACGAGCCTATCAGAC 5708  
QY 6008 AACGCTGGGCTCAGCTGAGAGTACTGCGCCCGGCTAATCCAGACGCTTGGCGAAA 6067  
DB 5709 CACTTGGGGGCGAAGAGGAGGTGTCTGCACTGTCTTCCAGCGCTGCTTACAGGAG 5768  
QY 6068 GCACAAAGCGCGCGCGCG 6084  
DB 5769 ACACCTGGCTAGGCGCGG 5785

RESULT 11  
ABT42021  
ID ABT42021 standard; DNA; 6586 BP.  
XX  
AC ABT42021;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Toxicity modelling related rat gene SEQ ID No 1723.  
XX  
KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
KW database; drug screening; toxicity assay; rat; ds.  
XX  
OS Rattus norvegicus.  
XX  
PN MO200295000-A2.  
XX  
PD 28-NOV-2002.  
XX  
PE 22-MAY-2002; 2002MO-US016173.  
XX  
PR 22-MAY-2001; 2001US-0292335P.  
PR 13-JUN-2001; 2001US-0297523P.  
PR 19-JUN-2001; 2001US-0298925P.  
PR 10-JUL-2001; 2001US-0303807P.  
PR 10-JUL-2001; 2001US-0303808P.  
PR 10-JUL-2001; 2001US-0303810P.  
PR 28-AUG-2001; 2001US-0315047P.  
PR 27-SEP-2001; 2001US-0324928P.  
PR 22-OCT-2001; 2001US-0330462P.  
PR 01-NOV-2001; 2001US-0330867P.  
PR 21-NOV-2001; 2001US-0331805P.  
PR 06-DEC-2001; 2001US-0336144P.  
PR 19-DEC-2001; 2001US-0340873P.  
PR 21-FEB-2002; 2002US-0357842P.  
PR 21-FEB-2002; 2002US-0357843P.  
PR 15-MAR-2002; 2002US-0357844P.  
PR 08-APR-2002; 2002US-0370144P.  
PR 08-APR-2002; 2002US-0370206P.  
PR 08-APR-2002; 2002US-0370247P.  
PR 17-APR-2002; 2002US-0372794P.  
PR 21-APR-2002; 2002US-0371679P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX  
DR WPI; 2003-148464/14.  
XX  
PT Predicting at least one toxic effect of a compound, useful for toxicity  
PT modelling, comprises preparing a gene expression profile of a tissue or  
PT cell sample exposed to the compound, and comparing the gene expression  
PT profile to a database.  
XX  
PS Example 4; Page; 446pp; English.  
XX  
CC The invention relates to a novel method of predicting at least one toxic  
CC effect of a compound. The method comprises a gene expression profile of a  
CC tissue or cell sample exposed to the compound, and comparing the gene  
CC expression profile to a database comprising at least part of the data or  
CC information given in the specification. The methods are useful for

CC predicting at least one toxic effect of a compound, predicting the  
CC progression of a toxic effect of a compound, predicting the renal  
CC toxicity of a compound, or identifying toxicity markers in tissues or  
CC cells exposed to known renal toxin. The genes are useful as toxicity  
CC markers in drug screening and toxicity assays, in monitoring disease or  
CC physiological states, or disease progression. This polynucleotide  
CC represents a rat DNA sequence relating to the toxic effect database  
CC described in the specification. NOTE: the sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the World Intellectual Property  
CC Organization  
SQ  
Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;  
XX  
XX  
Query Match 15.7%; Score 1019.4; DB 10; Length 6586;  
Best Local Similarity 52.8%; Pred. No. 7.3e-245;  
Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;  
QY 186 CGCAAGAAAAAACAAGAAATCCGATATGATGACGAGAGAGAGATGCCAA 245  
DB 268 CTCAAGAAACCAACAAAGCGGATGCGACGCCGAGGAGAGATGAAGACAGAGCC 327  
QY 246 CCGATCCCTACACTTGAACAGGGTGTGCAATACCTGTTGATTGACAGGAGCTTCCG 305  
DB 328 AAGCCAAACAGTGAACCTGAGGCTGGAGAGTTTGCCTTCACTACAGGAGATCCG 387  
QY 306 CCGAATTGGCTTCACCTCTCTCGAGATATGATCCCTAACAAGATGTAAGCA 365  
DB 388 CAAAGCCTGTTGGGTTCCCTCGAGGACTTGAACCTTACTATTGACCAAGAAAC 447  
QY 366 TTGATGTTGATGAGAAAGAAAGATATTTTGGCTTTTGTGATCAAAAGCAATGCG 425  
DB 448 TTGTGATATTAACAGGAGAAACTCTCTCAATTTAGTGGACACCTGCTTAC 507  
QY 426 ATGCTCATTCATTCATTCGATAGTGTGSCCATTTTACCTTATGATCATCATTA 485  
DB 508 ATTTTAAGCCCTTTTAACCTGATGAAGATAGCTATTAATTTGATATACAGTT 567  
QY 486 TTTTCCCTATTCATTCATTCACCAATTTCTGTAACATGATCTGATGATATGCCACA 545  
DB 568 TTGACATGATCATCATGATGATCATCTGACCACTGTGTGTTCAATGATAGTATAC 627  
QY 546 AAGCCCAAGGTTGATGATCAGAGGTG---ATATTCACCGGAATCTTACATTTGAATCA 602  
DB 628 CTTCAGAAATGCTCAAGAAATGTAAGTACATTCACAGGATTTTACATTTGAATCA 687  
QY 603 GCTGTTAAGATGATGACAGAGTTTCAATTTATGCGCGTTTATGATGATGATGCA 662  
DB 688 CTAGTGAATATCATCGAAGAGTTTCTGCTATGACGCTTACCTTCTGCGAGACCG 747  
QY 663 TGAATTGGCTGACCTTGTATGATATAGCTTTAGCTTATGATGATGATGATGATTA 722  
DB 748 TGAATCTGTTAGACTTCAGTGTATCATATGATGATGATGATGATGATGATGATGAT 807  
QY 723 GGTATATCTAGAGAGCTTGCAGAGCTTTAGAGTGTGAGAGGCTTAAACCGTAGCAT 782  
DB 808 GGCATATCTTCAAGCTGAGAGCAATTCAGAGTTTCTCGAGCTTGAAGAAATATCTGTA 867  
QY 783 GTGCCAGGCTTGAAGACATGATGTCGAGCGCTCATGCAATGCTGAAGAAATCTGCGAT 842  
DB 868 ATTCAGGCTTGAAGACATGATGTCGAGCGCTTATTCAGTCTGAGAAAGCTTTCGAC 927  
QY 843 GTGATTAATCTGACCATGTTCTCCCTGTGCTGTGCTGATGAGGCTTACAGATCTAT 902  
DB 928 GTGATATCTGACAGTGTCTGCTGAGTGTTCGCCCTGATGAGCTGACACTCTTC 987  
QY 903 ATGGCGCTGCTACCCGAGAGTGAAT-----CAAGAGTTCCCGCTGAGAGGTTCC 953  
DB 988 ATGGGAACCTTCAAGAAACAGTGTGTGTGTGCGCCATTAACAGAGAGTACCTG 1047  
QY 954 TGAGGCAATCTGACGAGAGAACTGAGACTATCATCATGATGATGATGAT 1013  
DB 1048 GAGAACGCAACAGAGCTTTGACTGGAGAGAAATATCAACATTAACAACTTTAC 1107

1014 TCCGAGAGAGAGGAGCTCATTTCCGTTATGCGGCAATATATCCGGTCGCGGAGCATGC 1073  
Db 1108 ATGGTTCCTGAGATGCTAGAACCCCTTGCTCTGCGGAGAACAGTTCTGATCTCGGAGATGC 1167  
Qy 1074 GACGACGATTACGTGTGCTGACAGGGGTTGTGTCGAAATCCGAATTATGCTACACAGC 1133  
Db 1168 CCGAGGAGATTCCAGTGCATGAAAG---CAGGAAGAACCCCACTACGATTACACACAGC 1224  
Qy 1134 TTGGATTGCTTCGAGATGGGCTTCCGTGCGCCTTCCGGTGATGACACAGGACTTCTGG 1193  
Db 1225 TTGGACCTTCAGCTGCGCTTCTTGGAATATTCGCTTATGACCAAGACATATGG 1284  
Qy 1194 GAGGATCTGACAGCTGTGTGTCGCGCGCCGACCATAGGACATGCTGTTCTTTATTA 1253  
Db 1285 GAGAACCTTATACAGCTGACCTTACAGCGCGCTGGGAAAAGTACATGATCTTCTGTTC 1344  
Qy 1254 GTCATCATCTTCTAGGTTCAATTCATCTTGTGAAATTTGTTGGCCATTTGTCATG 1313  
Db 1345 TTGGTCATCTTCGTGGGTTCTTCTATCTGTGAACTTGATCTTGGCTGTGTGGCCATG 1404  
Qy 1314 TCCGATGACGATTGCAAGAGAGCGGAGAAAGAAAGAGAGCTGCCGAAAGAGAGGATTA 1373  
Db 1405 GCTTATAGAAA---CAGAACAGGCAACACTGAGAGAGGCAAGCAAAAGAGGC---- 1457  
Qy 1374 CGTGAAGCGAAGAGAGCTGCGCGCCGCAAGCGGCAAGCTGAGAGAGCGGCAATGCG 1433  
Db 1458 CGAGTTCAAGGCAATGCTGGAGCAACTCAAG---AAGCAGCAGGAGAGGACAGGGCT 1512  
Qy 1434 CAGGCTCAGGACAGAGGAGATGCGGCTGCGCGCCGAAAGAGCTGACCTGCACTCGGAAATG 1493  
Db 1513 GCTGCAATGGCCACTCAGCGGAGCACTGTCTCGAACA---CGCATTTGAAGAAAGGG 1569  
Qy 1494 GCCAAGAGTCCGAGGTATTTCTTCATCAGCTATAGCTATTTTGGCGCGAGAAAGGC 1553  
Db 1570 GAAATGGGATGAGGCTCTCGAGAGAGCTCTTGAACGTCTTAACTCAAGTCCAAAGAGC 1629  
Qy 1554 AACGATGCAACAAAGAGAGATGCTTCTGAGAGCTGAGAGGTGAGTGGAGTGC 1613  
Db 1630 GCGAAGGAGCGGCGGAA-----CCGACGGAAGAGAGAGGAGAGGAA 1673  
Qy 1614 GTGAGCGTTATCAAAAGCAACAGACCTTACACAGACACCAAGCTAACAAAGTTGCT 1673  
Db 1674 GCTCTCGAAGGCGAGAGAGAGGAGACCGGAGAAAGGTGTTAA-----GT 1720  
Qy 1674 AAGGTGAGCAGACATCTTATCTTACCTGTTTACCGTTTACATACGAGGGATCA 1733  
Db 1721 CAGAGTCGAGAGCGGTATGAGAGAGAGGCTTCCGGCTGCCAGACAAACAGATAGGGA 1780  
Qy 1734 GGTAGTTCTCAAGATACAGATACGAAACGGAAGCTGCGCTTGTGATACCGGATAGC 1793  
Db 1781 GGAAGTTTTCATCATGATGATGATGCTGCTCAGCATTCAGGCTCGCCCTTCTCTCC 1840  
Qy 1794 GATGTAGGCAATGGTATGTTGTCACATATCAGATGCGCAGACACTTTCCTATGCC 1853  
Db 1841 GACATTAACAGAAAGCAGCATTTCACTTCGCGGAGCCG-GTGCGTTCGCGGAGCCCG 1899  
Qy 1854 GACGATCGAATGCGGTACCCCGATGTCCGAGAGATGAGGAGGAGGAGGAGGAG 1913  
Db 1900 GGGCTCGAAGATG-----AGTTCCAGAGATGAACACAGACCGTGGAGAG 1947  
Qy 1914 TACTATGGCAATCTAGGCTCCCGACATCATGATTACTTCCGATCAAGTCCGGAATG 1973  
Db 1948 ACGGAGGCGCGGAGCTGCTGCTTTCATCCGATTCGCGCGCGGAGCGCGGAGAGC 2007  
Qy 1974 TATACCTCAATGGGATCTACTCGCGGCAATGCGGCTCATAGGCGTACGACATAGCC 2033  
Db 2008 TACAGTGGCTACAGCGGCTACAGCAGTGCAGCGCTGTGCGGATCTTCCCGAGCTG 2067  
Qy 2034 AAGGAGAGCAATTTGCGCAACGCGCAACAGCAATCAATCAGTGGGCGCAACCATGGC 2093  
Db 2068 CGGCGCAGGCTGAGACGCGCAACAGCA-----CGTGGACTGCAACGCGC 2109

2094 GCGACACACTGTCTGACACCAATCAAGCTGATCATCGGCAATGCAAAATTGGCTG 2153  
Db 2110 G-----TAGTGTCACTATGCGGCGCGGCTCACACATCGG 2144  
Qy 2154 GAGTGCAGGACGAAAGCTGGCAAGTTAAACATCATGACATCTTTTATGAGCCGCTC 2213  
Db 2145 GCGGCTCTGCTGAGAGTGAATAA-----GATAGGCAAGCTACGAGACGCGCA 2193  
Qy 2214 CAGACACAAAGGTGGTGTGATATGAAG---ATGTGATGTCTCGAATGACATCATGGA 2270  
Db 2194 ACGACTGAGTGAATTAAGAAAGAAAGCCCTGATCTCTTTAGTTTCTATGAGCCAA 2253  
Qy 2271 CAGGCGGCTGGTCCGACAGCTCGGCAAGCATGCGGCTGTCTCGTTACTATTTCCCA 2330  
Db 2254 CTGCGCTCTTACGACGAGAGAGCAAGATCAACAGCAATTAAGAGGTGTCAACAAACG 2313  
Qy 2331 ACAGAGGACGATGACGAGATGGCGGACGTTCAAAAGCAAGCACTGAAATGATCTC 2390  
Db 2314 CTAGTGAAGAGCTGGAAGA-----GCTTCAGAAAGTGCACCGGTGTGTA 2363  
Qy 2391 AAGGCAATGATGTGTTTGT-GTGTGGACCTGTGCTGGGTTGGTGAATTTCAAGA 2449  
Db 2364 TAAGTTTGCACAACCTTTCATCTCATCTGGAAGTGAACCTTACTGATTAACAGAGA 2423  
Qy 2450 GTGGGATGCGTCATGCTCTTCATCTCCTTGTGAGCTTTCATCAGCTGTGATGT 2509  
Db 2424 GATCTGAACCTTAATCTCATGATGACCTTTTGTATACCTTAGCAATCACATCTGATCT 2483  
Qy 2510 GGTCAACAGATGTTCTATGGAATGATATCAACGATATGAACAAAGAGATGGAACGGT 2569  
Db 2484 TCTGAATACGTAATTAATGCAATGAGACATCCATGACACCAAGTTGGAACAGCT 2543  
Qy 2570 GCTCAAGAGTGGCACTAATTTCTCACCGGCACTTTGCGCATCGAGGCAACCATAGGT 2629  
Db 2544 CTGGCGCTGAGAAATCTGTGTTTCAACGGGATCTTCAAGCGGAAATGTTCTGAGCT 2603  
Qy 2630 AATGGCCATGAGCCCACTACTATTTCCAGAGGCTGGAACATCTTGCATCTTATAT 2689  
Db 2604 CATAGCATGAGCCCTTACTATTTCCAAAGAGCTGGAACATTTTGAAGGATTAAT 2663  
Qy 2690 CGTGGCCCTATGCTATTTGGAATCTGGACTGAGAGGTCCAGGGTGTGCTGTAATGG 2749  
Db 2664 TGTCTCCCTCAGTTTAATGAGCTGAGTCTGAGAGTGGAGGAGGCTCTCAGTGTGCG 2723  
Qy 2750 TTGCTTGCATGCTGCTGATTAATCAACTGGCCAAAGCTTGGCCCACTTAATTACT 2809  
Db 2724 GTCTTTCGAGTCTCCAGTCTTCAAGCTGGAAGTCTGAGCCCACTCGAACAATGCT 2783  
Qy 2810 CATTCGATTAATGAGACGACCAATGGGCGCTTGGTAACTTGAACATTTGACTTTGAT 2869  
Db 2784 GATCAAGATCATCGGAACTCCGTGGGTCCCTGGGCAACTGACCCTGTGCTGGCAT 2843  
Qy 2870 TATCATCTTCAATTTGCGGTATGGAATGCAAGCTTCCGAAAGATTTATCATGA--- 2926  
Db 2844 CATGCTTCATATTTGCGGTGAGAGTGAAGCTGTTTGAAGAGTTTACAGAGAG 2903  
Qy 2927 TCAAGAGACCGCTTTCGAGATGCGACCTGCGCGCTGGAACCTTACCGACTTATGCA 2986  
Db 2904 CGTCTGTAAGATCAACAGAGAGTGAAGTCCGCGCTGACATGAAAGACTTCTTCCA 2963  
Qy 2987 CAGCTTCATGATGTGTTCCGGGTGCTCTGCGAGAAATGATGATTCATGAGGAGACTG 3046  
Db 2964 CTCCTTCCTCATGTCTTCCAGTGTGCTGTGGAGAGTGAATGAGACATGAGGAGACTG 3023  
Qy 3047 CATGTAAGT---GGGAGTGTGAGCAATCTCTTCTTGGCCACGTTGTGATCGG 3103  
Db 3024 CATGAGAGTCCGCGGACAGGCAATGCTCATATGCTTCTTATGATGATTAATGCTATGG 3083  
Qy 3104 CAATCTTGTGTATTAACCTTTTCTTGAAGCTTGTGCTTGTCAATTTGGCTCATCTAG 3163  
Db 3084 CAACCTGTGTGTGATATTAATCTCGGCTTGTGAGCTCTTCAAGCCAGACAGCA 3143  
Qy 3164 CTATATCAGCCGACATGCGGATACGATACGATTAATTAATGAGGAGGCTTCAATGAAAT 3223

DB 3144 CTGCGCGCCACAGACGACGCGGGAAATGACAA----- 3179  
QY 3224 TGGCCGATTTAAAGTTGGTTAAGCGTAATATGCTGATTTTCAAGTAATATACGTAA 3283  
DB 3180 ----- 3179  
QY 3284 CAATTTGCAAAATCAATTAAGTATCAACCATCAGGTGAGAGACCAACAGATCAGTTG 3343  
DB 3180 -----CTGCAAGATCTCAGT 3194  
QY 3344 GATTTGGAGCGAAGAGCATGTGTGACAAACAACTGAGCTGGGCCACGACGAGATCTCGC 3403  
DB 3195 GATCCGAGATCAAGAGGCGGTGGCTTGACCAAAAGTGAAGTGCACGCTTCATCATCAGGC 3254  
QY 3404 CGAGCGCTCATCAAGAGGGGATCAGAGACGACACTGAGGTGGCCATCGGGA 3463  
DB 3355 TCACCTTCAAGCAGCGGGAGCGGATGAAGTGAACCCCTCGACGAGCTGTATGAGAA 3314  
QY 3464 TCGGATGGAATTCACGATTAACGGGACATGAGAAACAAACCGGAAAGAAATCCAAATA 3523  
DB 3315 GGCCTACTGCATTCGCAACCAACGCGGCGTGAATATCAACGGAAACGGCCTTCAGAA 3374  
QY 3524 TCTAAATTAACGACGATGATTGGCACTCAATTAACCAACGACAAATAGACTGGAACA 3583  
DB 3375 GAAGGGGAACGGAAACCAACGCGCATCGCAGCAGCTGGAAGTATCATATGACGA 3434  
QY 3584 CGAGCTAAACATAGAGGTTTGTCTTACAGACGACACACTGCCAGCATTAATCTATA 3643  
DB 3435 GGACACACA-----TGTCTTCAATTAACAC-----CCAAACCTGACCGTCC 3475  
QY 3644 TGTGACCATTAAGATGACCATTCACAGACGAGACCAAGGCGACGCGGACGAT 3703  
DB 3476 GGGTGCCTATGCTGTGGGCAAGTC-----TGACTTGAAGACCTCAACACAGAGATGT 3530  
QY 3704 GAGGGGCGAGGAGAGACGCGACGCGCAAGAGAGATTAGTCTCGACGAGAACTGGA 3763  
DB 3531 TAGACGCAATACAGACCTGTAAGGACGAAAGATTA-----ACTGACGATACCAAGTC 3584  
QY 3764 CGAGAGGGCGAATGCGAGAGGGCGCTGACGCGTATCATTAATTCATGACACGA 3823  
DB 3585 CTCGAAAGGAATGACATGACATCAAGCTGAGGTGAAAGATTTCCGTGAGCAACC 3644  
QY 3824 CGAGGATTAATTCGATGAATATCCAGCTGATTTGCTGCCCCCATTCGTATTAAGAAAT 3883  
DB 3645 TGAGAAATACTTGG-----ATCGGACGCTGCTTTACAGAGGTTGCGTCCAGCGGT 3698  
QY 3884 TCCGATCTAGCCGCTGACGATGACTCGCGCTTCTGGCAAGATGGGCAATTTACGACT 3943  
DB 3699 CAAATGCTGCAAGTCAACATCGAGAGAGACTAGGCAAGTGTGTGATCTTGGCGAA 3758  
QY 3944 GAAAACTTTCAATTAATTAATAATTAATTTGAAACAGCTGTTACTATGATTTT 4003  
DB 3759 AACCTGCTCTCAATGTGAGCAAAATGTTGAGACTTTCATCATCTTCATGATTTCT 3818  
QY 4004 AATGATGACTTACTTGTGATTAAGAAATGATACATGTGCCAACAAGAACCATATGCA 4063  
DB 3819 GCTAGAGAGTGGCGCCCTGGCTTTGAGACATCTACATGAGACAGAAAGACATCCG 3878  
QY 4064 GGAATTTTATCTATATGACAGAAATTTTACGTTTATTTCTTTGAAATGTTAT 4123  
DB 3879 CACATCTCGAAGTATGAGCAAGTCTTCACTACATCTTCACTCGAGATGTTGCT 3938  
QY 4124 CAAATGTTGGCGCTCGGCTTCAAAAGTATCTTCAACAAACGCGTGTGTTGCTGATTT 4183  
DB 3939 CAAATGAGACCGCTACGCTTGTCAAGTTCTTCAACCAATGCTGTGTGTTGACTT 3998  
QY 4184 CGTATTTGATGATGATTCGCTTATCAACTTGTGTTCACTTGTGGAAGCTGTGTGAT 4243  
DB 3999 CCTATTTGTGCTGTCTTTTATGACGCTTATAGCTAATGCTCCGTGGGCTACCTCGAACT 4058  
QY 4244 TCAAGCTTCAAGACTATGCAAGCTTAAAGACATGAGACCACTACGTCGATGTCGG 4303

DB 4059 AGTGTCCATTAAGTCCCTTAGACCCCTTAAGACTTTGAGACCCCTTAAGACCTTATACG 4118  
QY 4304 TATGACGGGCAATGAGGCTGTGTTAATGCGCTGTGACAACTATACCTGCATCTTCAA 4363  
DB 4119 ATTTGAAGGATGAGGGGTGTGTGAATGCTGTGTGGGCCCATCCCTCATCATGAA 4178  
QY 4364 TGTGCTATTTGCTGTCTAATATTTTGGCTAATTTTCCCTAATTTGCTGTAAGCTTTT 4423  
DB 4179 TGTGCTGTGTGTCTCATCTTCTGTGATTTTTCAGCATTCATGGAAGTTAACCTGTT 4228  
QY 4424 TGTGGAATAATTTTAAAGTGC-----GAGACATGAATGCGAGAGCTCAGCCACGAGAT 4480  
DB 4239 TGGCGGGAATTAACACTACTCTTTAATGACACTTGAATTCGGTTTGAATTCGATAT 4298  
QY 4481 CATACCAATGCAATGCTGTGAG-----AGCGAACTACAGCTG 4522  
DB 4299 TGTCAACAATTAACGACTGTGAGAGCTCAGAGGCAACGACGAGATCCGATG 4358  
QY 4523 GGTGAATTCAGCANTGAATTTGATCATGTAGGTAAGCGGATCTGTGCTTTTCCAAAT 4582  
DB 4359 GAAATGTCAGATCAACTTTGAACATGTGAGACAGGTAACCTGCTTCTTCAAGT 4418  
QY 4583 GGCACCTTCAAGGCTGATATCAAAATCATGAAGTCTATGATTCAGACAGAGTGA 4642  
DB 4419 GCGAATCTTCAAGGCTGATGACATCATATGCGCTTATAGATTCGGAAGCCAGA 4478  
QY 4643 CAAGCAACCAATTCGTGAACGAACATCTACATATTAATTTGTAATTTCTTCATCAT 4702  
DB 4479 CGAGCAGCTGACATCAAGAGGCAACATCATATGATACATCACTTCGTCATCTCATAT 4538  
QY 4703 ATTTGATCCCTTTTCACTCATATGTTGATGTTGTTATGTAATTTTAAATGA 4762  
DB 4539 CTGCGCTCTTCTTCACTTCACTTCACTGTTATGTTGTTATGTAATTTTAAATGA 4598  
QY 4763 GCAAAAGAAAAACAGGTGATCATTAAGAAATTTATGACAGAGTCAAGAAAAATGA 4822  
DB 4599 GCAAGAAAAA-----GTTTGAAGTCAAGACATCTTATGACAGAGAAAGAAATGA 4655  
QY 4823 CTATATGCTATGAAAAAGATGAGCTTAAAAAACAATTAAGCCATTTCAAGACCAAG 4882  
DB 4656 CTACAAATGCAATGAAAAAGCTGAGCTCAAGAAACCAAGAACCCATCCCGACCTT 4715  
QY 4883 GTGGGACCAACAAACATATGCTTTGAAATGTAACGATTAAGAAATTCGATATATCAT 4942  
DB 4716 GAACAAATTCAGAGGATGTCTTTGATTTGTAATCTCAACAGACCTTTGACATTTGAT 4775  
QY 4943 TATGTAATTCATGCTGAACATGTTCAACCATGACCTCGATGTTACGATGCTCGGA 5002  
DB 4776 CATATGCTCATCTGCTTAAACATGTGACATATGATGTGAGACAGACACTCAGAGAA 4835  
QY 5003 CAGGTATACGCGGTCTTAACATATCTCAATGCAATGCGAATTTGATTTTCACTTCGA 5062  
DB 4836 GCAATGAGAAACATTTCTTAATGATTAATCTGCTCTTTGTCATCTTCACTCGCA 4895  
QY 5063 ATGTCTATTAATAATTTGCTTTAGATATCACTATTTTAATGAGCAATGAAATTAAT 5122  
DB 4896 GTGTGTCTCAAAATGTTGCTTGAAGACATCTATTTTCACTTAATGAGTGAACATCTT 4955  
QY 5123 TGATGATGATGTTGCTCAATTTTATCCATCTTAAGTCTTGTACTTAAGCATAATTAAGGAA 5182  
DB 4956 TGACTTTGTGTGTATCTCTTCACTTTGTGGAATGTTCTGTGCTATATTAATGAGAA 5015  
QY 5183 GTACTTGTGTGCGGACCTGCTCGAGTGTGTGCTGTGTGCGAAAGTGTGGCGTGTCT 5242  
DB 5016 GTACTTGTGTGCGGACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 5075  
QY 5243 TCGAGTGTGAAGGAGCCAAAGGCAATTCGGAACATGCTCTGCGGTTGCGCATGTGCT 5302  
DB 5076 GCGTCTATCAAGGCGCCAAAGGATCCGACCTGCTCTTTGCTTAAATGATGTGCT 5135  
QY 5303 GCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362  
DB 5136 GCGGCGCTGTTCAACATGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195

QY 5363 CGGATGTCGTTCTGATGACGTGAAGAGAGAGGCGCATTAACGAGTCTACACTT 5422  
 DB 5196 TGGCATGTCGATCTGATGAGTGAAGACGAGGCGGCGATTTGACATGTTCACTT 5255  
 QY 5423 CAAGACCTTTGGCCAGAGATGATCTGCTCTTTTCAGATGTCAGCGTTCAGGTTGGGA 5482  
 DB 5256 CGAGCATTTGGCAAGCATGATCTGTTGTTCCAGATCAACAAGTCTGCTGGCGGGA 5315  
 QY 5483 TGGTGTACTGAGACCCATTATCA-----TGAGAAAGCATGGGATCCACCGCAGAG 5533  
 DB 5316 TGGCTGCTGCTGCTCAATCTGAAACGCGCCCTGAGCTGAGCAAGAGACCC 5375  
 QY 5534 CGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTCGAAATACGTTTCTCTTC 5593  
 DB 5376 AGGAGAGGCTTCGAAAGGGAAGTGGGAACCCCTGGTGGGATCTTCTTTGTGAG 5435  
 QY 5594 ATACCTAGTTAAAGCTTTTGTAGTATTAATGATGATGCTGCTCTTCTTCAGAA 5653  
 DB 5436 CTACATCATCATCTCTCTCTGATGTGTGAACATGTATCATGCGCATCTCTGAGAA 5495  
 QY 5554 CTATATGACAGCCAGACGAGACGTCGAAGAGGGGTCTAACCGACGACGATACGATGTA 5713  
 DB 5496 CTTCAGGTTGACCAAGAGAGAGCGCCGACCTCTGATGAGATGATCTTCAGACTT 5555  
 QY 5714 CTATGAGATCTGAGAGCAATTCGATCCGAGGGGACCCAGTACATACGTTATGATGCT 5773  
 DB 5556 CTATGAGATCTGAGAGAGAGTTTGAACCCAGACCGCATTCATGATGATGTAAGCT 5615  
 QY 5774 GTCCGAATTCCTGAGAGTACTGAGGCGCCGCTGCAATCCAAACCGAAAGTACAA 5833  
 DB 5616 GGCAGAGCTTTGCGACCGCCCTGAGACCGGCTCGAGTACCCAAAGCCCAACCATCA 5675  
 QY 5834 GATCATATTCATGAGACATACCATCTGTGCGGAGTACCTGATGATGCTGCAATCT 5893  
 DB 5676 GCTATGCGCATGATGATCTGCGCATGATGAGAGAGATGATGATGATGATGATGAT 5735  
 QY 5894 CGAGCGCTTTTACGAAGAAGCTTTCTTGGCGGAGAGGCAATCCGATGAGAGAGGCTGA 5953  
 DB 5736 TTTGCGCTTACCAAGAGAGTCTGAGAGACAGTGGGAGTTGACATCTCTGCGGAGCA 5795  
 QY 5954 GATTGTGTAG-----ATAGCGGCGCGCGCGGATACGAGGAGGCTACAGCGCTCTCATC 6007  
 DB 5796 GATGAGAGAGCGGTTCTGAGCATCAATCTTCCAAAGTGTCTTACGAGCTTATCAGAAC 5855  
 QY 6008 AACCGTGTGAGTACGCTGAGAGTACTGCGCCGCGCTAATCCAGACGCTTGGCGAAA 6067  
 DB 5856 CACTCTGCGGCGCAAGCAGAGAGAGTGTCTGAGTGTCTGAGAGCGGCTTACAGGCGG 5915  
 QY 6068 GCACAGAGCGCGCGCGG 6084  
 DB 5916 ACACCTTGGCTAGGCGGG 5932  
 RESULT 12  
 ADS16302  
 ID ADS16302 standard; DNA; 6586 BP.  
 AC ADS16302;  
 XX  
 DT 02-DEC-2004 (first entry)  
 DE Rat voltage-gated type 8 alpha protein (Scn8a) sodium channel DNA.  
 XX  
 KW Voltage-dependent ion channel; drug candidate; aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;  
 KW anticonvulsant; antiarrhythmic; rat; type 8 alpha protein; ds.  
 OS Rattus norvegicus.  
 XX  
 PN US2004175761-A1.  
 XX  
 PD 09-SEP-2004.

XX PF 01-MAR-2003; 2003US-00377139.  
 XX PR 01-MAR-2003; 2003US-00377139.  
 XX PA (MACK/) MACKINNON R.  
 XX PA (MACK/) MACKINNON A L.  
 XX PA (JIAN/) JIANG Y.  
 XX PA (RUTA/) RUTA V.  
 XX PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
 XX DR WPI: 2004-642122/62.  
 XX REFSEQ; NM\_019266.  
 PT Screening drug candidates that target voltage dependent ion channel  
 PT protein, involves contacting screening protein with chemical compound,  
 PT which is drug candidate and determining whether chemical compound binds  
 PT to screening protein.  
 XX  
 PS Disclosure; SEQ ID NO 14; 61bp; English.  
 CC The invention relates to the composition of matter suitable for use in  
 CC identifying chemical compounds that bind to voltage-dependent ion channel  
 CC proteins. The composition comprises a screening protein that consists of  
 CC an ion channel voltage sensor domain of the ion channel protein  
 CC immobilised on a solid support. The invention is useful for identifying  
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
 CC channel proteins. The drug candidate of the invention is utilised for  
 CC treating a condition mediated by aberrant electrical activity that  
 CC initiates uptake or release of neurotransmitters and contraction of  
 CC muscles. The drug candidate of the invention is also utilised for  
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-gated  
 CC sodium channel DNA.  
 CC  
 SQ Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;  
 Query Match 15.7%; Score 1019.4; DB 13; Length 6586;  
 Best Local Similarity 52.8%; Pred. No. 7.3e-245;  
 Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;  
 QY 186 CCGAAGAAAAACAAAGAAATTCGATATGATGACGAGACGAGATGAAGTCCACAA 245  
 DB 268 CTCAGAAAACCAACCAAGCGAGTGGACACCCGAGAGAGATGAACAGCAAGCC 327  
 QY 246 CCGATCTCACTTAACGAGGAGTGGCCATTAATCTGTTGATGAGGAGGAGCTTCCG 305  
 DB 328 AACCAAAAGTACGCTGAGAGCTGGAGAGTTGCTTATCATCAAGGAGCATCCG 387  
 QY 306 CCGAAATGGCTCCACTCTCTCGAGATATGATTCCTTACACGAAATGATGACA 365  
 DB 388 CAAAGCGCTGGTTCGGTCCCTGAGAGACTTGAACCTTATATTTGACGCAAAAAC 447  
 QY 366 TTGATGTTAGCAAGAGAAAGATTTTGGCTTTTCGATCAAAAGCATGTGG 425  
 DB 448 TTTGATATTAACAGAGGAAACCTCTTGAATTAATGATGACACCTGCTGTAC 507  
 QY 426 ATGCTGATCCATTCATCCGATACGTGTCGAGCAATTAATCTGATGATCAATTA 485  
 DB 508 ATTTAAGCCCTTTTAACGATTAAGAAATGATTAATTTGATATCACTAGTT 567  
 QY 486 TTTTCCCTATTCATATCAACAATTTCTGATGATCTCTGATGATTAATGCGACA 545  
 DB 568 TTCAGATGATCATCATGTCACACATCTGACCAACGTTGTGATGACCTTATGATAC 627  
 QY 546 AGCGCCAGGTTAGTCCAGTGAAGTGG--ATATTCACCGAATCTACATTTGATCA 602  
 DB 628 CTTCAAGATGTTCCAAAGATGAGATACATTCACAGGATTTACATTTGATCA 687  
 QY 603 GCTGTAAAGTATGAGCAGAGGTTTCAATTTATGCCGCTTTACGATCTTAAGATGCA 662  
 DB 688 CTATGAAAATCATGCAAGAGGTTTCTGATGAGAGGCTTCAACCTTCTGCAAGACCG 747

Qy 663 TGAATGCTGACCTGCTGATATAGCTTATGATGACCATGGATATGATTA 722  
Db 748 TGAATGCTGACCTGCTGATATAGCTTATGATGACCATGGATATGATTA 807  
Qy 723 GGTATCTAGACGCTGCGAAGCTTTAGGGTCTGCGAGCGCTTAAACGTAGCCATT 782  
Db 808 GGCATGCTCAGCGCTGAGAACATTCAGGGTCTTCCGAGCTTTGAAAATCATCTCTGTA 867  
Qy 783 GTGCGAGCTTGAAGACCATGTGGGCGCGCTCATCCAAATCGGTGAAGAACTGCGGAT 842  
Db 868 ATTCAGAGCCCTGAAGAACATGTGGGCGCGCTTAAATCCAGTCCGGAAGAACCTGTGGAC 927  
Qy 843 GTATATCTGACCATGCTCTCCCTGTGGGCTTGGGCTGATGGGCTTACAGATCAT 902  
Db 928 GTATGATCTGACCATGCTCTCCCTGTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTTC 987  
Qy 903 ATGGGCGCTGCTCAGCGAAGTGCAT-----CAGAAAGTTCCCGCTGACGCTTCC 953  
Db 988 ATGGGGAACCTTCGAAACAGTGTGTGTGGCCCATTAACCTTCAAGAGAGCTACCTG 1047  
Qy 954 TGGGCGCATCTGACCGAGACATCTGGGACATATCAATCGCATAGCTTCCATTGGTAT 1013  
Db 1048 GAGAACGCGACCAAGGCTTTGACTGGAGGAAATATCAACATTAACAACTTTTAC 1107  
Qy 1014 TCCGAGGACGAGGCTATCTATTCCTTATGCGGCAATATATCGGCTGCGGCGCAATGC 1073  
Db 1108 ATGCTTCTGCGACATGCTAAGAACCTTGTCTTGGCGGAAACATTTGATGCTGGGCAATGC 1167  
Qy 1074 GACGACGATTAAGTGTGCTGCGAGGGGTTTGTCCGAATCCGAATTAATGCTTACACGAC 1133  
Db 1168 CAGAGGGAATTCAGTGCATGAAAG---CAGAAAGAACCCCACTACGCTTACACGAC 1224  
Qy 1134 TTGCAATCTGCGAGATGGGCTTCTGTCCGCTTCCGGCTGATGACACAGACTTCTG 1193  
Db 1225 TTGTACACCTTACCTGCGGCTTCTTGTGCAATATTCGCTTATGACCCAGACTTATTTG 1284  
Qy 1194 GAGGATCTGACGAGCTGTGTGCGCGCGCGGACCATGACATGCTTCTTATA 1253  
Db 1285 GAGAACCTTATACGAGCTGACCTTACGAGCCCTGGGAAACGTCATGATCTTCTTGTTC 1344  
Qy 1254 GTCACTATCTTCTAGGCTTCTATCTTGTGATTTGATTTTGGCATTTGTCATG 1313  
Db 1345 TTGCTCATCTTCTGCGGCTTCTTCTATCTGTGAACTTGTGCTGTGTGGCCATG 1404  
Qy 1314 TCGTATGACGATTCGAAAGAGCGCGAAGAAAGAGGCTGCCGAAGAGAGCGGATA 1373  
Db 1405 GCTTATGAGAA---CAGAACAGGCAACCTGAGAGGCGAGAGCAAAAGAGGC--- 1457  
Qy 1374 CGTGAACGGAAGAGCTGCCCGCCCAAGCGCCCAAGCTGAGAGCGCGCCCAATGCG 1433  
Db 1458 CGAATTCAGAGCAATGCTGAGCAATCCAG---AAGCAGCAGAGAGAGGCAAGGCT 1512  
Qy 1434 CAGGCTCAGGACGAGCGGATGCGGCTGCGCGCAAGAGGCTGACCTCCGAAATG 1493  
Db 1513 GCTGCAATGCGCACTGAGCGGCACTGTCTCGAAG---CGCATTTGAAGAGAGG 1569  
Qy 1494 GCCAAGAGTCCGACGATTTCTTCACTAGCTATAGCTATTTGTTGGCGCGAAGAGGC 1553  
Db 1570 GAGGATGGGATAGCTCTCCAGAGAGCTTCTTCACTAGCTATTTCCAAAGAGC 1629  
Qy 1554 AAGCATACAAACAAAGAGAGATGTCATTCGAGCGCTGAGGCTGAGGATCGGAGTGC 1613  
Db 1630 GCGAAGAGCGCGGAA-----CCGACGGAAGAGAGAGAGAGAGAGAG 1673  
Qy 1614 GTGACGCTTATACAAAGCAACAGCACTTACCAAGCAACAGCTACCAAGATTCTG 1673  
Db 1674 GCTCTGAGAGGCGAG 1720  
Qy 1674 AAGATGAGCAGCATCTTATCTTACCTGCTTACCGTTTAAACATACGAGAGGATCA 1733  
Db 1721 CAGAGTGGAGAGAGGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780  
Qy 1734 CGTAGTCTCAAGTACAGATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793

Db 1781 GGAAGTTTTCATCATGATATCACTGCTGCTCAGCATTCAGAGCTGCGCTTCTCTCC 1840  
Qy 1794 GATCTAAGCCATTGTTATGTCACATATCAGAGATCCAGACGACTTGCCTTATGCC 1853  
Db 1841 GACATTAACAGCAAAAGAGAGATCTTACGCTTCCGAGAGAGAGAGAGAGAGAGAG 1899  
Qy 1854 GAGCAGCTGAAAGCGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913  
Db 1900 GGTCTGAGAAATG-----AGTTCGACAGCATGAAACACAGCAGCTGAGAGAG 1947  
Qy 1914 TACTATGCAATCTAGGCTCCCGACACTCATCTGATATCTTCTGATCAGTCCGAAATATG 1973  
Db 1948 AGCAGAGGCGCGGCTGATCTGCTTATCCCATCCGCGCGCGAGCGCGAGAGAGAG 2007  
Qy 1974 TATATCTCAATGCGCATCTTACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2033  
Db 2008 TACAGTGGCTACAGCGCTACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
Qy 2034 AAGAGAGCAAAATGCGCAACCGCAACAGCAATCAATCAATGAGGCGCGCAATGAGC 2093  
Db 2068 CGGCGAGCGTGAAGCGCAACAGCA-----CGTGAAGCTGACAGGCG 2109  
Qy 2094 GGCACGACTGTCTGACACCAATCAGACCTGATCATGCGACTACGAAATGGCTG 2153  
Db 2110 G-----TAGTCACTCATGAGGCGCGGCTCAGCATTCG 2144  
Qy 2154 GAGTGCAGAGCAGAGCTGCGAAGATTAACATCAGACATCTTTATGAGCCGCTC 2213  
Db 2145 GCGGCTCTCTGAGAGTGAAGATA-----GATTAAGCAGCTACGAGAGAGGCA 2193  
Qy 2214 CAGACCAAAAGCTGTGATATGAAG---ATGTATGCTCTGATGATCATGAGAA 2270  
Db 2194 ACGACTAGGTGAATTAAGAAAGAGCGCTGATCTCTTATGATTTCTATGAGACAA 2253  
Qy 2271 CAGGCGCTGCTGCGCAGCTGCGGAGAGATGCGAGCTGCTCTCTTACTATTTCCCA 2330  
Db 2254 CTGCGCTCTTACGAG 2313  
Qy 2331 ACAGAGAGAGATGAGAGAGATGGGCGAGCTTCAAGACAGCAAGCTTGAAGTATCTC 2390  
Db 2314 CTAGTGAAAGCTGGAAGA-----GTCTCAGAGAAAGGCGCACCGTCTGATTA 2363  
Qy 2291 AAGGCAATCATGCTTGTGTG-GTGTGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2449  
Db 2364 TAAATTTGCAACACTTCTCTCATCTGAGAGTGCACCTTACGATGAATAAAGAGAG 2423  
Qy 2450 GTGGGATGCTCATGCTTCTGATCCCTGCTGAGCTCTTCTCATGAGCTGATCTGT 2509  
Db 2424 GATGTAACCTTATGCTGATGAGCTTCTTGTGATCTTATGATCATCATCTGATCTGT 2483  
Qy 2510 GGTCAACAGATGTTTCAATGAGATGATCAACAGATATGAACAGAGATGAAGCGCT 2569  
Db 2484 TGTGAATAGCTATTTATGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2543  
Qy 2570 GCTCAAGAGGCACTATTTCTTACCGGCACTTTGGCATGAGGCGACATGAAGCT 2629  
Db 2544 CTGGCGGTAGGAATGTGTGTTCACCGGAGCTTTCACGCGGAAATGTTTCTGAAGCT 2603  
Qy 2630 AATGGCATGAGCGCCCAAGTATTTCCAGAGAGGCTGGAACATCTTCACTTAT 2689  
Db 2604 CATAGCATGAG 2663  
Qy 2690 CGTGGCCCTATGCTATGGAAGCTGAGAGCTGAGAGGCTGAGAGGCTGCTGATTTGCG 2749  
Db 2664 TGTCTCCCTCAGTTATATGAGAGCTGAGCTGCGAGAGTGAAGAGGCTCTCAGTCTGCG 2723  
Qy 2750 TTGCTTCTGATGCTGTGTATTTCAAACTGGGCAAGCTTTGGCGCCCACTTATTTACT 2809  
Db 2724 GCTTTCGAGCTGCTGAGATCTTCAAGCTGGGCAAGCTCTGAGCCCACTTGAACAGCT 2783  
Qy 2810 CATTTCATATGAG 2869

Db 2784 GATCAAGATCATCGGAACTCCGTGGGTCCCTGGGCAACTGACCTGTGCTGCCAT 2843  
QY 2870 TATCATCTTCATCTTGGCGTGAATGGAAATGCAACTGTTCGGAAGAATATCATGA--- 2926  
Db 2844 CATCTGCTTCATCTTGGCGTGAATGGAAATGCAACTGTTCGGAAGAATATCATGAAG 2903  
QY 2927 TCAACAAGACCGCTTTCGGAATGGCACTGCGCGCTGGAACTTCAACGACTTATGCA 2986  
Db 2904 CGCTGTAAAGATCAACACGAGAGTGAAGCTCCGCGCTGGCAATGAAGACTTCTTCCA 2963  
QY 2987 CAGCTTCATGATGTGTTCGGGTGCTTCGCGAAGATGATGATGATGATGATGATGATG 3046  
Db 2964 CTCTCTTCATGATGTGTTCGGGTGCTTCGCGAAGATGATGATGATGATGATGATGATG 3023  
QY 3047 CATGTAAGT---GGCGATGCTGCTGATCTCCCTCTTCTTGGGCAACGCTGTCTCATCG 3103  
Db 3024 CATGAGATGCGCGGCAAGGCTATGCTCATGCTTCATGATGATGATGATGATGATGATG 3083  
QY 3104 CAATCTGTGTGTAATTAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3163  
Db 3084 CAACCTGTGTGTAATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3143  
QY 3164 CTATATGCGCGCACTGCGGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGA 3223  
Db 3144 CTGCGCGGCAACAGACAGACGCGGAATGAACA----- 3179  
QY 3224 TGGCCGATTTAAAGTTGGTTAAGGTTAATTTGCTGATTTGTTCAAGTTAAAGCTAA 3283  
Db 3180 ----- 3179  
QY 3284 CAATATGCAATCAATTAATGATCAACCATAGGTGAAGAGCAACCAACGATCACTTG 3343  
Db 3180 ----- 3179  
QY 3344 GATTGGAGCGAAGAGCATGTGTGCAACGAATGAGCTGGCGCAGACAGATCTCTCG 3403  
Db 3195 GATTCGATTAAGAAAGGCTGTGCTTGGACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3254  
QY 3404 CGACGCGCTCATCAAGAAAGGGAATCAAGAGCAGACGCAACTGAGGTGGCATCGGGGA 3463  
Db 3255 TCACTTCAAGAGCGGAGGCGGATGAAGTGAAGCCCTCGACGAGCTGTATGAAGAA 3314  
QY 3464 TCGGATGAATTCAGATCAACGCGGCACTGAAGAAACAACAGCCGGAAGAAATCAAAATA 3523  
Db 3315 GGGCAACTGATCGCCCAACCAACGCGGCTGGAATACCGGAGCGGCACTTCCGAA 3374  
QY 3524 TCTTAATTAAGCAAGATGATGAGTGGCACTCAATTAACCAAGACAAATAGACTGAAACA 3583  
Db 3375 GAACGGAAGGAAACCAACGCGGCACTGCGAGAGGTGAAGAAATCAATCAATCAAGCA 3434  
QY 3584 CGAGCTAAACCTAAGAGTTTGTCTTACAGAGCAGACGACACTGCCAGATTAATCTATA 3643  
Db 3435 GGAACACA-----TGTCTTCAATTAACA-----CCAAACCTGACCTGCC 3475  
QY 3444 TGGTGAAGCAATGAAGATGACATTCAGAGCAGAGCAGAGGCGGCGGAGAT 3703  
Db 3476 GGGTGCCTATGCTGTGGGAGATC-----TGACTTGAAGACTTCAACAGAGATGT 3530  
QY 3704 GGAAGGCGAGAGAGAGCGCGACGCGCAAGAGAGATTTAGTCTGACAGAGAACTGGA 3763  
Db 3531 TAGAGAGCAATCAACCTGGAAGGCAAGAAATGA-----ACTGAGCAATACAGCTC 3584  
QY 3764 CGAGAGGCGAATGCGAGAGGCGCGCTGACGAGTATCTTATATGACAGCA 3823  
Db 3585 CTCGAAGAGAGTACCATGACATCAAGCTGAGGTGAAGAAATTTCCGAGAGAAC 3644  
QY 3824 CGAGAGTATCTGATGAATTCAGAGTATGCTGCGCGGCACTTCTATATGAAGAT 3883  
Db 3645 TGAAGATATCTTG-----ATCGAGAGCTGCTGCTTACAGAGGTTGCGCGAGCTT 3698  
QY 3884 TCCGATCTTACCGGTGAGTGAATCTGCGCTTCTGCGAGAGATGGGCAATTTAGACT 3943  
Db 3699 CAATGTCTGCAAGGTCAATGAGAGAGCACTAGGCAAGTGTGTGATCTTTCGGA 3758

QY 3944 GAAAACCTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4003  
Db 3759 AACCTGCTCTCATTTGAGAGCAAAATGATTTGAGCTTCAATCATCTTCAATGATCT 3818  
QY 4004 AATGAGTGTAGCTTTGGCAATTAAGATGATGATGATGATGATGATGATGATGATGATG 4063  
Db 3819 GCTCAGAGTGGCGGCTGCTGCTTTGAGAGCATCTACATTAAGAGAGAGAGAGAGAGAG 3878  
QY 4064 GGAATATTTTAATCTATGAGAGAAATTAAGGTTAATTTTATTTCTTGGAAATGTAAT 4123  
Db 3879 CACCATCTGAGATGAG 3938  
QY 4124 CAAGTGTGGGCGCTGCTGCTTCAAGTGTGATCTTCAAGAGAGAGAGAGAGAGAGAGAG 4183  
Db 3939 CAAGTGTGAG 3998  
QY 4184 CGTGAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4243  
Db 3999 CTTCTATTTGGCTGCTCTTTAGTACGCTTATAGCTATAGCTTATAGCTTATAGCTTAT 4058  
QY 4244 TCAAGCTTCAAGACTATGCGAAGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4303  
Db 4059 AGGTGCAATTAAGTCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4118  
QY 4304 TATGAG 4363  
Db 4119 ATTGAAG 4178  
QY 4364 TGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4423  
Db 4179 TGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4238  
QY 4424 TGTGGAAGATTTTAAAGTGC---GAGGACATGAATGAGAGAGAGAGAGAGAGAGAG 4480  
Db 4239 TGGGAGAGATTAACACTACTGCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4298  
QY 4481 CATACCAATTCGAATGCTGCGAG-----AGCGAGAGAGAGAGAGAGAGAGAGAGAG 4522  
Db 4299 TGTCAACATTAACAG 4358  
QY 4523 GGTGAATTCAGAGATGAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 4582  
Db 4359 GAAGATGTCAAGATCACTTGAACATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4418  
QY 4583 GGCACCTTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4642  
Db 4419 GGCACCTTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4478  
QY 4643 CAAAGCAACCAATTCGGAAG 4702  
Db 4479 CGAG 4538  
QY 4703 ATTTGATCTTTTCAACTCAATCTGTCATGATGATGATGATGATGATGATGATGATGAT 4762  
Db 4539 CTTCGCTCTTCTTCACTCACTGTCATGATGATGATGATGATGATGATGATGATGATGAT 4598  
QY 4763 GCAAG 4822  
Db 4599 GCAAG 4655  
QY 4823 CTATATGCTATGAG 4882  
Db 4656 CTCAATGATGAG 4715  
QY 4883 GTGCGAG 4942  
Db 4716 GAACAAATTCAG 4775  
QY 4943 TATGATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5002  
Db 4776 CATGATGCTATGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4835

```

Qy 5003 CACGTATACGCGGCTAGACTATCTCATGCGATATTCGGATTATTTTCAGTCCGA 5062
Db 4836 GCAATGAGAAACATCTTTTACTGATTAATCTGCTTTTGTGATCTTTCACCTCGCA 4895
Qy 5063 ATGCTATTAATAATATTCGCTTACGATATCACTATTTATTTGAGCAATGGAATTAT 5122
Db 4896 GTGTGTCTCAAAATGTTGCTTGAGACACTACTATTTTACCATTTGGCTGGAACATCT 4955
Qy 5123 TGAATGATAGTGTGATTTATTCATCTTAGGTCTTGTACTTACCATTTATGAGAA 5182
Db 4956 TGACTTTGTGTGTGCTCTCTCCATGTGTGGAATGTTCTGGCTGATTCATTTAGAA 5015
Qy 5183 GTACTTGTGTGCGGACCTGCTCCGATGTGTGTGTGTGTGGAAGTGGGCGGTCTCT 5242
Db 5016 GTACTTGTGTGCGGACCTGCTCCGATGTGTGTGTGTGTGGAAGTGGGCGGTCTCT 5075
Qy 5243 TCGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5302
Db 5076 GCGTGTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5135
Qy 5303 GCGGCGCTGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362
Db 5136 GCGGCGCTGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195
Qy 5363 GCGGATGTGCTTTCATGACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5422
Db 5196 TGGGATGTGCTTTCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5255
Qy 5423 CAAAGCTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5482
Db 5256 CAAAGCTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5315
Qy 5483 TGGTGTACTGAGAGCATTATCA-----TGAGAGAGATCCGATCCAGCCGACAG 5533
Db 5316 TGGGCTGTGTGCTCAATCTGAAACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 5375
Qy 5534 CGAAGAGGCTATCGGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5593
Db 5376 AGGAGATGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5435
Qy 5594 ATACCTAGTTTAAAGCTTTTGTATGATTTATTAATGATGATGCTGCTGCTGCTGAG 5653
Db 5436 CTACATCATCATCTCTCTGATGTGTGTAATGATGATGATGATGATGATGATGATG 5495
Qy 5654 CTATATGTCAGGCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5713
Db 5496 CTTCAGGCTGTGCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5555
Qy 5714 CTATGAGTCTGGAGAGCAATTCGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5773
Db 5556 CTATGAGTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5615
Qy 5774 GTCCGAATTCCTGAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5833
Db 5616 GGCAGACTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5675
Qy 5834 GATCATATTCGATGAGATACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5893
Db 5676 GCTCATGCGCATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5735
Qy 5894 CGAGAGCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5953
Db 5736 TTTTGGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5795
Qy 5954 GATTGTGAG-----ATAGCGGCGCGCGCGAGATACGAGAGAGAGAGAGAGAGAG 6007
Db 5796 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5855
Qy 6008 AAGCGTGTGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6067
Db 5856 CACTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5915
Qy 6068 GCACAGAGCGCGCGCGCG 6084

```

```

Db 5916 ACACCTTGGCTAGCGCGG 5932

RESULT 13
AAV58420
ID AAV58420 standard; cDNA; 5977 BP.
AC AAV58420;
DT 01-DEC-1998 (first entry)
DE Tetrodotoxin-sensitive sodium channel PN4 coding sequence.
XX
XX Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;
XX nervous system disorder; epilepsy; brain injury; diabetic neuropathy;
XX AIDS-associated neuropathy; therapy; ss.
OS Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 22..5958
XX FT /tag= a
XX
XX MO9838302-A2.
XX
XX 03-SEP-1998.
XX
XX 20-FEB-1998; 98WO-EP000997.
XX
XX 26-FEB-1997; 97US-0039447P.
XX
XX (HOF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;
XX WPI; 1998-481204/41.
XX P-PSDB; AAM69361.
XX
XX New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for
XX detecting inhibitors which alleviate pain, and treating nervous system
XX disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.
XX
XX Claim 2; Page 30-32; 87bp; English.
XX
XX This sequence represents the isolated rat PN4 sodium channel cDNA clone
XX of the invention. This sequence was isolated from a peripheral nerve from
XX a rat dorsal ganglia. The PN4 sodium channel sequences are tetrodotoxin-
XX sensitive sodium channels. The protein is used in assays for detecting
XX inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate
XX pain. The probes can be used to detect and isolate the DNA or protein in
XX tissues. The antibodies can also be used to isolate the protein. The
XX protein is used as a therapeutic target for compounds to treat disorders
XX of the nervous system, such as epilepsy, stroke and brain injury,
XX diabetic neuropathy, and AIDS-associated neuropathy, etc
XX
XX Sequence 5977 BP; 1478 A; 1554 C; 1600 G; 1345 T; 0 U; 0 Other;
XX
XX Query Match 15.2%; Score 993; DB 2; Length 5977;
XX Best Local Similarity 52.4%; Pred. No. 3e-238;
XX Matches 3121; Conservative 0; Mismatches 2460; Indels 372; Gaps 28;
Qy 186 CGCAAGAAAAAAGAAAAAATCCGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
Db 121 CTCAGAAACACCAAGAGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 246 CCGGATCTTACATTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305
Db 181 AAGCAAAACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 306 CCGGAATTTGGCTTCACTCTCTGAGAGATATGATCCCTACTACAGCAATGTATGAGCA 365
Db 241 CAAAGCGCTGTGGCTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

```

QY 366 TTGATGTTAGTGAAGAAAGAAATATTTTTCGCTTTTCGATCAAAAGCAATGCG 425  
DB 301 TTGTTGTTATTAAGAGAGAAACTCTCTTCAATTTAGTGCACACCTGCTGTAC 360  
QY 426 ATCTCGATTCATCAATCCGATAGCTGCTGCGCAATTTACATTAGTGCATCATTA 485  
DB 361 ATTTTAAGCCCTTTTAACCTGATAGAAAGATAGCTAATTAATTTTGTATACCTAGTT 420  
QY 486 TTTTCCCTATTCATTCACCAATTTCTGTCATCGCATCTGATGATTAATGCCACA 545  
DB 421 TTGACATGATCATCATGTCACACATCTGATCAAACTGTGTCTTATGATTAAC 480  
QY 546 ACCGCCACGGTTAGTCCACTGAGTG-ATAATCAACGAAATCTACATTTGATCA 602  
DB 481 CTTCCGAATAGTCCAAAGATGTGGAGTACATTCACAGGAAATTAACATTTGATCA 540  
QY 603 GCTGTTAAATGATGCGACAGAGTTTCAATTTATGCCGTTTACGTAATCTTAAGATCA 662  
DB 541 CTAGTGAATTCATCGCAAGAGTTTCTGATAGACGGCTTACCTTTGCGAGACCG 600  
QY 663 TGAATTTGCGTGAAGCTTGTATATAGCTTTAGCTTATGATGATGAGGATATTA 722  
DB 601 TGAATCTGTTAATCTTCACTTATCATGATGATGATGATGATGATGATGATGATG 660  
QY 723 GGTATCTAGCAGCCCTGCGAAGCTTTAGGCTGCTGAGCGCTTAAACCGTACCAT 782  
DB 661 GCGAATGTCTAGGCGTGAAGAACTTCAAGGTTCTCCGAGCTTTGAATATCTCTGTA 720  
QY 783 GTGCGAGCTTTGAAGACATCTGTGCGGCGCTGATGCAATCGGTAAGAAATCTGCGCAT 842  
DB 721 ATTCAGGCGTGAAGAAATGCTGCGGCGCTTATTCAGTCTGTAAGAAAGCTGTGCGAC 780  
QY 843 GTGATTTCTGACCATATGTTCTCCCTGCTGCGTGTTCGCGTGTGATGAGGCTTACATATAT 902  
DB 781 GTATGATCTGACAGAGTTCTGCTGATGTTTTCGCTGATGAGCTGCGAGCTTTC 840  
QY 903 ATGCGCTGTCTCACGAGAAAGTGCAT-----CAAGAAATTCGCGTGCAGAGTTCC 953  
DB 841 ATGCGGGAACCTTCGAAACAGATGTGTGCTGCGCCATTAACCTTCAACGAGAGTACTTG 900  
QY 954 TGGGCGCATTCGACCGACGAACTGGAGCATACATCGCAATGCAATGCTCAATTTGAT 1013  
DB 901 GAGGAACGACACAGAGCTTTGACTGGAAGAAATTAATCAACATTAATAACAACTTTTAC 960  
QY 1014 TCCGAGACGAGGCAATCTATTTCCGTTATGCGGCAATATATCCGCTGCGGCGCAATGC 1073  
DB 961 ATGTTCTGCGCATGCTAGAACCTTGTCTGCGGGAAGATTCGATGCTGCGGCAATGC 1020  
QY 1074 GACGACATTAAGTGTGCTGCGAGGCTTGTGCTCGAATCCGATTTATGCTTACACAGC 1133  
DB 1021 CCAAGGGAATTCAGATGATGAAG--CAAGAAAGAAACCCCACTACGCTTTTACACAGC 1077  
QY 1134 TTGATTTGTTGCGATGAGGCTTTCTGTCCGCTTCCGCGTATGATGACACAGACCTTCTG 1193  
DB 1078 TTTTACACTTCAAGCTGAGCTTTCTTGGCATTAATTTCCGCTTATGACCCAGAGACTATTTG 1137  
QY 1194 GAGGATCTGACAGCTGCTGTGCGCGCCGCGACCATGAGCAATGCTGTCTTTATA 1253  
DB 1138 GAGAACTTAACAGGCTGACCTTACGAGCGCTGGGAAAGATGATGATCTTCTTTGTC 1197  
QY 1254 GTCAATCATCTTCTAGGTTCAATTTCTATTTGTGATTTGATTTTGGCATTTGTTGCCATG 1313  
DB 1198 TTGTCATCTTCTGAGGTTCTTTCTATCTGTGAACTTGATCTTGGCTGTGTGTGCGCATG 1257  
QY 1314 TCGATGACGAATTCGAAGAGGCGCGAAGAAAGAGGCTGCGCAAGAGAGGCGATA 1373  
DB 1258 GCTTATGAGAA--CAAGAACAGGCAACCTGAGAGAGCGAGAGAAAGAGGCG----- 1310  
QY 1374 CGTGAAGGGAAGAGGCTGCGCGCGCAAGCGCGCAAGCTGTGAGAGCGGCGCAATGCG 1433  
DB 1311 CGAGTTCAAGGCAATGCTGAGCAACTCAG-----AAGCAGACGAGAGAGGCGACAGGCT 1365

QY 1434 CAGGCTCAGCAGCAGCGGATGCGGCTGCGCGCGAAGAGGCTGCATGCTCCGAAATG 1493  
DB 1366 GCTGAATGCGCACTTCAGCGGCACTGTCTGAGAA-----CGCATTTGAAGAAAGAGG 1422  
QY 1494 GCCAAGATCCGACCTATTTCTTTCATCAGCTATGAGCTATTTGTTGGCGCGAAGAGGCG 1553  
DB 1423 GAAGATGGGTATGGCTCTCCGAGAGCTCTTCTGAATCTGTCAAACTCAGTTCCAAAGAGC 1482  
QY 1554 AAGATGACACACAAAGAGAAATGTCTCATTTCCGAGCGTGCAGAGTGGAGTGGAGTGC 1613  
DB 1483 GCGAAGAGCGCGGAA-----CCGAGGAAAGAAAGAGAGCAAGAGGA 1526  
QY 1614 GTGAGGTTATCAAAAGCAACAGACCTTACACAGACACCAAGTACCAAGTTCGT 1673  
DB 1527 GCTCTGAGAGCGAGAGAAAGGAGACCGGAGAAAGCTTTAA-----GT 1573  
QY 1674 AAGTGAACACACATCTTTATCTTACCTGCTTACCGTTTAACTATGACAGGAGATCA 1733  
DB 1574 CAGAGTGGAGACCGTATGAGAGAAAGGCTTCCGCGCTGCAGACAAACAGATAGGGA 1633  
QY 1734 CCGATTTCTCAAGTACAGATACGGAACGAGCGTGGCGCTTGTGTATACCGGATAGC 1793  
DB 1634 GGAAGTTTTCATCATGATGATGATGCTGCTGAGATTCAGAGCTGCGCTTCTCTCC 1693  
QY 1794 GATCGTAACCATTTGGTATTTGTCACATATCAGATGCCCCAGACACTTGCCTATAGCC 1853  
DB 1694 GACATTAACGAAAGACAGATCTTACGCTTCCGAGAACCG-GTGCGTTCCGAGACCC 1752  
QY 1854 GACGACTCGAATGCGCTACCCCGATGTCGAAAGAAATGGGCGCATCATGTCGCCGTG 1913  
DB 1753 GGTCTGAGAAATG-----AGTTCGAGACGATGAACACAGCACCGTGAAGAG 1800  
QY 1914 TACTATGGAATCTAGGCTCCCGACATCATGATTAATCTGATCAGTCCGAAATATG 1973  
DB 1801 AGGAGAGGCGGCTATCTGCTTTATCTTATCCGATCCGCGCCGAGAGCGCGGACAGC 1860  
QY 1974 TATACCTCATATGCGCATTAATCTGCGGCAAGCGCTGATGAGGCGCTGACCAATAGC 2033  
DB 1861 TACAGTGGCTACAGCGGCTACAGCCAGTCAAGCGCTGCTGCGCATCTTCCAGGCTG 1920  
QY 2034 AAGAGACCAATTTGGCAACCGCAACACAGCATTAATCAGTGGCGCCACCAATGGC 2093  
DB 1921 CCGCGCAGCGTGAAGGCGAA-----CAGCAGGTG 1950  
QY 2094 GGCACACCGTGTGACACCAATCAACAGCTGATCATCGGATACAGAAATTTGCGCTG 2153  
DB 1951 GACTGACAGCGCTATGCTATCATCTGCGGCGCGCTCACATTCGGGCGCTCTGCT 2010  
QY 2154 GAGTGAACGACAGACAGCTGCAAGATTAACATCATGACATCTTTTATGAGCCGCT 2213  
DB 2011 GAGGCAACAGCTGAGGTGAATTAAGAAAGGCGCTGSAATCTCTTTAGTTTCTATG 2070  
QY 2214 CAGACCAAAAGGTGTTATTAAGAAAGATGTGATGTCTGAAATGACATCATCGAAGC 2273  
DB 2071 GACCAACTGCGCTTCAACGAGCGAAGGA-----CAGATCAACAGATTAATGAG 2120  
QY 2274 GCGGCTGTGGGACAGTGGGCAAGGATCGCGGTCTCGCTTACTATTTCCAAACA 2333  
DB 2121 CGTGTCAAAACAGCTATGAAAGAGCTGGAAGAGTCTCAGAGAA----- 2167  
QY 2334 GAGGACGATGACAGAGATGGGCGCAGCTTCAAAAGACAGGCACTCGAAGTATCTCAAA 2393  
DB 2168 -----AGTCCCAACCGTGTGATTAAGTTTCCAAACTTCTCTCA-- 2209  
QY 2394 GGCATGATGTGTTGTGTGTGTGAGCTGTGCTGGTTGTGTAATTTGAGAGTGG 2453  
DB 2210 -----CTGGAGTGTACCCCTTACATGATTAATACTGAAGAGATC 2250  
QY 2454 GTATGCTCATGCTTTCATCTTTCATGAGCTCTTTCATCAACGCTGTGCTATTTGCTC 2513  
DB 2251 GTGAATTAATGCTATGAGACCTTTTGTGATCTTACCATTCATCTGATCTGTTCTG 2310  
QY 2514 AACAGATGTTTATGCAATGATGATCAACAGATTAAGAAAGAGATGAGACGCTGCTC 2573

[illegible]

Db	3262	CACA-----TGTCTTCAATTAAC-----CMAACTGACCTCCGGGT	3302
OY	3648	AGCCATAAATGCACTTCAAGGACGACCAAGGGCAGCGCCGACGATGGAG	3707
Db	3303	GCCATTGCTGTGGCGAGTCT-----GACTCGAAGACCTCAACAGAGGATGTTAGC	3357
OY	3708	GGCCAGGAAAGCGGACGCCAGCAGAGGATTTAGTCTCGACGAGAACTGACGAG	3767
Db	3358	AGCGAATCAGACCTCGAAGGACGAAAGATTA-----ACTGACGATACCGCTCTCA	3411
OY	3768	GAGGGCGAATGCGAGGAGGGCCGCTCGACGGTGATATCATTTATTCAGCAGAGGAG	3827
Db	3412	GAGGAGATACCATGCAATPAACTGAGGTGAGAGATTTCCCGTGGAGCACTGAG	3471
OY	3828	GATATACTCGATGAAATTCACAGTGAATTCGCCCCGATTTGGTACTAATAGAAATTTCCG	3887
Db	3472	GAAATCTTGG-----ATCCGAGCGCTGCTTTACAGAGGGTTGCTCCAGCGGTTCAAG	3525
OY	3888	ATCTTAGCCGGTACGATGACTCGCCGTTCTGCGAAGAGTGGGCAATTTACGACTGAA	3947
Db	3526	TGCTGCCAGGTCAACATCGAAGAAAGACTAGGCAAGTGTGTGATCTTTCGGAAAAAC	3585
OY	3948	ACTTTCAATTAATTGAAAAATTAATTTTGAACAGCTGTATACATAGATTTTATG	4007
Db	3586	TGCTTCTCATGTGGAGCACAATTTGGTTGAGACTTTCATCATCTTCATGATTTCTGCT	3645
OY	4008	AGTAGCTTAGCTTTGGCATTGAGAGATGATCATCTGCCACAAAGACCATCTCAGGAT	4067
Db	3646	AGCAGTGGCGCCCTGGCTTTGAGACATCTCACTTGAGCAGAGAAAGACATCCGACC	3705
OY	4068	ATTTTATATCTATATGACAGAAATTTTACGGTTATTTCTTCTTGAATTTGTAATCAG	4127
Db	3706	ATCTGAGATATGGGACAAAGTCTTCACTCAATCTTCACTCGAGAGTGTCTCAAG	3765
OY	4128	TGCTTGGCGCTCGGCTTCAAGTGTACTTCCACACGCGTGTGTGTGCTCGATTTGTG	4187
Db	3766	TGGACAGCTTAACGGCTTCGTCAATTTCTTCAACATGCTGTGTGCTGTGGACTTCTCTC	3825
OY	4188	ATTGTCAATGATGCGCTTATCAACTTCGTTGCTTCACTGTGTGAGCGTGGTATTCAA	4247
Db	3826	ATTGTGCTGTCTCTTTAGTACCTTATAGCTTAATGCTTGGGCTACTGGAACTAGGT	3885
OY	4248	GCTTCAAGACTATGCGACGTTAAGACACTGAGACCACTACGTGCATGTCCGATAG	4307
Db	3886	GCCATTAAGTCCCTTAGGACCTTAAGAGCTTTGAGACCTTAAAGCCTTATCAGATTT	3945
OY	4308	CAGGGCATGAGGGTCTGTGTTAATGCGCTGTACAAAGTATCCGTCATCTTCAATGTG	4367
Db	3946	GAAAGGATGAGGGGTGTGTGTAAGCCTTGGTGGGCCCATCCCTCATCATATAAATGTG	4005
OY	4368	CTATTGGTGTCTCAATATTTTGGCTAATTTTTCSCAATAAGGGTGTACAGCTTTTGCT	4427
Db	4006	CTGCTGTGTCTCTCATCTTCTTGGCTATTTTTCAGCATCATGGAGTTAACTGTTTGCG	4065
OY	4428	GAAAAATATTTTAAAGTGC--GAGCAGATGAATGGCAGAACTCAAGCAGAGATCATTA	4484
Db	4066	GGAATAATCACTACTGTTTAAATGAGACTTCTGAATCCGGTTGCAAAATGATTAATGTC	4125
OY	4485	CCMAATGCAATGCTCTGGAG-----AGCGAATCTACCTGGGTG	4526
Db	4126	AACATATTAACGCGCTGTGAGAGCTCATGAGGGCAACAGCAGGATCCGATGAGAG	4185
OY	4527	AATTCACGAATGAATTTTGCATCATGTAGTAAAGCGATATCGTGGCTTTTTCGAAGTGGCC	4586
Db	4186	AATGTCAAGATCAATTTTGAACATGTGAGACAGAGGTAACCTGGCTTTTTCGAATGGCA	4245
OY	4587	ACCTTCAAAGCTTGATACAAATCATGAACGATGCTATTCGATTTACGAGAGGTGACAG	4646
Db	4246	ACCTTCAAAGGCTGTGAGCATCATGTATAGCGGCTGTATATTCGGAAGCCAGAGAGAG	4305
OY	4647	CAACCAATTTGTGAAGCAACATCTACATGATATTTATTTTCTGTATTTCTTCATCATATTT	4706
Db	4306	CAGCTTAATAAGGGCAACATCTACATGATATCTACTTGTGTATCTTTCATCATCTTCTC	4365

OY	4707	GAATCTTTTTCACACTCAATCGGTCATTGGGTATCATATGATAATTATTAAGGCAA	4766
Dd	4366	GGGCTCTTTTCACCCTCAACCTGTCATCGGGTCAATCGACAATTCCACACGACG	4425
OY	4767	AAGAAAAAAGCAGGTGATCATTAAGAATGTTTCATGACAGAAATCAGAAAAATCTAT	4826
Dd	4426	ANAAAAA---GTTTGAGGTCAAGACATCTTCATGACAGAGAAACAGAAAGATCTAC	4482
OY	4827	AATGCTATGAAAAAGATGGGCTCTAAAACATTTAAAGCCATTCACAGAACCAAGTGG	4886
Dd	4483	AATGCCATGAAAAAGCTGGGCTCCAGAAACCCACAGAGCCATCCCCGACCTTGAAC	4542
OY	4887	CGACCAACAGCAATAGCTTTGAAAATAGTAAACCGATTAAGAAATTCGATTAATCATTA	4946
Dd	4543	AAATCCAAAGGATGTGCTTTGATTTGGTCATCTCACTCAACAAACCTTTGACATTTGATCAT	4602
OY	4947	TATATCTAGGTCTGAACATGTTTCAACATGACCCCTGCATCGTTACATGCTGTGGACAG	5006
Dd	4603	ATGCTCATCTGCCCTTAACATGATGACATATATGTTGAGACAGACATCCAGAACAGAC	4662
OY	5007	TATTAACCGGCTCCAGACATATCCAAATGCGCATATGCTAGTTATTTCACTCCGAATG	5066
Dd	4663	ATGGAACAATCTTTACTGGATTAATCTGTCTTTGTCACTTTCTCACCTGGAGTGT	4722
OY	5067	CTATTAATAAATATTCGCTTAAAGATATCACTATTTTAATGACCATGAATTAATTGAT	5126
Dd	4723	GTGCTCAAAATGTTGCTTGAGACACTACTATTTCCACATGGCTGGAAACATCTTGGAC	4782
OY	5127	GTATAGTAGTTCATTTTATTCATCTTATAGTCTGTGACTTGAACGATATTAACGAAGTAC	5186
Dd	4783	TTTTGTGGTGCATCTCTCCATTTGTGGAAATGTTCTCGGTGATATCATTTGAAGATAC	4842
OY	5187	TTCTGTCTCGCGACCCCTGCTCCGATGAGTGTGGCGAAGATGGGCGGTGCTTTCGA	5246
Dd	4843	TTCTGCTHCCCACACCTATTTCCAGTTATCCGATTTGGCCCGATTTGGCGATCTTGGT	4902
OY	5247	CTGTGAAAGGAGCCAAAGGCAATTGCGACATGCTCTTTCGGGTTGGCCAATGCGTCGCG	5306
Dd	4903	CTGATCAAGGGCGGCCAAAGGATCCGACCTGTGCTTTGGCTTAATGATGTCCCTGCC	4962
OY	5307	GGCCGTTTCACATCTGCTGCTGCTGTTCTGTGTCATGTTCACTTTTGCCATTTTGGC	5366
Dd	4963	GGCTGTTTCACATCGGCTCTGCTCTTCTCTCGCANGTTCATCTTCCATATTTTGGC	5022
OY	5367	ATGTGCTTTCTTCATGACGCTGAAGAGAAAGCGGCATTAACAGACGTCTAACACTTCAAG	5426
Dd	5023	ATGTCCAACTTCGCATATCGTAAAGACAGAGGCCGCGATTTGACGACATGTTCAACTTGAAG	5082
OY	5427	AACCTTGGCCAGAGATGATCTGTCTTTAGATGTGACGTCAGCGGTTGGGATGAT	5486
Dd	5083	ACATTTGGCAACAGATATATCTGTTTGTTCAGATCAAAAGTCTGCTGGCTGGGAATGCG	5142
OY	5487	GTACTGACGCGCATATATCA-----TGAAGAGATCGATCAACCCGACAGCGAC	5537
Dd	5143	CTGCTGCTGCAATCTCTGAACGCGCCCTGATCTGCACTTGGACAAAGACACCCAGGG	5202
OY	5538	AAAGGCTATCCGGGCAATTTGTGTTCACGACCCGTGGAATAAAGTTCCTCTCTCATAC	5597
Dd	5203	AGTGGCTTCMAAGGGGACGTGTGAAGACCCCTCGGTGGGCATCTTCTTCTTGTGAGCTAC	5262
OY	5598	CTAGTTATTAAGCTTTTGTAGTATTAATAATGTACATTTGCTGTCACTTCOGAATACTAT	5657
Dd	5263	ATCATATCTCTTCTCTGATTTGTGTGTAACATGTACATCGGCATATCTCTGSAAGACTTC	5322
OY	5658	AGTCAGGCCACCGAGACGTCGAAGAGGCTTAACCGACAGACGATACGACATGTACTAT	5717
Dd	5323	AGCGTGGCCACCGAGAGAGCGCCACCTCTGAATGTAGATGATCTTGAGACTTCTAT	5382
OY	5718	GAGATCTGGCACACNTGATCCGAGAGGCAACCGATCATATCGCTATGATCAGCTGCC	5777
Dd	5383	GAGATCTGGGAAGTTTACCAAGCCGACCCAGCTTCATGAGTACTGTAAAGCTGGCA	5442

Qy	5778	GAATTCCTGGACCGACTAGAGACCCCGCTCAGATCCACAACCAACGAAAGTCCAGATC	5383
Db	5443	GACTTTGGCCGACGGCCCTGGAGNACCCGCTCCAGATCCAAAGCCCAACCATCATGACCTC	5502
Qy	5838	ATATCGATTGGACATATCCCATCTGTGCGGGGTGACCTCATATGTATACCGCGTCGACATCTCGAC	5897
Db	5503	ATCCGCATGGACCTGCCCATATGATGGAGGAGGAGATGCATCCATCTGCTTGACATCTTTTC	5562
Qy	5898	GCCCTTACGAAAGACTCTTTGCGCGGAGAGGGCAATCCGATAGAGAGACGGGTGAGATT	5957
Db	5563	GCTTTTCAACAAAGCAGATCTCTGGAGAGACATGGGGAGTTTGGACATCTTCGCGCAGCAATG	5622
Qy	5958	GGTGAG-----AATGGGCGCCCGCCCGGATATCGAGGGGCTACAGAGCCCGTCTCATCAAG	6011
Db	5623	GAGAGCGGGTTCTGGCAATCCATCTTCCAAAGTGTCTTAGAGGCTATTCACAACCACT	5682
Qy	6012	CTGTGGCGTCAAGCGTGAAGAGTACTGCGCCCGGCTAAATCCAGCAAGCCTTGCGCAAAAGCA	6071
Db	5683	CTGCGGGCCCAAGCAGAGAGAGTGTCTTGCAAGTGTCTCTGACGCGTGTCTTACAGGGGACAC	5742
Qy	6072	AAGGCGCGCGGCG	6084
Db	5743	TTGGCTAGCGGG	5755

XX	AAV58419	standard; cDNA; 6556 BP.
XX	AAV58419;	
XX	01-DEC-1998	(first entry)
XX	PN4 sodium channel clone.	
XX	Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;	
XX	neurov system disorder; epilepsy; brain injury; diabetic neuropathy;	
XX	AIDS-associated neuropathy; therapy; ss.	
XX	Rattus sp.	
XX	WO9838302-A2.	
XX	03-SEP-1998.	
XX	20-FEB-1998;	98WO-EP000997.
XX	26-FEB-1997;	97US-0039447P.
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
XX	Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;	
XX	WPI; 1998-481204/41.	
XX	New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for	
XX	detecting inhibitors which alleviate pain, and treating nervous system	
XX	disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.	
XX	Claim 1; Page 54-58; 87pp; English.	
XX	This sequence represents the isolated rat PN4 sodium channel cDNA clone	
XX	of the invention. This sequence was isolated from a peripheral nerve from	
XX	a rat dorsal ganglia. The PN4 sodium channel sequences are tetrodotoxin-	
XX	sensitive sodium channels. The protein is used in assays for detecting	
XX	inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate	
XX	pain. The probes can be used to detect and isolate the DNA or protein in	
XX	tissues. The antibodies can also be used to isolate the protein. The	
XX	protein is used as a therapeutic target for compounds to treat disorders	
XX	of the nervous system, such as epilepsy, stroke and brain injury,	
XX	diabetic neuropathy, and AIDS-associated neuropathy, etc	
XX	Sequence 6556 BP; 1620 A; 1727 C; 1736 G; 1471 T; 0 U; 2 Other;	



Db 2268 CGTGGTCAACAAACCGCTAGTGGAGAGCTGGAAAGTCTCAGAGAA----- 2314  
Qy 2334 GAGAGCAGATGACGAGATGGGCGGACGTTCAAAAGAACGCACTCGAAGTGAATCCTCAAA 2393  
Db 2315 -----AGTCCCAACCGTGTGGTAATGATTGGCAACCTTTCCTCA-- 2356  
Qy 2394 GGCATGATGTGTTTGTGTGGGACTGTGGGGTGTGTTGAAATTTCCAGAGTGG 2453  
Db 2357 -----TCTGGAGTGTCAACCCCTAATGATAAATCGAAGGAGATC 2397  
Qy 2454 GATCCGCTCATGCTCTTCGATCCCTTGTGTGAGCTCTTCATCAACGCTGTGATGTGTG 2513  
Db 2398 GTGACCTTAATCCCTATGACCCCTTTGTGACTTGACCTACCAATCTGCAATGTCTTG 2457  
Qy 2514 AACACAGTGTTCATGGAATGATGATCAACGATATGAAACAAAGAGATGGAACGCTGTCT 2573  
Db 2458 AATACGCTATTATATGGCAATGAGACACATCCATGACACCAACATTCGAACGCTTG 2517  
Qy 2574 AAGATGGCAACTAATTTCTTCAACCGCAACCTTGCATCGAGGCCAATGAAGCTPATG 2633  
Db 2518 GCGGTAGGAATCGGTGTTCACCGGATCTTCAACGCGGAAATGTTCTGAAGCTCATG 2577  
Qy 2634 GCCATGAGCCCCAGTAATCTATTTTCAGAGAGGCTGGAAACATTTCCATTCATTCG 2693  
Db 2578 GCCATGAGCCCTACTAATTAATTTCCAAAGAGGCTGGAAACATTTTGAAGGATTTATG 2637  
Qy 2694 GCCCTATCGCATTTGAACTGGGACTCGAGGGTGTCCAGGGGTGTCTGCTCCATTTGCTTC 2753  
Db 2638 TCCCTCAGTTTAATGAGCTGAGTCTGTGCAAGATGTGAAAGGGGTCTCAGTGTGCGGTCT 2697  
Qy 2754 TTTGATGTGCTGTGATTAATCAACCTGGCAAGCTTTGGCCCACTTAATTTACTCAT 2813  
Db 2698 TTCCGATGCTCCGAGCTTCAAGCTGGCAAGCTCGGCCCAACCTGGAACATGTCTGATC 2757  
Qy 2814 TCGATTAATGAGAGCCACCATGAGGCGCTTTGGGTAACTGACATTTGACTTTGATATC 2873  
Db 2758 AAGATCACTGGGAACTCCGTGGGTGCCCTGGCAACCTGACCTGTGCTGGCCATATC 2817  
Qy 2874 ATCTTCATCTTTGGGTGATGGAATGCAACTGTTCCGAAAGAAATTAATCAAGA---TCAC 2930  
Db 2818 GTCTTCATCTTCGCGGTGTGGGATGCAAGCTGTTTGGAAAGTTTCAAGAGTGTGCTC 2877  
Qy 2931 AAGAGCCGCTTTCCGATGAGGACTGCGCGCTGGAATTCAACCGACTTAATGACAGC 2990  
Db 2878 TGTAAATCAACACGAGATGCAAGCTCCGCGCTGGACATGAAACGACTTCTCCACTCC 2937  
Qy 2991 TTCAATGATGCTGCTCCGCGGTCTCTGGGAGATGATGAGTCAAGTGTGAGGACTGTGATG 3050  
Db 2938 TTCTCATGCTCTTCGAGTGTGTGTGGAGTGAATCGAGACCAATGTGGAGCTGATG 2997  
Qy 3051 TACGTG---GGCGATGTCTCTGCAATCCCTTCTTGTGGCCACCGTGTTCATCGCAAT 3107  
Db 2998 GAGGTGCGCGCCAGGCGCATGTGCTCATGTCTTCAATGATGTATGTCATATGGCAAC 3057  
Qy 3108 CTGTGTGATTAACCTTTTCTTACGCTTGTGTTTGTTCCAATTTGGCTCATCTAGCTTA 3167  
Db 3058 CTGTGTGTGTGAATCTAATCTGACCTTGTCTTCAAGCTCTTCAGGCGACACACTG 3117  
Qy 3168 TCAGCGCCGACTGCGCGATTAAGATACGAATAAATAGCCGAGGCTTCATCGAATTGGC 3227  
Db 3118 GCGGCAACAGACGACGCGGGAATGAACA----- 3149  
Qy 3228 CGATTTAAAGTGTGTAGCGTAATATGCTGATGTGTTCAAGTTAATACGTACAAA 3287  
Db 3150 ----- 3149  
Qy 3288 TTGACAAATCAATATGATCAACCATCAGGTGAGAGACCAACCATGATGATTTGAT 3347  
Db 3150 -----CTGCAATATCTAGTATC 3168  
Qy 3348 TGGAGCGAAGCAGATGTGACAAAGAACTGGAGCTGGCGACGACAGATCTCGCCGAC 3407

Db 3169 CGGATCAAGAAAGGCGCTGCGCTGACCAAGTAAGTGCACGCTTCATGCAAGGCTCAC 3228  
Qy 3408 GGCCTCATCAAGAAAGGATCAAGAGACAGACGCACTGAGTGTGCCATCGGGATCGG 3467  
Db 3229 TTCAAGCAGCGGAGGCGGATGAAAGTGAACCCCTCGACGAGCTGTATGAGAAAGAGCC 3288  
Qy 3468 ATGGAATTCAGATTCACGCGGACATGAAGAACAAACAAAGCGGAAGAAATCCAAATATCTA 3527  
Db 3289 AACTGCATGCGCAACCAACGCGGCTGTGATTCACCGGAACGCGGACTTCCAGAAAGAAC 3348  
Qy 3528 AATTAAGCAACGATGATTGGCAACTCAATTAACCAACAGACAAATAGA CTGGAACAGAG 3587  
Db 3349 GGAAGGAAACCAACGAGGATCGGACGACGCTGGAAGTATCATCATGACAGAGAC 3408  
Qy 3588 CTAAACATAGAGTGTGTCTTACAGACGACGACCTGCCAGATTAATCATATAGT 3647  
Db 3409 CACA-----TGTCTTCAATTAACA-----CCAAACTGACGCTCGGCT 3449  
Qy 3648 AGCCATTAAGATCGACATTCAGAGACGAGCCCAAGAGGCGCGGACGAGATGAG 3707  
Db 3450 GCCATGTCTGTGGGAGTCT---GACTTCGAGAACCTTCAACAGAGATGTTAGC 3504  
Qy 3708 GCGCAGAGAAACGCGGACGCGACAGAGAGATTTAGTCTGACGAGAGACTGACAG 3767  
Db 3505 AGCGATCAACCTGAAAGCAGCAAAAGTAA-----ACTGAGCATACAGCTCTCA 3558  
Qy 3768 GAGGCGAATGCGAGAGGAGCCGCTCGACGTTGATATCATATTCATGACACAGCAG 3827  
Db 3559 GAAGGAATGATGACATCAACGCTGAGTGAAGAAATTCCTGTGAGCAACCTGAG 3618  
Qy 3828 GATATATCGATGAATATCACTGATGCTGCTCCCGATTCGATATTAAGAAATTTCCG 3887  
Db 3619 GAATCTTGG-----ATCCGAGCGCTGCTTTACAGAGGTGTGGTCAAGGGTTCAG 3672  
Qy 3888 ATCTTAACCGGATGACATGCTGCGCTTCTGCAAGATGAGGCAATTTAGCATGA 3947  
Db 3673 TGCTGCAGGTCAACATCGAGAGAGCACTAGGCAAGTCTGTGTGATCTTGGGAAAC 3732  
Qy 3948 ACTTTTCATTAATTAATAATTAATTTTGAAGAGCTGTATCATCTATGAATTTATG 4007  
Db 3733 TGCTTCCTATGTGAGGACATTTGTTGAGACCTTATCATATCTTCATGATTTGCTC 3792  
Qy 4008 AGTAGCTTACCTTGGCATTAAGATGTACATCTGCCAAGAACCCATCTGACAGAT 4067  
Db 3793 AGCAGTGGCGCCCTGCTTTAGACATCTACATTTAGACAGAGAAACATCCGAC 3852  
Qy 4068 ATTTTACTATATGACAGATATTTACGTTATATTTCTTGGAAATGTTAATCAAG 4127  
Db 3853 ATCTGAGATACGGAACAAAGCTTTCACCTTACATCTTCACTGAGATGTTGCTCAG 3912  
Qy 4128 TGTGTGCGCTGGCTTCAAGATGTACTTCAACCAAGCGGCGTGTGGCTGCAATTCG 4187  
Db 3913 TGAACAGCTTACGGCTTGTCAAGTCTTTCACCAATGCTGTGTGTGAGACTTCTC 3972  
Qy 4188 ATGTGATGTATGCTTATCACTTGTGCTTCACTGTGTGAGCTGTGTATTCAA 4247  
Db 3973 ATGTGTGTGTCTTTTATGACCTTATAGCTAATGCTGTGAGTCTGCAATCAGAT 4032  
Qy 4248 GCTCTTAAGACTATGGAAGTTAAGACATGAGACCACTACGTCATGTCGATG 4307  
Db 4033 GCCATTAAGTCCCTTGAAGCCCTTAAGAGCTTGAAGCTTGAAGCTTATACAAAT 4092  
Qy 4308 CAGGGCAGAGGAGCGTGTATATGCGTGTACAAGCTTACCTGATCTTCAATG 4367  
Db 4093 GAAGGATGAGGAGTGTGATATGCTGTGTGTGAGGCGCATCCCTTCATCATGATGTG 4152  
Qy 4368 CTATGTGTGTCTAATATTTTGGCTAATTTTGCATTAATGAGTGAACGCTTTTGT 4427  
Db 4153 CTGTGTGTGTCTAATCTTCTGCTGATTTTCAAGATCAATGGAAGTAACTGTTTGC 4212  
Qy 4428 GAAATATTTTAATGCTC---GAGGACATGAATGAGCAAGAGCTGACGACGAGATCAT 4484  
Db 4213 GGGAAATACACTAATGCTTTAATGAGACTTGTGAATCCGTTTCAATTCGATTTGCTC 4272

QY	4485	CCAAATGCGCAGTGGCTGGAG-----AGCGAAGATCAACCGGGTGG	4526
Db	4273	AACATATAAAGCGACTGTGAAGAGCTATGAGAGGCCAACAGACGSAATCGATGGAAAG	43323
QY	4527	AATTGACGAATGAATTTTGATCATGTAGTGAACGGTATCTGTGCTTTTCCAACTGGCC	45868
Db	4333	AATGTCAGATCAACTTTGACAAATGTGGAAGAGGGTACTGGCCCTTCTTCAAGTGGCA	43929
QY	4587	ACCTTCAAAAGGCTGGATATCAAAATATCAATGAAAGATGCTATCGATTTCAACGAGTGGACAG	46464
Db	4393	ACCTTCAAAAGGCTGGATGAGATCATGTATGAGGGGTGTAGATTTCCGGAACCCAGACAG	44525
QY	4647	CAACCAATTCGTGAACAGACATCTACATGTAATTTATTTTCGTATTTCTTCATCATATTT	47060
Db	4453	CAGCTGACTACGAGGGGACAAATCTACATGTACATCTACTCTTCGTATCTTTCATCATCTTC	45122
QY	4707	GGATTCCTTTTTCACATCATATCTGTTCATTTGAGTGTATCATTTGATTAATTTAATGACAA	47666
Db	4513	GGCTTCCTTTTCACCTTCACCTTCACCTGTTCATTCGGTGCATATCGACAACTTCAACACAG	45727
QY	4767	AAGAAAAAGACGGGTGATCTATTGAATGTTCATGACAGAAAGATCAGAAAAAGTACAT	48268
Db	4573	AAGAAAAA--GTTTGGAGTCAAGACATCTTCATGACAGAGAACAGAAAGCCATCCCCCGAC	46229
QY	4827	AATGCTATGAAAAAGATGGGCTTAAAAAACCATTTAAAGCCATTTCCAGAACCAAGGTGG	48868
Db	4630	AATGCTATGAAAAAGCTGGGCTCCAGAAAGCCACAGAAAGCCATCCCCCGACCTTTGAC	46899
QY	4887	CGACCAAGACGAATAGTCTTTGGAAATAGTAAACCATTAAGAAATTCGATATATATCATTTAG	49466
Db	4690	AAATATCCAAAGGATGTGTTTGGATTTGGTCACTCAACAGCCTTTGACATTTGTATGTATG	47494
QY	4947	TTATTCATTTGGTCTGCAACATGTTCACCATGACCTCGATCGTTACGATGCGCTGGACAGC	50066
Db	4750	ATGCTCATCTGCTTTAATCATGTGACATGATGTGTGAGACAGACACTCAGACAGACAG	48099
QY	5007	TATTAACGGGTCTTAGACTATCTCAATGCGAATTCGTAGTTATTTCAGTTCCGAATGT	50666
Db	4810	ATGAGAAACATCTTCTTACTGTGATTAATCTGGCTTTGTTCATCTTCCACCTGGACGATGT	48659
QY	5067	CTATTAATAAATATTCGCTTTACGATATCACTATTTTATGAGCAATGGAATTTATTTGAT	51266
Db	4870	GTGCTCAAAATATGTTTGCCTTGAGACACTACTATTTTACCATTTGGCTGGAACATCTTGAC	49299
QY	5127	GTAGTAGTGTTCATTTTATTCATCTTAGTCTTGTACTTACGCAATATTTATGAGAAGTAC	51866
Db	4930	TTTGTGTGTGTCAATCTCTCTCATATTGTGGAAATGTTCTGTGATATCATTTGAAGAATAC	49899
QY	5187	TTTGTGTGCGCGACCTCTGCTCCAGATGTGCTGTGGAGAAAGTGGCCGTGTCTCTTGA	52466
Db	4990	TTTGTGTGCGCGACCTTATTCGAGTTATTCGATTTGGCCGTATTTGGCGCATCTTGTGT	50499
QY	5247	CTGTGTGAAGGAGCCAAAGGCGATTTCGACACTGCTCTTGGGTGGCCATGTCGTGGCG	53066
Db	5050	CTGATTCAGAGGCGCCAAAGGATTCGACACTGCTCTTGGCTTAAATGATGTGCTGCTCC	51099
QY	5307	GCCCTGTTCAACATCTGCTGTGCTGTGTTCTGTGTCATGTTCAATCTTTCGATTTTGGC	53666
Db	5110	GCCCTGTTCAACATCTGCGCTCTCTGCTCTCTCTGTCATGTTCAATCTTCTCATTTTGGC	51699
QY	5367	ATGTGCTTTTCATGACGCTGAAGAGAGACGGCCATTACGACGCTTCAACTTCAAG	54266
Db	5170	ATGTTCACATTTGCAATGATGATGAAGACGAGGCGGCATGACGACATGTTTCACTTGAAG	52299
QY	5427	ACCTTTGGCCAGACATGATCTGCTCTTTTCAGATGTGACGTCGACGCGTGTGGATGTGT	54866
Db	5230	ACATTTGGCAACACATGATCTGTGTTGTTCCAGATTCACAACTGTGCTGCGCTGGGAATGCG	52899
QY	5487	GTACTGCAAGCCATTATCA-----TAGAAGATATGCAATCCACCCGACAGCAGAC	5537
Db	5290	CTGCTGTGCGCAATCTGGAACGCGCCCTTACTGACGCTTGGACAAAGACACCCAGCG	53499

OY		5538	AAAGGCAATCCGGGCACATTGGGTTCAGCACCCTTGAATAAGTTTCTCTCATAC	5597
Dd		5350	AGTGCGTTCAAAGGGACTGTGGGAACCCCTCGGTGGGCACTCTTCTTTGTGAGCTAC	5409
OY		5598	CTAGTTAATACCTTTTTTGATTAATTAAATATGTAATCTGCTGATTTCTGAGAATCTAT	5657
Dd		5410	ATCATCATCTCTCTTCCGATATTGTGGTAAACAATGATACCTGCCATCATCTGGAGAACCTTC	5469
OY		5658	AGTAGGCGCACCCGAGGACGTGSCAAGAGAGGTCTAACGACACGATCGAGCATGACTAT	5717
Dd		5470	AGCGTGGCGACCCGAGAGAGCGCCGACCCTCTGATGAGATGACTTGAGACTTTCTAT	5529
OY		5718	GAGATCTGCGACGAACTTCGATCCCGAGGGGCACCCAGATACATACGCTATGATCAGCTGTCC	5777
Dd		5530	GAGATCTGGAGGAAGTTGACCAGACGACCAACCCAGTTCAATCGAGTACTGTAAAGCTGGCA	5589
OY		5778	GAATTTCTGACGATCTGAGAGCCCGCTGCGATCCAACAAACGAACTAGTACAAGATC	5837
Dd		5590	GACTTTGCGCGACGCGCTGTGAGCAACCGCTCCGATACCCAAAGCCCAACACCATGAGACTC	5649
OY		5838	ATATCGATGAGCATATACCCATCTGTGCGGGTGAACCTCAATGTACTGCTGCATCTCGAC	5897
Dd		5650	ATCGCCATGAGACCTGCCCCATGTGAGAGCGAGATGCGATCCACTCTGTTGACATCTTTTC	5709
OY		5898	GCCCTTACGAAAAGACTTCTTTGCGCGGAGAGGGCAATCCGATGAGAGAGACGGGTGAGATT	5957
Dd		5710	GCTTTTACCAAGCAGACTCTGGGAGACAGTGGGAGATTGGACATCTGCGCGACAGAAATG	5769
OY		5958	GGTAG-----ATAGGGGCGCGCGCGGATATACGAGAGGGCTTACGAGCGCGTCTCATCAAG	6011
Dd		5770	GAGAGGGCGTTCGTGGCATTCATCTCTTCCAAATGTCTTTACGAGCCTTATACACCACT	5829
OY		6012	CTGTGCGGTCAAGCGTGTGAGAGTACTGCGCCCGCTAATCCAGCAAGCGCTGGCGAAACAC	6071
Dd		5830	CTGCGGGCGCAAGCAGAGGAGGTGTCTGCAGTGTCTCTGACAGCGGTGCTTACAGGAGCAC	5889
OY		6072	AAGCGCGCGCGCGC 6084	
Dd		5890	TTCGCTAGCGCGG 5902	
<hr/>				
RESULT 15				
ADP71901				
ID	ADP71901	standard; DNA;	6556 BP.	
XX	AC			
XX	ADP71901;			
XX				
DT	26-AUG-2004	(first entry)		
DE				
XX		Renal toxin progression gene marker #490.		
KW	dsj; toxic effect; gene expression profile; kidney tissue;			
KW	differential gene expression; toxicity progression; toxicity marker;			
KW	drug screening; toxicity assay; kidney pathology; nephritis;			
KW	kidney neurosis; glomerular injury; tubular injury;			
KW	focal segmental glomerulosclerosis.			
XX				
OS	Rattus norvegicus.			
XX				
PN	MO2004048598-A2.			
XX				
PD	10-JUN-2004.			
PF	24-NOV-2003; 2003WO-US037556.			
XX				
PR	22-NOV-2002; 2002US-00301856.			
PA	(GENE-) GENE LOGIC INC.			
PI	Mendrick DL, Porter MW, Johnson KR, Caastle A, Higgs B;			
EI	Elashoff M;			
XX				
RR	WPI; 2004-460771/43.			

XX Predicting (the progression of) a toxic effect of a compound, for  
 PT monitoring the progression of renal disease states, comprises preparing a  
 PT gene expression profile of a kidney tissue or cell sample exposed to the  
 PT compound.

XX Claim 11; SEQ ID NO 490; 266bp; English.

XX The invention relates to a method of predicting (the progression of) a  
 CC toxic effect of a compound by preparing a gene expression profile of a  
 CC kidney tissue or cell sample exposed to the compound and comparing the  
 CC gene expression profile to a database, or detecting the level of gene(s)  
 CC expression in a tissue or cell sample exposed to the compound, where  
 CC differential gene expression compared to a control indicates a toxic  
 CC effect (toxicity progression). The method is useful for predicting (the  
 CC progression of) at least one toxic effect of a compound. The genes are  
 CC useful as toxicity markers in drug screening and toxicity assays. The  
 CC methods are useful for predicting the likelihood that a compound or test  
 CC agent will induce various specific kidney pathologies, such as nephritis,  
 CC kidney necrosis, glomerular and tubular injury, or focal segmental  
 CC glomerulosclerosis. The methods are useful for determining the similarity  
 CC of a toxic response to one or more individual compounds and for  
 CC predicting or elucidating the potential cellular pathways influenced,  
 CC induced or modulated by the compound or test agent. The kit is useful for  
 CC predicting or modelling the toxic response of a test compound, for  
 CC monitoring the progression of renal disease states, for identifying genes  
 CC that show promise as new drug targets and for screening known and newly  
 CC designed drugs. This sequence corresponds to a gene marker used in the  
 CC method of the invention. (Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pcr\_sequences).

XX Sequence 6556 BP; 1620 A; 1727 C; 1736 G; 1471 T; 0 U; 2 Other;

XX Query Match 15.2%; Score 993; DB 12; Length 6556;

XX Best Local Similarity 52.4%; Pred. No. 3.2e-238; Indels 372; Gaps 28;

XX Matches 3121; Conservative 0; Mismatches 2460; Indels 372; Gaps 28;

QY 186 CGCAGAAAAAAGAAAAAATCCGATATGATGACGAGACGAGATGAAAGTCCACAA 245  
 DB 268 CTCAGAGAAACCAAGGCGATGAGCAGCCAGCGAGACGATGAGAGACAGAGCC 327  
 QY 246 CCGATCTTACATTTGAAACGGGTGTCATACCTTTGATGAGGAGGAGTCCG 305  
 DB 328 AAGCAAAAGTGAAGCTGAGAGCTGAGAGAGTTGCTTCTTCACTGAGGACATCCG 387  
 QY 306 CCGAATTTGGCTTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAATGACA 365  
 DB 388 CAGGCTGTGTGGGTTCCCTTGGAGGACCTTGAACCTTATTTGAGCAGAGAAACC 447  
 QY 366 TTGGTATGTTAGCAAGAAAGATATTTTGTCTTTTGTGATCAAAAGCAATGTGG 425  
 DB 448 TTTGTAGATTAACAGAGGAGAAACCTCTTCAGATTAGTGTGACACCTGCTTTTAC 507  
 QY 426 ATGCTCATTCATTCATTCGATCGTGTGAGCAATTTACATTTAGTGCATCATTA 485  
 DB 508 ATTTAAAGCCCTTTTAACTTATTAAGAAATAGCTATTAATTTTGTATGATCATCTG 567  
 QY 486 TTTTCCCTATTCATTCATTCAGCAATTTCTGTCATGTCATCTGATGATTAATCCGACA 545  
 DB 568 TTGAGCATGATCATTCATTCAGCAATTTCTGTCATGTCATCTGATGATTAATCCGACA 627  
 QY 546 AGGCCACGTTGAGTCCATGAGGTG---ATATTTCCCGGAATCTTCAACATTTGATCA 602  
 DB 628 CCTCCAGATGATGTCAGAAATGAGATGACATTTCAAGGATTTTAACTTTGATTA 687  
 QY 603 GCTGTTAAAGTATGAGGACGAGAGTTTCAATTTTATGCGGTTTATGATCTTAAAGATGCA 662  
 DB 688 CTATGAAATCATTCAGAGAGGTTTCTGATAGAGGCTTCACTTTCTGAGAGACCG 747  
 QY 663 TGAATTTGCTGAGCTTGTATGATTAATGCTTATGATGATGATGATGATGATGATGAT 722  
 DB 748 TGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807

QY 723 GGTATCTAGAGCCCTTCGAAAGCTTTAGGCTGTCGAGGCGCTTAAACCGTAGCCAT 782  
 DB 808 GGCAATGCTCAGCCCTTAGAACAATTCAGAGGTTCTCCAGGCTTTGAAATCTTGTGA 867  
 QY 783 GTCCAGGCTTGAAGACCATGTCGAGCGCGCTCATCGATCGTGAAGATCTGCGCAT 842  
 DB 868 ATTCAGGCTGAGAAACAATGTCGAGCGCGCTCATCGATCGTGAAGATCTGCGCAT 927  
 QY 843 GTGATATCTGAGCAATGTCCTCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTC 902  
 DB 928 GTGATATCTGAGCAATGTCCTCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTC 987  
 QY 903 ATGCGGCTGTCAGCAAGTGCAT-----CAAGAGTTCGCGTGAAGCTTCC 953  
 DB 988 ATGCGGCAATCTGAGCAAGTGCAT-----CAAGAGTTCGCGTGAAGCTTCC 1047  
 QY 954 TGGGCAATCTGAGCAAGTGCAT-----CAAGAGTTCGCGTGAAGCTTCC 1013  
 DB 1048 GAGAACGCAACAGAGGCTTTGACCTGAGAGAAATATCAACATTAACAACTTTAC 1107  
 QY 1014 TCCGAGAGCAGAGGATCTCATTTCCGTTATGCGCAATATATCCGTCGCGGCAATGC 1073  
 DB 1108 ATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167  
 QY 1074 GAGACGATTAAGTGTGCTGAGAGGCTTTGCTCCGAATTCGAATTTAGCTACACAGC 1133  
 DB 1168 CAGAGGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1224  
 QY 1134 TTGATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1193  
 DB 1225 TTGATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1284  
 QY 1194 GAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253  
 DB 1285 GAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1344  
 QY 1254 GTCATCATCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313  
 DB 1345 TTGATTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1404  
 QY 1314 TCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1373  
 DB 1405 GCTTATGAGGAA---CAGAACAGAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457  
 QY 1374 CCGTGAAGCGGAAAGCTGAG 1433  
 DB 1458 CGAGTTCAAGGCAATGTCGAGCACTCAAG---AAGCAGAGAGAGAGAGAGAGAGAGAG 1512  
 QY 1434 CAGGCTCAGGAG 1493  
 DB 1513 GCTGCAATGAGGAG 1569  
 QY 1494 GCCAAGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553  
 DB 1570 GAAGATGAGGAG 1629  
 QY 1554 AAGGATGAG 1613  
 DB 1630 GCGAG 1673  
 QY 1614 GTGAGGATTAACAAAG 1673  
 DB 1674 GCTCTGAG 1720  
 QY 1674 AAGGATGAG 1733  
 DB 1721 CAGAGTCCGAG 1780  
 QY 1734 CGTATGCTCAG 1793  
 DB 1781 GAGAGTTTTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840

QY 1794 GATGTAAGCATTTGATGTGACATATGAGATGCCAGACGACTTGCCCTATGCC 1853  
DB 1841 GACATTAACAGCAAAAGCAGATCTTACCTTCGCGGACCCG-CTCGGTTCGCGGACCC 1899  
QY 1854 GACGACTCGAATGCGCTGACCCCGATGTCGGAAGAATGCGGCGCATATGATGCCCTG 1913  
DB 1900 GGCCTGTGAGATG-----AGTTCCGAGCGATGAACACAGACGCTGGAGAG 1947  
QY 1914 TACTATGCGAATCTAGGCTCCGACATCTATGTAATCTTGCACTGATCCCGAATATCG 1973  
DB 1948 AGCGAGGCGCGCGTGAATCTGCTCTTCAATCCGATCCGCGCGCGAGCGCGCGAGCAGC 2007  
QY 1974 TATACCTGACATGCGGATCTACTCGGCGGCAATGCGCGCATGCGGCGTGAAGCAATGACC 2033  
DB 2008 TACAGTGGCTACAGGCTTACAGCCAGTGCAGCGCGCTGTCGCGATTTCCCAAGCTG 2067  
QY 2034 AAGGAGCAAAATTTGCGCAACCGCAACACAGCAATCAATGATGGCGCGCAACCAATGCG 2093  
DB 2068 CGGCGAGCGTGAAGCGCA-----CAGCACGGTG 2097  
QY 2094 GGCACCACTCTCTGAGACCAATCAAGCTCGATCACTCGGACTACGAAATGGCGCTG 2153  
DB 2098 GACTGCAACGCGGATGCTACTCATCGGCGCGGCTCACATCGGCGGCTCGTGCCT 2157  
QY 2154 GAGTGCACGCAAGCAAGCTGGCAATTAACATCATGACATCTTTTATGAGCGCTC 2213  
DB 2158 GAGGCAACGACTGAGTGAATTAAGAAAGGCGCTGAGATCTTTTATGATTTATG 2217  
QY 2214 CAGACACAAACGAGTGTGATGATGAATGATGCTGTAATGACATCATCGAACAG 2273  
DB 2218 GACCACTCGCTCTACGAGCGAAGGA-----CAGATCAACACATCATATGAG 2267  
QY 2274 GCGCGTGTGCGGACAGTCCGCGCAAGCGAGTCCGCTGCTCCGTTACTATTTCCCAACA 2333  
DB 2268 CGTGTGTCAAAACGCTAGTGAAGAGCTGAAGAGTCTCAGAGAA----- 2314  
QY 2334 GAGGACGATGACGAGATGCGCGCGAGCTTCAAAAGCAAGGCACTCGAATGATCTCTCAA 2393  
DB 2315 -----AGTCCACACGCTGCTGATTAAGTTTGCACACATTTCTCTCA-- 2356  
QY 2394 GGCATCGATGTTTTGTGTGTGAGACTGTGCTGGTGTGTTGTAATTTCAAGAGTGG 2453  
DB 2357 -----TCTGGAGTGTCAACCCCTTACTGATTAATCTGAAGAGATC 2397  
QY 2454 GTATGCTCATGCTGCTTGATGATCCCTTGTCGAGCTCTTCAATCAGCTGTGATGTC 2513  
DB 2398 GTGAATTAATGCTATGAGACCTTTTGTAGACTTACCATCATCTGATGCTGTCG 2457  
QY 2514 AACGAGATTCATGCGCAATGAGATCAACGATATGAACAAGAGATGGAACGGTGTCTC 2573  
DB 2458 AATAGCTATTATGAGCAATGAGACCATTCAGACCAACAGTTGGAACAGCTCTTG 2517  
QY 2574 AAGAGTGAACATAATTTCTTACCGCCACCTTTGCAATGAGGCGCAACCATAGCTAATG 2633  
DB 2518 GCGGTAGGAATCTGAGTGTCAACGGGATCTTCAACGGCGGAAATTTCTGAAGCTCA 2577  
QY 2634 GCGATGAGCCCAAGTACTATTTCCAGAGAGGCTGGAACATCTTCACTTATATGCTG 2633  
DB 2578 GCGATGAGCCCTCTATTTATTTCCAGAAAGGCTGGAACATTTTGAAGGATTAATGTC 2637  
QY 2694 GCGCTATGCTATGGAATGGAATCGAGCTGAGGCTGTCAGGCTCTGCTGATATGCTTCC 2753  
DB 2638 TCCCTCAGTTTAAAGAGAGTGAATGCTGCAATGAGGAGGCTCTCAGCTCGGCT 2697  
QY 2754 TTTGATTTGCTGCTGATTAACAATGCGCAAGTCTTGGCGCAACTTAATTTACTACT 2813  
DB 2698 TTTCCGATGCTCTCGAGTCTTGAAGTGCAGAGTCTGCGCAACCTGGAATGCTGATC 2757  
QY 2814 TCGATTAATGAGCAAGCGAGCGCTTTGGGTATCTGACATTTGATCTTTGATATC 2873  
DB 2758 AAGATCATCGGGAATCGCTGGGCTGCGCTGCGCAACCTGAGTCTGCGCATATC 2817  
QY 2874 ATCTTCAATCTTTGGGAGATGGAATGCACTGTTGGAAAGATTAATCATGA---TCAC 2930

DB 2818 GTCTTCAATCTTCCGCTGCTGAGTGAATGCACTGTTTGAAGAGATTACAGAGTGCCTC 2877  
QY 2931 AAGACCGCTTTCCGATGCGGACTCGCGCTGGAATTACCGACTTAATGACAGC 2990  
DB 2878 TGTAAGATCAACCAAGAGTGAAGTCCCGGCTGGGCAATGAACGACTCTTCCACTCC 2937  
QY 2991 TTTCAATGCTGTTCCGAGTCTCTGCGGAAATGATTCGATGCTCATGTGGGACTGCTG 3050  
DB 2938 TTTCTCATGCTTCCAGATGCTGTGGGAGTGAATGAGACCATGTGGGACTGCTG 2997  
QY 3051 TACG---GGCGATGCTCGTGCATTCCTTTCTTTGGCGCACCGTTGTGATCGGCAAT 3107  
DB 2998 GAGGTGCGCGCGCAGGCGATGCTCTATGTTCTTCAATGATGATGATGATGCGCAAC 3057  
QY 3108 CTGTGATCTTAACCTTTCTTATGCTGCTTTTGTCCAAATTTTGGCTCATAGCTTA 3167  
DB 3058 CTGGTGGTGTGAATTAATCTATCTGCTTGTGAGCTCTTCAAGCGAGAACCTG 3117  
QY 3168 TCAGCGCGGACTGCGGATTAACGATTAAGATTAATAATAGCCGAGGCTTCAATCGAATGGC 3227  
DB 3118 GCGGCAACAGACGAGCGGGAATGAACA----- 3149  
QY 3228 CGATTTAAAGTTGGGTAAAGCTAATATGCTGATGTTTCAAGTTAATAGTAACAA 3287  
DB 3150 ----- 3149  
QY 3288 TTGAACAATCAATTAAGTATCAACATCAAGTGAAGAGCAACCAAGATCATGTAAT 3347  
DB 3150 -----CTGCAATCTCATGATC 3168  
QY 3348 TGAAGCGAAGCATGCTGACACAAAGTGAAGTGGCGCGACGAGATCTTGGCGAC 3407  
DB 3169 CGGATCAAGAGGCGGCTGAGCCAGCAAGTGAAGTGAAGTGCAGGCTTCAATGCAAGCTCAC 3228  
QY 3408 GGCCTCAAGAGGAGATCAAGAGCAAGCAAGCACTGAGGAGTGCATCGGAGATCGG 3467  
DB 3229 TTCAAGAGCGGAGGAGGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3288  
QY 3468 ATGGAATTCAGATACACGCGGACATGAAGAACCAAGCGGAAGAAATCCAAATATCTA 3527  
DB 3289 AATGATGCGCAACCAACGCGGCTGATATCCACCGGAACGCGCACTTCCAGAGAAC 3348  
QY 3528 AATTAACGCAACGATATGAGCACTCAATTAACCAAGCAATGAGTGAACAGAG 3587  
DB 3349 GGGAAACGAACCAACAGGAGTGCAGAGCTGGAAGATGATCATCATGAGAGAGAC 3408  
QY 3588 CTAAACATAGAGTGTGCTTACAGAGCAAGCACTGCGACATTAATCTATATGCT 3647  
DB 3409 CACA-----TGTCTTCAATTAACAC-----CBAACCTGACGCTCGGCT 3449  
QY 3648 AGCCATAAGATCGACCATTCAGAGAGCAAGGCGCAAGGCGAGACGATGAG 3707  
DB 3450 GCCCATTTGCTGTGGGAGTCT-----GACTTGAAGAACCTCAACAGAGGATGTTAGC 3504  
QY 3708 GCGGAGGAAGCGCGGACGCGAGCAAGAGAGATTTAGTCTCGACGAGAACTGAGAG 3767  
DB 3505 AGCCAAATCAACCTTGAAGGAGCAAGATTA-----ACTGAGCAATACCAAGCTCTCA 3558  
QY 3768 GAGGCGAATGCGAGAGGCGCGCTGAGCGGTATCATTAATTAATGACAGAGAG 3827  
DB 3559 GAAGGAAGTACATCATGACATCAACCTGAGGTGGAAGAGTTCCCGTGAAGCAACCTGAG 3618  
QY 3828 GATTAATCTGATGAATATCAAGCTGATGCTGCCCGATTTGTAATTAAGAAATTTCCG 3887  
DB 3619 GAATACTTG-----ATCGGAGCGCTGCTTTAACAAGGTTGCGTCAAGCGTTCAAG 3672  
QY 3888 ATCTTACCGGTGACGATGCTGCGCTTCTGCGAAGATGCGGCAATTTACACTGA 3947  
DB 3673 TGCTGCGAGGTCAACATCGAGAGAGACTAGGCAAGTCTGAGTGAATTTGCGGAAAC 3732  
QY 3948 ACTTTCAATTAATGAATAATTAATTTGAACAGCTGTTATCATATGATTTATG 4007

Db 3733 TGGTTCATGTTGAGACAAATTGGTTGAGACCTTACATCTTCATGATTCGCTC 3792  
QY 4008 AGTAGCTTAGCTTTGGCATTTAGAAAGATGATCATCTGCCAAAGACCCTACTGACAGAT 4067  
Db 3793 AGCAGTGGGCGCCCTGGCTTTGAGGACATCTACATTTAGACAGAGAAACATCCGAC 3852  
QY 4068 ATTTTACTATATGACAGAAATATTTACGGTTATATCTTTGGAAAATGTTATCAAG 4127  
Db 3853 ATCTGAGATATCGGACAGAGTCTTCACTACATCTTCATCTGAGATGTTGCTCAAG 3912  
QY 4128 TGGTGGCGCTGGGCTTCAAGTGTACTTCAACGCGGTGGTGGCTGCATTTGCG 4187  
Db 3913 TGGACAGCTTACGGCTTCTGCAAGTCTTCAACAAAGCTGGTGTGACCTTCTC 3972  
QY 4188 ATGTGATGATGCTGCTTATCACTTCGTTCACTTCTGTTGAGCTGGTGTATCAA 4247  
Db 3973 ATTTGGCTGTCTCTTTAGTACGCTTATAGCTAATGCCCTGGGCTAATCGGAATAGGT 4032  
QY 4248 GCGTTCAAGATATGCGAAGGTTAAGACATGACACTACGTGCAATGTCCTGATG 4307  
Db 4033 GCCATTAAGTCCCTTAGGACCTTAAGAGCTTTGAGACCTTTAAGACCTTATCAGATTT 4092  
QY 4308 CAGGCGATGAGGTCCTGCTTATGGCGGTGTAACGCTATACCGTCAATCTCAATG 4367  
Db 4093 GAAGGATGAGGTTGGTGTGAATGCTTGGTGGCGCCATCCCTTCATCATGAATG 4152  
QY 4368 CTATGGTGTCTAATATTTGGCTAATTTTGGCATAATGGGTGATACGCTTTTGGCT 4427  
Db 4153 CTGCTGTGTCTCATCTTCTGCTGATTTTCAAGATCATGGAGTTAACCTGTTGG 4212  
QY 4428 GGAATAATTTTAAGTGC--GAGACATGAATGGCAGAGCTCAGCCACGAGATCAT 4484  
Db 4213 GGGAAATATCACCTACTGCTTTAATGAGACTTGAATCCGTTCCGAATGATATGTC 4272  
QY 4485 CCAATTCGAATGCTGCGAG-----AGCGAAGATCTACAGTGGGTG 4526  
Db 4273 AACATTAACGACATGTGAGAACTCATGAGGCGAAGCAGACAGATCCGATGGAAG 4332  
QY 4527 AATTGACGAATGAATTCGATGATGATGATGATGATGATGATGATGATGATGATG 4586  
Db 4333 AATGTCAAGATCACTTTGACATGTGAGAGGAGGATGCTGAGCTTTCTTCAAGTGGCA 4392  
QY 4587 ACCTTCAAGAGCTGATACAAATCATGATGATGATGATGATGATGATGATGATG 4646  
Db 4393 ACCTTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 4452  
QY 4647 CAACCAATTCGTGAAGGACATCTACATGATTTATTTATTTATTTATTTATTT 4706  
Db 4453 CAGCTTGAATCAAGAGGACATCTACATGATCTTATCTTATCTTATCTTATCTT 4512  
QY 4707 GGAATCTTTTCACTCAATCTGTTGATGTTGATGATGATGATGATGATGATG 4766  
Db 4513 GGGCTCTTCTTCACTCAATCTGTTGATGTTGATGATGATGATGATGATG 4572  
QY 4767 AAGAAAAAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 4826  
Db 4573 AAGAAAAA--GTTTGAAGGTGAGACATCTTCAATGACAGAGGACGAAAGATCTAC 4629  
QY 4827 AATGCTATGAAAAAGAGGTGCTTAATAAAACATTAAGGCAATTCGAAGACCAAGGTG 4886  
Db 4630 AATGCTATGAAAAAGGTGCTGCTCAAGAGGCAAGAGGCAAGGCAAGGCAAGG 4689  
QY 4887 CGACCAAGCAATGATCTTTGAAATGATGATGATGATGATGATGATGATGATG 4946  
Db 4690 AATATCAAGGAGTGTCTTGAATGTTGATGTTGATGATGATGATGATGATG 4749  
QY 4947 TTATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 5006  
Db 4750 ATGCTCATCTGCTTAACTGATGATGATGATGATGATGATGATGATGATGATG 4889  
QY 5007 TATACCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 5066  
Db 4810 ATGAGAAACATTTCTTACTGATGATGATGATGATGATGATGATGATGATG 4869

QY 5067 CTATTAATAATATTCGCTTTAAGATATCACTATTTTATTGAGCCATGGAATTTATGAT 5126  
Db 4870 GTGCTCAAAATATGTTGCTTGAAGACATATTTACCATTTGCTGGAACATCTTTAGC 4929  
QY 5127 GATGATGTTGATCTTTATTCATCTTATGATGATGATGATGATGATGATGATGATG 5186  
Db 4930 TTGATGATGATCTCTTCAATTTGATGATGATGATGATGATGATGATGATGATG 4989  
QY 5187 TTGATGATGATCTCTTCAATTTGATGATGATGATGATGATGATGATGATGATG 5246  
Db 4990 TTGATGATGATCTCTTCAATTTGATGATGATGATGATGATGATGATGATGATG 5049  
QY 5247 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5306  
Db 5050 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5109  
QY 5307 GCGCTGTTCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5366  
Db 5110 GCGCTGTTCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5169  
QY 5367 ATGTGTTCTTATGACATGATGATGATGATGATGATGATGATGATGATGATG 5426  
Db 5170 ATGTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 5229  
QY 5427 ACCTTGGCAGAGCATGATCTGCTCTTTCATGATGATGATGATGATGATGATG 5486  
Db 5230 ACATTTGGCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 5289  
QY 5487 GTACTGAGCGCATTAATCA-----TGAGAAAGATGCGATCAACCCAGACGAC 5537  
Db 5290 CTGCTGTGCAATCTGATCAACGCGCCCTGATGCTGATGATGATGATGATGATG 5349  
QY 5538 AAAGGCTATCGGCAATTTGATGATGATGATGATGATGATGATGATGATGATG 5597  
Db 5350 AGTGGCTTCAAGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATG 5409  
QY 5598 CTAGTTATGATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 5657  
Db 5410 ATCATATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 5469  
QY 5658 AGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5717  
Db 5470 AGGTGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5529  
QY 5718 GAGATCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5777  
Db 5530 GAGATCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5589  
QY 5778 GAATTCCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5837  
Db 5590 GACTTTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5649  
QY 5838 ATATGATGAGATCAATCTGATGATGATGATGATGATGATGATGATGATGATG 5897  
Db 5650 ATGCGATGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 5709  
QY 5898 GCGCTTACGAAGATCTTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5957  
Db 5710 GCGCTTACGAAGATCTTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5769  
QY 5958 GGTGAG-----ATAGCGGCGCGCGGATGATGATGATGATGATGATGATGATG 6011  
Db 5770 GAGAGGCGGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 5829  
QY 6012 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6071  
Db 5830 CTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5889  
QY 6072 AAGCGCGCGGCG 6084  
Db 5890 TTGCTAGGCGGG 5902

Tue May 10 12:01:09 2005

us-08-554-424-7.rng

Page 51

Search completed: May 9, 2005, 04:52:59  
Job time : 3212 secs

---

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 04:00:40 ; Search time 962 Seconds  
(without alignments)

11078.036 Million cell updates/sec

Title: US-08-554-424-7

Perfect score: 6513

Sequence: 1 TCTAGAGCTTGCCGCATAG.....ACGCGATTTAGCTCTAGA 6513

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6513	100.0	6513	1	US-08-338-702-7
2	6513	100.0	6513	1	US-08-337-339-7
3	6513	100.0	6513	1	US-08-724-095-7
4	6513	100.0	6513	5	PCT-US95-14262-7
5	6513	100.0	6513	5	PCT-US95-14378-7
6	6163.8	94.6	6519	2	US-08-808-793-24
7	5233.2	80.4	6519	2	US-07-998-289B-7
8	4447.8	68.3	6318	2	US-08-808-793-1
9	4447.8	68.3	6318	3	US-08-772-512A-1
10	4447.8	68.3	6318	4	US-09-428-371-1
11	4434.2	68.1	6315	2	US-08-808-793-2
12	4434.2	68.1	6315	3	US-08-772-512A-2
13	4434.2	68.1	6315	4	US-09-428-371-2
14	1021.4	15.7	6586	3	US-09-024-020B-43
15	1021.4	15.7	6586	3	US-09-425-043-43
16	1019.4	15.7	6007	3	US-09-024-020B-2
17	1019.4	15.7	6007	3	US-09-425-043-2
18	993	15.2	5977	3	US-09-024-020B-1
19	993	15.2	5977	3	US-09-425-043-1
20	993	15.2	6556	3	US-09-024-020B-7
21	993	15.2	6556	3	US-09-425-043-7
22	958.6	14.7	6826	3	US-09-024-020B-8
23	958.6	14.7	6826	3	US-09-425-043-8
24	944.8	14.5	7052	3	US-08-669-656A-5
25	940.2	14.4	6048	4	US-09-514-907A-1
26	940.2	14.4	6048	4	US-09-896-994-1
27	939.4	14.4	6048	3	US-09-634-920-3

28	939.4	14.4	6048	4	US-09-840-125-3	Sequence 3, Appli
29	927.8	14.2	6452	3	US-08-836-325-9	Sequence 9, Appli
30	927.8	14.2	6452	4	US-09-457-571-9	Sequence 9, Appli
31	921.2	14.1	6882	4	US-09-949-016-4205	Sequence 4205, Ap
32	904	13.9	6332	4	US-09-949-016-5117	Sequence 5117, Ap
33	899.8	13.8	6404	3	US-08-836-325-14	Sequence 14, Appl
34	899.8	13.8	6404	4	US-09-457-571-14	Sequence 14, Appl
35	880	13.5	6344	3	US-08-843-417-1	Sequence 1, Appli
36	880	13.5	6344	4	US-09-527-013-1	Sequence 1, Appli
37	878.4	13.5	6527	3	US-08-669-656A-7	Sequence 1, Appli
38	873.6	13.4	6524	3	US-08-669-656A-1	Sequence 1, Appli
39	870.6	13.4	6348	4	US-09-976-594-756	Sequence 756, App
40	870.6	13.4	6348	4	US-09-919-039-366	Sequence 366, App
41	870.6	13.4	6371	3	US-08-836-325-13	Sequence 13, Appl
42	870.6	13.4	6371	4	US-09-457-571-13	Sequence 13, Appl
43	837.4	12.9	5874	4	US-08-843-417-9	Sequence 9, Appli
44	837.4	12.9	5874	4	US-09-527-013-9	Sequence 9, Appli
45	696.2	10.7	3033	3	US-08-836-325-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1

US-08-338-702-7

Sequence 7, Application US/08338702

Patent No. 5550049

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: PARA SODIUM CHANNEL

ADDRESSEE: John W. Wallen III

STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,702

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wallen III, John W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 19338

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6513 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-338-702-7

Query Match 100.0%; Score 6513; DB 1; Length 6513;

Best local similarity 100.0%; Pred. No. 0;

Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTAGAGCTTGCCGCATAGCAATGACAGAAAGTTCGACTCATATCTGAGGAAGAC 60  
DB 1 TCTAGAGCTTGCCGCATAGCAATGACAGAAAGTTCGACTCATATCTGAGGAAGAC 60

QY 61 GCAGTTGTTCCGTCCTTACCCGCGAATCATTTGTGCAATCGAACAACGATTTGCCG 120  
| | | | |  
Db 61 GCAGTTGTTCCGTCCTTACCCGCGAATCATTTGTGCAATCGAACAACGATTTGCCG 120  
| | | | |  
QY 121 CTGAACATGAAAAGCAGAAAGAGCTGGAAAAGAAAGAGCCGAGAGAGTCCCGCAT 180  
| | | | |  
Db 121 CTGAACATGAAAAGCAGAAAGAGCTGGAAAAGAAAGAGCCGAGAGAGTCCCGCAT 180  
| | | | |  
QY 181 ATGTGCGCAAGAAAAAACAAGAAATCCGATATGATGAAGAGACGAGATGAAGATC 240  
| | | | |  
Db 181 ATGTGCGCAAGAAAAAACAAGAAATCCGATATGATGAAGAGACGAGATGAAGATC 240  
| | | | |  
QY 241 CACAAACCGATCTCACTTGAACAGGTTGCCAATACCTGTTCCATTTGCAAGGCGACT 300  
| | | | |  
Db 241 CACAAACCGATCTCACTTGAACAGGTTGCCAATACCTGTTCCATTTGCAAGGCGACT 300  
| | | | |  
QY 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
| | | | |  
Db 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
| | | | |  
QY 361 TGACATTCGTAGTTGTAAGCAAGAAAGATAATTTTCGCTTTTCTGCAATCAAAAGCAA 420  
| | | | |  
Db 361 TGACATTCGTAGTTGTAAGCAAGAAAGATAATTTTCGCTTTTCTGCAATCAAAAGCAA 420  
| | | | |  
QY 421 TGTGATGCTCGATCCATTCGATCCGATACGTCGTGTGCGCAATTTACATTTCTAGTGCATC 480  
| | | | |  
Db 421 TGTGATGCTCGATCCATTCGATCCGATACGTCGTGTGCGCAATTTACATTTCTAGTGCATC 480  
| | | | |  
QY 481 CATTTATTTCCCTATTCATTCATCCACCAATTCCTGCAATGCGATCCTGATGATATGC 540  
| | | | |  
Db 481 CATTTATTTCCCTATTCATTCATCCACCAATTCCTGCAATGCGATCCTGATGATATGC 540  
| | | | |  
QY 541 CGAACACGCCACCGGTTGAGTCCACTGAGTGATATTCACCGAATCTTACCATTTGGAAT 600  
| | | | |  
Db 541 CGAACACGCCACCGGTTGAGTCCACTGAGTGATATTCACCGAATCTTACCATTTGGAAT 600  
| | | | |  
QY 601 CAGCTGTAAGTGAAGAGAGAGAGTTCATTTATAGCCGTTTACGATCTTAGAGATG 660  
| | | | |  
Db 601 CAGCTGTAAGTGAAGAGAGAGTTCATTTATAGCCGTTTACGATCTTAGAGATG 660  
| | | | |  
QY 661 CATGAAATTTGGCTGAGCTTCTGTAATAGCTTTAGCTTATGTAACATGGGATATGATT 720  
| | | | |  
Db 661 CATGAAATTTGGCTGAGCTTCTGTAATAGCTTTAGCTTATGTAACATGGGATATGATT 720  
| | | | |  
QY 721 TAGGTAATCTAGACCCCTGCGAAGCTTTAGGGTCTGCGAGCCCTTAAACCGTATGCCA 780  
| | | | |  
Db 721 TAGGTAATCTAGACCCCTGCGAAGCTTTAGGGTCTGCGAGCCCTTAAACCGTATGCCA 780  
| | | | |  
QY 781 TTGTCGACAGCTTGAAGACATCGTCGGCGCCGTCATCGAATCGGTGAAGATCTGCGCG 840  
| | | | |  
Db 781 TTGTCGACAGCTTGAAGACATCGTCGGCGCCGTCATCGAATCGGTGAAGATCTGCGCG 840  
| | | | |  
QY 841 ATGTGATTAATCTGACCATGTTCTCCCTGTGCGATGTTGCGCGTTATGGGCTTACAGATCT 900  
| | | | |  
Db 841 ATGTGATTAATCTGACCATGTTCTCCCTGTGCGATGTTGCGCGTTATGGGCTTACAGATCT 900  
| | | | |  
QY 901 ATATAGGCGCTCTCAACCGAAGATGCAATCAAGAAAGTTCCGCTGACGCTTCTGCGGCA 960  
| | | | |  
Db 901 ATATAGGCGCTCTCAACCGAAGATGCAATCAAGAAAGTTCCGCTGACGCTTCTGCGGCA 960  
| | | | |  
QY 961 ATTCGACCGAGAGAACTGGAGCTATCACAATCGCAATAGCTCAATTTGATTTCCGAGG 1020  
| | | | |  
Db 961 ATTCGACCGAGAGAACTGGAGCTATCACAATCGCAATAGCTCAATTTGATTTCCGAGG 1020  
| | | | |  
QY 1021 ACGAGGGGATCTCAATTTCCGTTATGCGGCAATATATTCGGTGGCGGCAATGCAACGACG 1080  
| | | | |  
Db 1021 ACGAGGGGATCTCAATTTCCGTTATGCGGCAATATATTCGGTGGCGGCAATGCAACGACG 1080  
| | | | |  
QY 1081 ATTATGCTGTGCTGAGAGGGTTTGTCCGGAATCCGAATTAATGCTACACGAGCTTCGATT 1140  
| | | | |  
Db 1081 ATTATGCTGTGCTGAGAGGGTTTGTCCGGAATCCGAATTAATGCTACACGAGCTTCGATT 1140  
| | | | |  
QY 1141 CGTTGCGATGGGCTTTCTGTCCGCTTCCGCGTGATGACACAGGACTTCTGCGAGGATC 1200  
| | | | |

Db 1141 CGTTGCGATGGGCTTTCTGTCCGCTTCCGCGTGATGACACAGACCTTCTGGAGATC 1200  
| | | | |  
QY 1201 TGTACAGCTGTGTGTGCGCGCGCGCGACATGCGACATGCTGTTCTTTATATGATCA 1260  
| | | | |  
Db 1201 TGTACAGCTGTGTGTGCGCGCGCGCGACATGCGACATGCTGTTCTTTATATGATCA 1260  
| | | | |  
QY 1261 TCTTCTAGTTCATTTCTATCTTTGGAATTTGATTTTGGCCATTTGGCATGCTGATG 1320  
| | | | |  
Db 1261 TCTTCTAGTTCATTTCTATCTTTGGAATTTGATTTTGGCCATTTGGCATGCTGATG 1320  
| | | | |  
QY 1321 ACGAATTCGAAGAAAGAGCCGAAGAAAGAGAGGCTGCCGAAGAGAGGCGATACGGAAG 1380  
| | | | |  
Db 1321 ACGAATTCGAAGAAAGAGCCGAAGAAAGAGAGGCTGCCGAAGAGAGGCGATACGGAAG 1380  
| | | | |  
QY 1381 CGGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
| | | | |  
Db 1381 CGGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCGCAGGCTC 1440  
| | | | |  
QY 1441 AGGACAGACGATGCGGCTGCGCGGAGAGAGGCTGCACTGATCCGGAATGGCCAGAC 1500  
| | | | |  
Db 1441 AGGACAGACGATGCGGCTGCGCGGAGAGAGGCTGCACTGATCCGGAATGGCCAGAC 1500  
| | | | |  
QY 1501 GTCCGACGATTTCTTGCATCAGCTATGAGCTATTTGTTGGCGCGGAGAAAGGCGACGATG 1560  
| | | | |  
Db 1501 GTCCGACGATTTCTTGCATCAGCTATGAGCTATTTGTTGGCGCGGAGAAAGGCGACGATG 1560  
| | | | |  
QY 1561 ACAACAAACAAGAAAGATGTCATTCGAGAGCTGCGAGCTGAGAGTCCGTGAGAGG 1620  
| | | | |  
Db 1561 ACAACAAACAAGAAAGATGTCATTCGAGAGCTGCGAGAGTCCGTGAGAGG 1620  
| | | | |  
QY 1621 TTATACAAAGACCAACGAGACCTACCAAGACGACACCAAGCTACCAAGTTCTGTAAGTGA 1680  
| | | | |  
Db 1621 TTATACAAAGACCAACGAGACCTACCAAGACGACACCAAGCTACCAAGTTCTGTAAGTGA 1680  
| | | | |  
QY 1681 GCAAGCATTCCTTATCTTAACTGTTCAACGTTTAACTATGCGAGGGGATACGTAAGTT 1740  
| | | | |  
Db 1681 GCAAGCATTCCTTATCTTAACTGTTCAACGTTTAACTATGCGAGGGGATACGTAAGTT 1740  
| | | | |  
QY 1741 CTGACAAATGACAGATACGGAACGGAAGGAGCGGCTTGGATACCGGGATGAGATCGTA 1800  
| | | | |  
Db 1741 CTGACAAATGACAGATACGGAACGGAAGGAGCGGCTTGGATACCGGGATGAGATCGTA 1800  
| | | | |  
QY 1801 AGCCATTTGATTTGTGAACATATCAGATGCGCAGAGACTTGCCTTATGCCAGACT 1860  
| | | | |  
Db 1801 AGCCATTTGATTTGTGAACATATCAGATGCGCAGAGACTTGCCTTATGCCAGACT 1860  
| | | | |  
QY 1861 CGAATGCGCTGACCCGATGTCGAAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920  
| | | | |  
Db 1861 CGAATGCGCTGACCCGATGTCGAAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920  
| | | | |  
QY 1921 GCAATGAGGCTCCGACACTCATGCTATACCTGAGTACGTCGGAATTCGATATCT 1980  
| | | | |  
Db 1921 GCAATGAGGCTCCGACACTCATGCTATACCTGAGTACGTCGGAATTCGATATCT 1980  
| | | | |  
QY 1981 CACATGCGATCTACTCGCGGAGATGCGCGCTCATGAGCGCTCAGACAAATGACCAAGAGA 2040  
| | | | |  
Db 1981 CACATGCGATCTACTCGCGGAGATGCGCGCTCATGAGCGCTCAGACAAATGACCAAGAGA 2040  
| | | | |  
QY 2041 GCAAAATGGCGCAACCGCAACACGCAATATATCAAGTGGGCGCACAAATGGGCGACCA 2100  
| | | | |  
Db 2041 GCAAAATGGCGCAACCGCAACACGCAATATATCAAGTGGGCGCACAAATGGGCGACCA 2100  
| | | | |  
QY 2101 CCGTCTGAGACCAATCAACAAGCTGATGCTGCGACTGAGAAATTTGCGTGGAGTGA 2160  
| | | | |  
Db 2101 CCGTCTGAGACCAATCAACAAGCTGATGCTGCGACTGAGAAATTTGCGTGGAGTGA 2160  
| | | | |  
QY 2161 CGAGCGAAGCTGCGCAAGATTTAAACATCATGACATCTTTATGAGCCCGTCCAGACAC 2220  
| | | | |  
Db 2161 CGAGCGAAGCTGCGCAAGATTTAAACATCATGACATCTTTATGAGCCCGTCCAGACAC 2220  
| | | | |  
QY 2221 AAACGGTGTGTTGATATGAAGATGATGCTCTGAAATGACATCATCGAACAAGCGCGCTG 2280  
| | | | |

Db	2221	AAACGGTGGTTGATATGAAAGATGTGATGTCCTGAAATGACATCATCGAACGCGCGCTG	2280
Qy	2281	GTCCGCAACGTCCGGCAAGCGATCGCGGTGTCTCCGTTACTATTCCCAACAGAGGACG	2340
Db	2281	GTCCGCAACGTCCGGCAAGCGATCGCGGTGTCTCCGTTACTATTCCCAACAGAGGACG	2340
Qy	2311	ATGACGAGGATGGGCGGACGTTCAAAAGACAGGCACTGAAAGTGATCTTCAAGGCATCG	2400
Db	2311	ATGACGAGGATGGGCGGACGTTCAAAAGACAGGCACTGAAAGTGATCTTCAAGGCATCG	2400
Qy	2401	ATGCGTTTGTGTGTGGGACCTGTGCTGGTGTGGTTGTAATTTACAGAGTGGGTATCG	2460
Db	2401	ATGCGTTTGTGTGTGGGACCTGTGCTGGTGTGGTTGTAATTTACAGAGTGGGTATCG	2460
Qy	2461	TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATACGCTGTCATTTGTGTCAACAGCA	2520
Db	2461	TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATACGCTGTCATTTGTGTCAACAGCA	2520
Qy	2521	TGTTTCATGGCAATGAGATCACACGATATGAAACAGAGATGGAACGCGTGTCAAGAGTG	2580
Db	2521	TGTTTCATGGCAATGAGATCACACGATATGAAACAGAGATGGAACGCGTGTCAAGAGTG	2580
Qy	2581	GCAACTATTTTCTTCAACCGCCACCTTTGGCATCGAGGCCACCATGAAAGTTATGGCCATGA	2640
Db	2581	GCAACTATTTTCTTCAACCGCCACCTTTGGCATCGAGGCCACCATGAAAGTTATGGCCATGA	2640
Qy	2641	GCCCCAATGATCATTTTCAGAGAGGGCTGGAAACATTTTGACCTTCATTCGTGGCCCAT	2700
Db	2641	GCCCCAATGATCATTTTCAGAGAGGGCTGGAAACATTTTGACCTTCATTCGTGGCCCAT	2700
Qy	2701	CGCTAATTGGAACGTGGACTCGAGGGGTGTCAGAGGTCTGTCCGTATTTGCGTTCCTTGCGAT	2760
Db	2701	CGCTAATTGGAACGTGGACTCGAGGGGTGTCAGAGGTCTGTCCGTATTTGCGTTCCTTGCGAT	2760
Qy	2761	TGCTGCGCGTATTCAAACTGTGGCCAAAGTCTTGGCCCACTTAATTTACTCATTTGCATTA	2820
Db	2761	TGCTGCGCGTATTCAAACTGTGGCCAAAGTCTTGGCCCACTTAATTTACTCATTTGCATTA	2820
Qy	2821	TGGGACGACCAATGGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTATCATCTTCA	2880
Db	2821	TGGGACGACCAATGGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTATCATCTTCA	2880
Qy	2881	TCTTTGCGGTATGGGAATGCAACTGTTCGAAAAAATTTATCATGATCACAAGAACCGCT	2940
Db	2881	TCTTTGCGGTATGGGAATGCAACTGTTCGAAAAAATTTATCATGATCACAAGAACCGCT	2940
Qy	2941	TTCCGGAATGGGACCTGCGCGCTGGAACTTACCGACTTATGACACAGCTTACTGATATCG	3000
Db	2941	TTCCGGAATGGGACCTGCGCGCTGGAACTTACCGACTTATGACACAGCTTACTGATATCG	3000
Qy	3001	TGTTCCGGGTGCTCTGCGGAAATGGAATCGAGTCCATGTGGACCTGACATGACGTGGGCG	3060
Db	3001	TGTTCCGGGTGCTCTGCGGAAATGGAATCGAGTCCATGTGGACCTGACATGACGTGGGCG	3060
Qy	3061	ATGTCTCGTGATTTCCCTTCTTCTTGGGCAACGTTGTCACTGGGCAATCTTGTGGTACTTA	3120
Db	3061	ATGTCTCGTGATTTCCCTTCTTCTTGGGCAACGTTGTCACTGGGCAATCTTGTGGTACTTA	3120
Qy	3121	ACCTTTTCTTAGCCTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180
Db	3121	ACCTTTTCTTAGCCTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180
Qy	3181	CCGATTAACGAATACGAATTAATAATAGCCGAGGCTTCATTCGAATTGGCCGATTTTAAAGTT	3240
Db	3181	CCGATTAACGAATACGAATTAATAATAGCCGAGGCTTCATTCGAATTGGCCGATTTTAAAGTT	3240
Qy	3241	GGGTTAAGCGTAAATTTGCTGATTTGTTCAAGTTAAATCGTAACAAATTTGACAAATCAAA	3300
Db	3241	GGGTTAAGCGTAAATTTGCTGATTTGTTCAAGTTAAATCGTAACAAATTTGACAAATCAAA	3300
Qy	3301	TAACTGATCAACCATCAGGTAGAGAGAACCAACAGATCACGTTGATTTGGAGCAAGAGC	3360
Db	3301	TAACTGATCAACCATCAGGTAGAGAGAACCAACAGATCACGTTGATTTGGAGCAAGAGC	3360

QY	3351	ATGCTGCAACAGAACTGGAAGCTGGGCCACGACGAGATCTCTGGCCGAGCGCTCATGAAGA	3420
Db	3361	ATGGTGAACAAGAACTGGAAGCTGGGCCACGACGAGATCTCTGGCCGAGCGCTCATGAAGA	3420
QY	3421	AGGGGATCAAGAGACACAGCCAACTGAGAGTGGCCATCGGGGATCGGATGGAATTCCGA	3480
Db	3421	AGGGGATCAAGAGACACAGCCAACTGAGAGTGGCCATCGGGGATCGGATGGAATTCCGA	3480
QY	3481	TACACGGCGCATGAGAAACAAGCCGGAAGAAATCTAAATATCTTAATATACGCAACGA	3540
Db	3481	TACACGGCGCATGAGAAACAAGCCGGAAGAAATCTAAATATCTTAATATACGCAACGA	3540
QY	3541	TGATTTGGCAACTCAATTAACCAACCAACAATTAAGTACGTGAAACAACGAGCTTAACCATAGAG	3600
Db	3541	TGATTTGGCAACTCAATTAACCAACCAACAATTAAGTACGTGAAACAACGAGCTTAACCATAGAG	3600
QY	3601	GTATTGTCTTACAGAGACGACGACACTGCCAGACTTAATCTATATGGTAGCCATPAAGATTC	3660
Db	3601	GTATTGTCTTACAGAGACGACGACACTGCCAGACTTAATCTATATGGTAGCCATPAAGATTC	3660
QY	3661	GACCATTTCAAGAGACGAGGCCACAAAGGGCAGCGCCGAGACGATGAGAGGGCGAGAGAAAC	3720
Db	3661	GACCATTTCAAGAGACGAGGCCACAAAGGGCAGCGCCGAGAGCAGATGAGAGGGCGAGAGAAAC	3720
QY	3721	GCGACGCGCAGCAAGAGAGATTTTAAAGTCTCGACAGAGAACTCGACGAGACGGCGGAATGCG	3780
Db	3721	GCGACGCGCAGCAAGAGAGATTTTAAAGTCTCGACAGAGAACTCGACGAGACGGCGGAATGCG	3780
QY	3781	AGGAGGGCCGCTCGACGCGTGATATCAATTAATTCATGCAACGACAGAGAGATATCTCGATG	3840
Db	3781	AGGAGGGCCGCTCGACGCGTGATATCAATTAATTCATGCAACGACAGAGAGATATCTCGATG	3840
QY	3841	AATATTCAGCGCATATGCTGCGCCCGAATTCGATACATATPAAGAAATTTCCGATTTPAACCGGATG	3900
Db	3841	AATATTCAGCGCATATGCTGCGCCCGAATTCGATACATATPAAGAAATTTCCGATTTPAACCGGATG	3900
QY	3901	ACGATGACCTCGCCGCTTCTGCGCAAGAGATGGGGCAATTTACGACTGAAACCTTTTCAATTAA	3960
Db	3901	ACGATGACCTCGCCGCTTCTGCGCAAGAGATGGGGCAATTTACGACTGAAACCTTTTCAATTAA	3960
QY	3961	TTTGAATTAATATATTTTGAACAACAGCTGTATTCATCTATGATTTTAAATGAGTAGCTTAGCTT	4020
Db	3961	TTTGAATTAATATATTTTGAACAACAGCTGTATTCATCTATGATTTTAAATGAGTAGCTTAGCTT	4020
QY	4021	TGCGATTAGAAGATGTATCTCTGCAACAAGACCCCATCTGCAAGATATTTTATCTATA	4080
Db	4021	TGCGATTAGAAGATGTATCTCTGCAACAAGACCCCATCTGCAAGATATTTTATCTATA	4080
QY	4081	TGACACAGAAATATTTACGGTTATATTTCTTCTTGGAAAATGTTAATCAAGTGGTGGCGCTCG	4140
Db	4081	TGACACAGAAATATTTACGGTTATATTTCTTCTTGGAAAATGTTAATCAAGTGGTGGCGCTCG	4140
QY	4141	GCTTCAAAAGTATCTTACCAAGCGCGGTGGTGGCTCCGATTTTCGATATGTCATAGGTAT	4200
Db	4141	GCTTCAAAAGTATCTTACCAAGCGCGGTGGTGGCTCCGATTTTCGATATGTCATAGGTAT	4200
QY	4201	CGCTTATCAACTTCGTGCTTCACTTGTGGAAGCTGGTGTATTAAGCCTTCAAGACTA	4260
Db	4201	CGCTTATCAACTTCGTGCTTCACTTGTGGAAGCTGGTGTATTAAGCCTTCAAGACTA	4260
QY	4261	TGCGAATGTTAAGACACTGAGACCACTACGTGCAATGTCCTGATATGACGGGCACTGAGGG	4320
Db	4261	TGCGAATGTTAAGACACTGAGACCACTACGTGCAATGTCCTGATATGACGGGCACTGAGGG	4320
QY	4321	TTCGTCGTTAATGCGCTGTACAAAGCTATACCGTCCATCTTCAATGTGCTAATTTGGTGTGTC	4380
Db	4381	TAAATATTTGGCTAATTTTTCGCAATATGGGTGTACAGCTTTTTCGCGAAAAATATTTTA	4440
QY	4381	TAAATATTTGGCTAATTTTTCGCAATATGGGTGTACAGCTTTTTCGCGAAAAATATTTTA	4440

4441 AGTCCAGGACATGATGCGACGAACTGACGCAAGATCATACCAATCCGATGCT 4500  
4441 AGTCCAGGACATGATGCGACGAACTGACGCAAGATCATACCAATCCGATGCT 4500  
4501 GCGAGAGGAGAACTACAGTGGGTGATTCAGCAATGATTCATGATGATGACG 4560  
4501 GCGAGAGGAGAACTACAGTGGGTGATTCAGCAATGATTCATGATGATGACG 4560  
4561 CGTATGTCCTCTTCCAAAGTGGCCACTTCAAAAGCTGATACAAATCATGAAGATG 4620  
4561 CGTATGTCCTCTTCCAAAGTGGCCACTTCAAAAGCTGATACAAATCATGAAGATG 4620  
4621 CATGATTCACGAGAGGTGAGCAAGCAACCAATGCTGAAAGCAATCATGATGAT 4680  
4621 CATGATTCACGAGAGGTGAGCAAGCAACCAATGCTGAAAGCAATCATGATGAT 4680  
4681 TATATTCGATTCCTCATCATATTTGGATCCCTTTTCACTCAATCTGTCATGATG 4740  
4681 TATATTCGATTCCTCATCATATTTGGATCCCTTTTCACTCAATCTGTCATGATG 4740  
4741 TATATTCGATTCCTCATCATATTTGGATCCCTTTTCACTCAATCTGTCATGATG 4800  
4741 TATATTCGATTCCTCATCATATTTGGATCCCTTTTCACTCAATCTGTCATGATG 4800  
4801 TGAAGAGATCGAAGAAAGTACTATATGCTATGAAAGATGGGCTCTAAAGCCAT 4860  
4801 TGAAGAGATCGAAGAAAGTACTATATGCTATGAAAGATGGGCTCTAAAGCCAT 4860  
4861 TAAAGCCATTCGAAAGCAAGGTGGGACACAGCAATAGCTTTGAAATGATACG 4920  
4861 TAAAGCCATTCGAAAGCAAGGTGGGACACAGCAATAGCTTTGAAATGATACG 4920  
4921 AATAAGAAATCGATATATATATGATGATGATGATGATGATGATGATGATGATG 4980  
4921 AATAAGAAATCGATATATATGATGATGATGATGATGATGATGATGATGATGATG 4980  
4981 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
4981 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
5041 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100  
5041 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5100  
5101 TTAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
5101 TTAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
5161 TACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
5161 TACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
5221 TGGGAGAAAGTGGGCGGTGCTTCCGATGATGATGATGATGATGATGATGATGATG 5280  
5221 TGGGAGAAAGTGGGCGGTGCTTCCGATGATGATGATGATGATGATGATGATGATG 5280  
5281 TCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
5281 TCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
5341 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
5341 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5400  
5401 GCATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
5401 GCATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5460  
5461 TGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
5461 TGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
5521 ATCCACCGGACGAGCAAAAGGCTATCCGGGCAATGATGATGATGATGATGATGATG 5580

5521 ATCCACCGGACGAGCAAAAGGCTATCCGGGCAATGATGATGATGATGATGATGATG 5580  
5581 CGTTTCTCTCTCACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 5640  
5581 CGTTTCTCTCTCACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 5640  
5641 TCAATCTGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
5641 TCAATCTGAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5700  
5701 ACTAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
5701 ACTAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
5821 CGAAGAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
5821 CGAAGAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
5881 GGTGCACTCTCTGACGCTTACGAAAGACTCTTTTGGGAGAGGCAATCCGATG 5940  
5881 GGTGCACTCTCTGACGCTTACGAAAGACTCTTTTGGGAGAGGCAATCCGATG 5940  
5941 AGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
5941 AGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
6001 TCTCATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
6001 TCTCATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
6061 GGGAGAGGCAAGAGGCGCGGAGAGAGGATGATGATGATGATGATGATGATGATG 6120  
6061 GGGAGAGGCAAGAGGCGCGGAGAGAGGATGATGATGATGATGATGATGATGATG 6120  
6121 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
6121 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
6181 CGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
6181 CGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
6241 AGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
6241 AGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
6301 CGCGGCGGCGGAGAGAGAGGATGATGATGATGATGATGATGATGATGATGATG 6360  
6301 CGCGGCGGCGGAGAGAGAGGATGATGATGATGATGATGATGATGATGATGATG 6360  
6361 CGCGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6420  
6361 CGCGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6420  
6421 ACTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
6421 ACTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
6481 CCCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540  
6481 CCCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540

RESULT 2  
US-08-337-339-7  
Sequence 7, Application US/08337339  
Patent No. 5593864  
GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.  
APPLICANT: Hall, Linda  
APPLICANT: Feng, Gouping  
APPLICANT: Van Der Ploeg, Leonardus  
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
TITLE OF INVENTION: PARA SODIUM CHANNEL  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: John W. Wallen III  
STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,339  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen III, John W.  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 19332  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6513 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-337-339-7

Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGAGCTTGGCCGCGATGACATGACAGAAATTCGATCTCATATCTGAGGAAGAC 60  
DB 1 TCTGAGCTTGGCCGCGATGACATGACAGAAATTCGATCTCATATCTGAGGAAGAC 60  
QY 61 GCAATTTGTTCCGTCCTTTACCGCGCAATCATTGGTGCAATGGAACAACGCAATTGCG 120  
DB 61 GCAATTTGTTCCGTCCTTTACCGCGCAATCATTGGTGCAATGGAACAACGCAATTGCG 120  
QY 121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAAAGAGCCGAGGAGAGGTGCGCGAT 180  
DB 121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAAAGAGCCGAGGAGAGGTGCGCGAT 180  
QY 181 ATGTGCGCAGAAAAAACAAGAAATCCGATATGATGACAGAGAGAGATGAGGTC 240  
DB 181 ATGTGCGCAGAAAAAACAAGAAATCCGATATGATGACAGAGAGAGATGAGGTC 240  
QY 241 CACAACCGGATCTTACCTTGAACAGAGGTGCGCAATTCCTGTTGATTTGAGGGGAGCT 300  
DB 241 CACAACCGGATCTTACCTTGAACAGAGGTGCGCAATTCCTGTTGATTTGAGGGGAGCT 300  
QY 301 TCCGCGCGAATTTGGCTCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
DB 301 TCCGCGCGAATTTGGCTCTCACTCTCTCGAGATATCGATCCCTACTACAGCAATGTAC 360  
QY 361 TGAATTCGTATGTTGAAGCAAGAAAGATATTTTTCGTTTTCGATCAAAAGCAA 420  
DB 361 TGAATTCGTATGTTGAAGCAAGAAAGATATTTTTCGTTTTCGATCAAAAGCAA 420  
QY 421 TGTGATGCTCGATCGATTCATCGATAGCTCGTGTGGCCATTACCTTAGTGATC 480  
DB 421 TGTGATGCTCGATCGATTCATCGATAGCTCGTGTGGCCATTACCTTAGTGATC 480

DB 421 TGTGATGCTCGATCGATTCATCGATAGCTCGTGTGGCCATTACCTTAGTGATC 480  
QY 481 CATATTTTCCCTATTTATCATCATCCACAAATTTCTGTCATGATCTGTATGATATGC 540  
DB 481 CATATTTTCCCTATTTATCATCATCCACAAATTTCTGTCATGATCTGTATGATATGC 540  
QY 541 CGACAAGCCCAAGGTTGAGTCCACTGAGGTATTTACCGGAATCTACACATTTGAAT 600  
DB 541 CGACAAGCCCAAGGTTGAGTCCACTGAGGTATTTACCGGAATCTACACATTTGAAT 600  
QY 601 CAGCTGTTAAAGTATGAGCAAGAGTTTCAATTTATGCGCGTTTACGTATTTAGATG 660  
DB 601 CAGCTGTTAAAGTATGAGCAAGAGTTTCAATTTATGCGCGTTTACGTATTTAGATG 660  
QY 661 CATGAAATTTGGCTGACCTTGTAGTAATAGCTTTAGCTTTATGTATGACATGGGTATGATT 720  
DB 661 CATGAAATTTGGCTGACCTTGTAGTAATAGCTTTAGCTTTATGTATGACATGGGTATGATT 720  
QY 721 TAGGTAATCTAGCAGCCCTGCGAAGCTTTAGGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780  
DB 721 TAGGTAATCTAGCAGCCCTGCGAAGCTTTAGGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780  
QY 781 TTGTGCGAGGCTTGAAGACCATGTCGAGCGCCGTATCATGATCGATGAGATCTGCGCG 840  
DB 781 TTGTGCGAGGCTTGAAGACCATGTCGAGCGCCGTATCATGATCGATGAGATCTGCGCG 840  
QY 841 ATGTGATTTATCTGACATGTTCTCTGTCGTGTTGCGGTTGATGGGCTTACAGATCT 900  
DB 841 ATGTGATTTATCTGACATGTTCTCTGTCGTGTTGCGGTTGATGGGCTTACAGATCT 900  
QY 901 AATAGGGCGGTCTACCGAGAGAGCATCAAGAGTTCCGCTGAGCGGTTCCGAGGCA 960  
DB 901 AATAGGGCGGTCTACCGAGAGAGCATCAAGAGTTCCGCTGAGCGGTTCCGAGGCA 960  
QY 961 ATCTGACCGACGAGAACTGGGACTATCAATCGCAATAGCTCCAAATTTGATTTCCAGG 1020  
DB 961 ATCTGACCGACGAGAACTGGGACTATCAATCGCAATAGCTCCAAATTTGATTTCCAGG 1020  
QY 1021 ACGAGGSCATCTCAATTTCCGTTATGCGGCAATATATCCGAGCGGAGCAATGCGACGCG 1080  
DB 1021 ACGAGGSCATCTCAATTTCCGTTATGCGGCAATATATCCGAGCGGAGCAATGCGACGCG 1080  
QY 1081 ATTACGTCGTCGACAGGGGTTGGTCCGAATCCGATTTATAGCTTACACGAGCTTCATT 1140  
DB 1081 ATTACGTCGTCGACAGGGGTTGGTCCGAATCCGATTTATAGCTTACACGAGCTTCATT 1140  
QY 1141 CGTTGCGATGGGCTTCTCTGTCGCTTCGCGCTGATGACACAGGACTTCTGGGAGGATC 1200  
DB 1141 CGTTGCGATGGGCTTCTCTGTCGCTTCGCGCTGATGACACAGGACTTCTGGGAGGATC 1200  
QY 1201 TGTACAGCTGTGTGTCGCGCGCGGACCATGACATGCTGTTCTTTATAGTCATCA 1260  
DB 1201 TGTACAGCTGTGTGTCGCGCGCGGACCATGACATGCTGTTCTTTATAGTCATCA 1260  
QY 1261 TCTTCCTAGGTTCAATTTATCTTGTGAATTTGATTTGGCATTTGGCATGTCGATG 1320  
DB 1261 TCTTCCTAGGTTCAATTTATCTTGTGAATTTGATTTGGCATTTGGCATGTCGATG 1320  
QY 1321 ACGAATTTGCAAGAGAGCGGAGAGAAAGAGGCTGCGAAGAGAGAGCGCATAGCTGAAG 1380  
DB 1321 ACGAATTTGCAAGAGAGCGGAGAGAAAGAGGCTGCGAAGAGAGAGCGCATAGCTGAAG 1380  
QY 1381 CGAAGAAAGCTGCGCGCGCAAGAGCGCAAGCTGAGAGAGCGGCAATGCGAGGCTC 1440  
DB 1381 CGAAGAAAGCTGCGCGCGCAAGAGCGCAAGCTGAGAGAGCGGCAATGCGAGGCTC 1440  
QY 1441 AGGCAAGAGCGGATGCGGCTGCGCGCAAGAGGCTGACCTGCAATCCGGAATGGCCAAAG 1500  
DB 1441 AGGCAAGAGCGGATGCGGCTGCGCGCAAGAGGCTGACCTGCAATCCGGAATGGCCAAAG 1500  
QY 1501 GTCCGAGCTATTTCTTGATCAGCTATGAGCTATTTGTTGGCGGAGAGAGGCAACGATG 1560  
DB 1501 GTCCGAGCTATTTCTTGATCAGCTATGAGCTATTTGTTGGCGGAGAGAGGCAACGATG 1560

QY 1561 ACAACAACAAGAAAGATGTCCATTGCGAGCGTGAAGTGGAGTGGAGTGGTGAAGG 1620  
DB 1561 ACAACAACAAGAAAGATGTCCATTGCGAGCGTGAAGTGGAGTGGAGTGGTGAAGG 1620  
QY 1621 TTATACAAAGACCAACAGCACTTACCAAGCAACCAAGCTACCAAGTTCGTAAGTGA 1680  
DB 1621 TTATACAAAGACCAACAGCACTTACCAAGCAACCAAGCTACCAAGTTCGTAAGTGA 1680  
QY 1681 GCAAGCATCTTATCTTACCTTACCTGTTTACCGTTTAACTACGAGGAGATCACTGATG 1740  
DB 1681 GCAAGCATCTTATCTTACCTTACCTGTTTACCGTTTAACTACGAGGAGATCACTGATG 1740  
QY 1741 CTCACAAAGTACAGATACGGAACGGAAGTGGCGCTTTGGTATACCGGATGAGATCGTA 1800  
DB 1741 CTCACAAAGTACAGATACGGAACGGAAGTGGCGCTTTGGTATACCGGATGAGATCGTA 1800  
QY 1801 AGCCATTGTAATGTGTAACATATCAGGATGCCAGAGCACTTGCCCTATGCCAGAGACT 1860  
DB 1801 AGCCATTGTAATGTGTAACATATCAGGATGCCAGAGCACTTGCCCTATGCCAGAGACT 1860  
QY 1861 CGAATGCCGTCAACCCGATGTCCGAAGAGATGGGCCCATATAGTCCCGTGTACTATG 1920  
DB 1861 CGAATGCCGTCAACCCGATGTCCGAAGAGATGGGCCCATATAGTCCCGTGTACTATG 1920  
QY 1921 GCAATCTAGGCTCCGACACTCATCGTATACCTCGATCATGCCAATATCGTATACCT 1980  
DB 1921 GCAATCTAGGCTCCGACACTCATCGTATACCTCGATCATGCCAATATCGTATACCT 1980  
QY 1981 CACATGCGCATCTACTCGCGCGAGCGCGTCAATGGAGCGTCAAGCAATGACCAAGAGA 2040  
DB 1981 CACATGCGCATCTACTCGCGCGAGCGCGTCAATGGAGCGTCAAGCAATGACCAAGAGA 2040  
QY 2041 GCAATTTGGGCAACCGCAACAACGATCATAGTGGCGCCCAATGGCGGCAACA 2100  
DB 2041 GCAATTTGGGCAACCGCAACAACGATCATAGTGGCGCCCAATGGCGGCAACA 2100  
QY 2101 CCGTGTGACACCAATCAAGCTGATCATGGCGCTACGAAATTTGGCTGGAGTGA 2160  
DB 2101 CCGTGTGACACCAATCAAGCTGATCATGGCGCTACGAAATTTGGCTGGAGTGA 2160  
QY 2161 CGAGCAGAGCTGGCAAGATTAAATCATATGACATCTTTATCGAGCCGCTCAAGCAC 2220  
DB 2161 CGAGCAGAGCTGGCAAGATTAAATCATATGACATCTTTATCGAGCCGCTCAAGCAC 2220  
QY 2221 AAAAGGTGTGATATGAAAGATGTGATCTGATGACATCATCGAAGAGGCGCTG 2280  
DB 2221 AAAAGGTGTGATATGAAAGATGTGATCTGATGACATCATCGAAGAGGCGCTG 2280  
QY 2281 GTGCGCAGAGTGGGCAAGGATCGAGGTCTCCGTTTACTATTTCCCAAGAGAGCG 2340  
DB 2281 GTGCGCAGAGTGGGCAAGGATCGAGGTCTCCGTTTACTATTTCCCAAGAGAGCG 2340  
QY 2341 ATGACGAGATGGGCGAGCTTCAAGAACAAGGCACTCGAAGTATCTTCAAGGATCG 2400  
DB 2341 ATGACGAGATGGGCGAGCTTCAAGAACAAGGCACTCGAAGTATCTTCAAGGATCG 2400  
QY 2401 ATGTGTTTGTGTGTGGGACTGTGTGCTGGGTTTGTGAAATTTGAGAAATTTGGATTCG 2460  
DB 2401 ATGTGTTTGTGTGTGGGACTGTGTGCTGGGTTTGTGAAATTTGAGAAATTTGGATTCG 2460  
QY 2461 TCAATGCTTCAATCCCTTGTGAGCTTTCATACGCTGTGATTTGTGTCAACGGA 2520  
DB 2461 TCAATGCTTCAATCCCTTGTGAGCTTTCATACGCTGTGATTTGTGTCAACGGA 2520  
QY 2521 TGTTCATGGCAATGATCAACAGATATGAAACAAGAGATGAAACGCGTCTCAAGAGTG 2580  
DB 2521 TGTTCATGGCAATGATCAACAGATATGAAACAAGAGATGAAACGCGTCTCAAGAGTG 2580  
QY 2581 GCAACTATTTCTTACCGGCACTTTGCCATCGAGGCAACATGAACTATATGCCATGA 2640  
DB 2581 GCAACTATTTCTTACCGGCACTTTGCCATCGAGGCAACATGAACTATATGCCATGA 2640  
QY 2640 GCAACTATTTCTTACCGGCACTTTGCCATCGAGGCAACATGAACTATATGCCATGA 2640

QY 2641 GCCCAAGTACTATTTCCAGAGGGGCTGGAACTCTTGCATCTTATATCGTGGCCCTAT 2700  
DB 2641 GCCCAAGTACTATTTCCAGAGGGGCTGGAACTCTTGCATCTTATATCGTGGCCCTAT 2700  
QY 2701 CGCTATTTGGAACCTGGACTCGAGGGTGTCCAGGGTGTCCGTATTTGCTTCTTTCAT 2760  
DB 2701 CGCTATTTGGAACCTGGACTCGAGGGTGTCCAGGGTGTCCGTATTTGCTTCTTTCAT 2760  
QY 2761 TGTGTGTGTATTTCAAACTGGGCAAGTCTTGGCCCACTTAAATTTACTATTTGATTA 2820  
DB 2761 TGTGTGTGTATTTCAAACTGGGCAAGTCTTGGCCCACTTAAATTTACTATTTGATTA 2820  
QY 2821 TGGAGCGCAACATGGGCGCTTGGGTAATCTGACATTTGATCTTGCATTAATCATCTTCA 2880  
DB 2821 TGGAGCGCAACATGGGCGCTTGGGTAATCTGACATTTGATCTTGCATTAATCATCTTCA 2880  
QY 2881 TCTTTGGGATGAGGATGCAACTGTTTGGGAAAGATTTATCATGATCAAGAGACCGCT 2940  
DB 2881 TCTTTGGGATGAGGATGCAACTGTTTGGGAAAGATTTATCATGATCAAGAGACCGCT 2940  
QY 2941 TTCCGATGGCGACCTGCGCGCTGGAACTTCAACGACTTTATGACAGCTTATGATCG 3000  
DB 2941 TTCCGATGGCGACCTGCGCGCTGGAACTTCAACGACTTTATGACAGCTTATGATCG 3000  
QY 3001 TGTTCGGGCTGCTGCGGAGATGGATGATGATCTGATGAGGACTGATGATGATGATG 3060  
DB 3001 TGTTCGGGCTGCTGCGGAGATGGATGATGATCTGATGAGGACTGATGATGATGATG 3060  
QY 3061 ATGTCTGTGCAATTCCTTCTTCTTGTGGCAACGTTGTCAATGGGCAATCTTGTGTACTTA 3120  
DB 3061 ATGTCTGTGCAATTCCTTCTTCTTGTGGCAACGTTGTCAATGGGCAATCTTGTGTACTTA 3120  
QY 3121 ACCTTTCTTACCTTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3180  
DB 3121 ACCTTTCTTACCTTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3180  
QY 3181 CCGATACGATACGATTAATAATAGCGAGGCTTCAATGAAATGGCCGATTTAAAGTT 3240  
DB 3181 CCGATACGATACGATTAATAATAGCGAGGCTTCAATGAAATGGCCGATTTAAAGTT 3240  
QY 3241 GGGTTAAGCTTAATATGCTGATTTGTTCAAGTTATAGTAAACAAATTTGACAAATTCAGA 3300  
DB 3241 GGGTTAAGCTTAATATGCTGATTTGTTCAAGTTATAGTAAACAAATTTGACAAATTCAGA 3300  
QY 3301 TAAAGTATCAACATAGGATGAGAGCAACAGATCAGTGTGATTTGAGGAGAGAGC 3360  
DB 3301 TAAAGTATCAACATAGGATGAGAGCAACAGATCAGTGTGATTTGAGGAGAGAGC 3360  
QY 3361 ATGTGACAAAGAACTGAGCTGGGCAAGAGATCTGCGCAAGGCTTCAATCAAGA 3420  
DB 3361 ATGTGACAAAGAACTGAGCTGGGCAAGAGATCTGCGCAAGGCTTCAATCAAGA 3420  
QY 3421 AGGGATCAAGAGCAAGCACTGAGAGTGGCTTGGGGATCGGATGAGAAATTCAGA 3480  
DB 3421 AGGGATCAAGAGCAAGCACTGAGAGTGGCTTGGGGATCGGATGAGAAATTCAGA 3480  
QY 3481 TACAGCGCAATGAAAGCAACAAAGCGAAGAAATCAAAATATCTTAATTAACGCAACA 3540  
DB 3481 TACAGCGCAATGAAAGCAACAAAGCGAAGAAATCAAAATATCTTAATTAACGCAACA 3540  
QY 3541 TGAATGGCAACTCAATTAACCAACCAAGATGATCTGAAACAGAGCTTAAACATATGAG 3600  
DB 3541 TGAATGGCAACTCAATTAACCAACCAAGATGATCTGAAACAGAGCTTAAACATATGAG 3600  
QY 3601 GTTTGTCTTAAAGAGCAAGCACTGCGAGATTTAATCTATGTTTGTACCTTAAGAAATC 3660  
DB 3601 GTTTGTCTTAAAGAGCAAGCACTGCGAGATTTAATCTATGTTTGTACCTTAAGAAATC 3660  
QY 3661 GACCAATTCAGAGCAAGCACTGAGGAGCGCGAGAGATGAGGCGAGAGAGAGC 3720  
DB 3661 GACCAATTCAGAGCAAGCACTGAGGAGCGCGAGAGATGAGGCGAGAGAGAGC 3720  
QY 3721 GCGAGCGCAGCAAGAGATTTAGTCTCGACGAGAACTGAGCAGAGAGGCGAATGCG 3780

Db 3721 GCGACGCGAGAGAGATTTAGGTCTCGACGAGGAACTGACGAGAGAGGCGCAATCG 3780  
Qy 3781 AGAGAGGCGCGCTGACGCGGTATCATTTATTCAGCACGACGAGATATCTCGATG 3840  
Db 3781 AGAGAGGCGCGCTGACGCGGTATCATTTATTCAGCACGAGAGATATCTCGATG 3840  
Qy 3841 AATATCAGCTGATTTGCGCCGATTCGTATTAAGAAATTTCCGATCTTACCGGTG 3900  
Db 3841 AATATCAGCTGATTTGCGCCGATTCGTATTAAGAAATTTCCGATCTTACCGGTG 3900  
Qy 3901 ACGATGACTGCGCGCTTGGCAAGATGCGGCAATTTACGACTGAAAATTTCAATTA 3960  
Db 3901 ACGATGACTGCGCGCTTGGCAAGATGCGGCAATTTACGACTGAAAATTTCAATTA 3960  
Qy 3961 TTGAAAATTAATTTTGAACAGCTGTATCATCTAGATTTTATAGTAGTCTAGCTT 4020  
Db 3961 TTGAAAATTAATTTTGAACAGCTGTATCATCTAGATTTTATAGTAGTCTAGCTT 4020  
Qy 4021 TGGCATTAAGAGATGATCATCTGCGACAAAGACCATCTGACGATATTTATATATA 4080  
Db 4021 TGGCATTAAGAGATGATCATCTGCGACAAAGACCATCTGACGATATTTATATATA 4080  
Qy 4081 TGGACAGATATTTACGTTATATCTTCTTGAATTTATCAAGTGTGGCGCTCG 4140  
Db 4081 TGGACAGATATTTACGTTATATCTTCTTGAATTTATCAAGTGTGGCGCTCG 4140  
Qy 4141 GCTTCAAGTGTACTTCAACAGCGGTGTGTGGCTGATTTGCTGATTTGCTGAT 4200  
Db 4141 GCTTCAAGTGTACTTCAACAGCGGTGTGTGGCTGATTTGCTGATTTGCTGAT 4200  
Qy 4201 CGCTTATCACTGTGTCTTCACTGTGTGAGGCTGTGTATCAAGCTTCAAGCTA 4260  
Db 4201 CGCTTATCACTGTGTCTTCACTGTGTGAGGCTGTGTATCAAGCTTCAAGCTA 4260  
Qy 4261 TGGCAAGCTTAAAGACATGACCACTACGTCATGTCCGTATGCAAGGCGATGAGG 4320  
Db 4261 TGGCAAGCTTAAAGACATGACCACTACGTCATGTCCGTATGCAAGGCGATGAGG 4320  
Qy 4321 TCGTGTAAATGCGTGTGATACGCTATACGTCATCTTCAATGTGTGTGTGTC 4380  
Db 4321 TCGTGTAAATGCGTGTGATACGCTATACGTCATCTTCAATGTGTGTGTGTC 4380  
Qy 4381 TAAATTTTGGCTAATTTTGGCCATATGCGTGTACGCTTTTGTGGAATATTTTA 4440  
Db 4381 TAAATTTTGGCTAATTTTGGCCATATGCGTGTACGCTTTTGTGGAATATTTTA 4440  
Qy 4441 AGTGCAGAGACATGATGACGAGAGCTCAGCCAGAGATCATATCAAAATGCAATGCT 4500  
Db 4441 AGTGCAGAGACATGATGACGAGAGCTCAGCCAGAGATCATATCAAAATGCAATGCT 4500  
Qy 4501 GCGAGACGAGAACTACACGTTGGTGAATTCAGCAATGAATTTGATCATGTAGTAA 4560  
Db 4501 GCGAGACGAGAACTACACGTTGGTGAATTCAGCAATGAATTTGATCATGTAGTAA 4560  
Qy 4561 CGTATCTGTGCTTTTCCAGTGGCACTTCAAAAGCGTGAATCAAAATCATGAAATG 4620  
Db 4561 CGTATCTGTGCTTTTCCAGTGGCACTTCAAAAGCGTGAATCAAAATCATGAAATG 4620  
Qy 4621 CTATGATTCAGAGAGTGTGACAAACCAATTCGTGAACCAATCTACATGTATTT 4680  
Db 4621 CTATGATTCAGAGAGTGTGACAAACCAATTCGTGAACCAATCTACATGTATTT 4680  
Qy 4681 TATATTCGATTTCTTCAATATTTGATCTTTTCACTCAATCTGTCTTATGCTG 4740  
Db 4681 TATATTCGATTTCTTCAATATTTGATCTTTTCACTCAATCTGTCTTATGCTG 4740  
Qy 4741 TTAATCATGTAATTTTAAAGAGAAAGAAAGAGAGATGATCTTAAATGTTCA 4800  
Db 4741 TTAATCATGTAATTTTAAAGAGAAAGAAAGAGAGATGATCTTAAATGTTCA 4800  
Qy 4801 TGAAGAGATCAGAAAAAGTATATATGCTATGAAGATGGCTTAAAAACAT 4860  
Db 4801 TGAAGAGATCAGAAAAAGTATATATGCTATGAAGATGGCTTAAAAACAT 4860

Db 4801 TGAAGAGATCAGAAAAAGTATATATGCTATGAAGATGGCTTAAAAACAT 4860  
Qy 4861 TAAAGCCATTTCCAAAGCAAGGTGGACCAAGCAATATGTCTTTGAATATTAACCG 4920  
Db 4861 TAAAGCCATTTCCAAAGCAAGGTGGACCAAGCAATATGTCTTTGAATATTAACCG 4920  
Qy 4921 AATAGAAATTCGAT 4980  
Db 4921 AATAGAAATTCGAT 4980  
Qy 4981 TCGATCGTATGATGCGTGGACAGATTAACGCGGTCTTGAATATCTCAATGCGAT 5040  
Db 4981 TCGATCGTATGATGCGTGGACAGATTAACGCGGTCTTGAATATCTCAATGCGAT 5040  
Qy 5041 TCGATGATTTTATGATTCGGAATGTCTATTTAAAAATTTGCTTTACGATATCAAT 5100  
Db 5041 TCGATGATTTTATGATTCGGAATGTCTATTTAAAAATTTGCTTTACGATATCAAT 5100  
Qy 5101 TTAATGAGCCATGGAATTTATGATGATGATGATGATGATGATGATGATGATGAT 5160  
Db 5101 TTAATGAGCCATGGAATTTATGATGATGATGATGATGATGATGATGATGATGAT 5160  
Qy 5161 TACTTACGATATATATGAGAGATCTTGTGTGCGGACCGCTCTCGAGTGTGCGTG 5220  
Db 5161 TACTTACGATATATATGAGAGATCTTGTGTGCGGACCGCTCTCGAGTGTGCGTG 5220  
Qy 5221 TGGGAAAGTGGGCGGTCTCTTCTGATGATGAAAGGAGCCAGAGGCAATTCGACCTGC 5280  
Db 5221 TGGGAAAGTGGGCGGTCTCTTCTGATGATGAAAGGAGCCAGAGGCAATTCGACCTGC 5280  
Qy 5281 TCTTGGGTTGGGCAATGCGTGGCGGCGGCTTCAATCTGCTGCTGCTGCTGCTG 5340  
Db 5281 TCTTGGGTTGGGCAATGCGTGGCGGCGGCTTCAATCTGCTGCTGCTGCTGCTG 5340  
Qy 5341 TCAATGTCATCTTGGCCATTTTGGGCAATGCTTCTTCAATGCAAGTGAAGAGAGAG 5400  
Db 5341 TCAATGTCATCTTGGCCATTTTGGGCAATGCTTCTTCAATGCAAGTGAAGAGAGAG 5400  
Qy 5401 GCATTAAGAGCTTCAACCTTCAAGACCTTTGGCCAGAGATATCTGCTCTTTTCA 5460  
Db 5401 GCATTAAGAGCTTCAACCTTCAAGACCTTTGGCCAGAGATATCTGCTCTTTTCA 5460  
Qy 5461 TGTGAGTGAAGCGGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5520  
Db 5461 TGTGAGTGAAGCGGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5520  
Qy 5521 ATCCACCCGACAGGCAAGAGGCTATCGGGCAATTTGTGTTCAAGACGTTGGAATTA 5580  
Db 5521 ATCCACCCGACAGGCAAGAGGCTATCGGGCAATTTGTGTTCAAGACGTTGGAATTA 5580  
Qy 5581 CGTTTCTCTCTCATATCTATATATATATATATATATATATATATATATATATAT 5640  
Db 5581 CGTTTCTCTCTCATATCTATATATATATATATATATATATATATATATATATAT 5640  
Qy 5641 TCAATTCGAGAACTATATGTCAGGCGCAGAGACGTCGAAAGGCTTAACGAGAG 5700  
Db 5641 TCAATTCGAGAACTATATGTCAGGCGCAGAGACGTCGAAAGGCTTAACGAGAG 5700  
Qy 5701 ACTACGACATGATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 5760  
Db 5701 ACTACGACATGATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 5760  
Qy 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5820  
Db 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5820  
Qy 5821 GGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880  
Db 5821 GGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880  
Qy 5881 GCGTGCATCTCTGACGCGCTTACGAAAGACTTTTGGCGGAGAGGCAATCCGATG 5940  
Db 5881 GCGTGCATCTCTGACGCGCTTACGAAAGACTTTTGGCGGAGAGGCAATCCGATG 5940

```

;
; REFERENCE/DOCKET NUMBER: 19332DA
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (908) 594-3905
;
; TELEFAX: (908) 594-4720
;
; INFORMATION FOR SEQ ID NO: 7:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6513 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; US-08-724-095-7

```

```

Query Match      100.0%; Score 6513; DB 1; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

;
; 1 TCTAGACGTTGGCCGACATGACATGACGAAAGATTCGACTGATATCTGAGAAAGAC 60
; 1 TCTAGACGTTGGCCGACATGACATGACGAAAGATTCGACTGATATCTGAGAAAGAC 60
;
; 61 GCAGTTTGTTCCTGCTCCCTTACCCCGAATCATTTGGTGAATGGAACATGTCG 120
; 61 GCAGTTTGTTCCTGCTCCCTTACCCCGAATCATTTGGTGAATGGAACATGTCG 120
;
; 121 CTGAACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
; 121 CTGAACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
;
; 181 ATGATGCGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
; 181 ATGATGCGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
;
; 241 CACAAACCGGATCTCTACCTTGAACAGGAGTGCCTGTTGATGATGAGAGAGCT 300
; 241 CACAAACCGGATCTCTACCTTGAACAGGAGTGCCTGTTGATGATGAGAGAGCT 300
;
; 301 TCCCGCGGAAATTTGGCTCCACTCTCTGAGAGATATCGATCCCTACAGCAATG 360
; 301 TCCCGCGGAAATTTGGCTCCACTCTCTGAGAGATATCGATCCCTACAGCAATG 360
;
; 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 420
; 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 420
;
; 421 TGTGATGCTGCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 480
; 421 TGTGATGCTGCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 480
;
; 481 CATTATTTTCCATATCATCATCATCACCAATTCCTGTCATCTGATGATATGTC 540
; 481 CATTATTTTCCATATCATCATCATCACCAATTCCTGTCATCTGATGATATGTC 540
;
; 541 CGACAAACGCCCGGAGTTGAGTGCATCTGAGAGATATTCACCGGAATCTACATTTGAAT 600
; 541 CGACAAACGCCCGGAGTTGAGTGCATCTGAGAGATATTCACCGGAATCTACATTTGAAT 600
;
; 601 CAGCTGTTAAAGGATGAGCAGAGAGTTTCAATTTATGACCGTTTACGATCTTAGAGATG 660
; 601 CAGCTGTTAAAGGATGAGCAGAGAGTTTCAATTTATGACCGTTTACGATCTTAGAGATG 660
;
; 661 CATGAATTTGGCTGACCTTGTAGTAATAGCTTTAGCTTATGTGACATGAGTATGAT 720
; 661 CATGAATTTGGCTGACCTTGTAGTAATAGCTTTAGCTTATGTGACATGAGTATGAT 720
;
; 721 TAGGTAATCTAGAGAGCCCTGCAAGAGTTTATGAGTGTGAGAGAGCTTAAACCGTGA 780
; 721 TAGGTAATCTAGAGAGCCCTGCAAGAGTTTATGAGTGTGAGAGAGCTTAAACCGTGA 780
;
; 781 TTGTGCAAGGCTGAGAGACCATGTCGAGCGCGCTCATCGAATGCTGAGAAATCTGCGG 840
; 781 TTGTGCAAGGCTGAGAGACCATGTCGAGCGCGCTCATCGAATGCTGAGAAATCTGCGG 840
;

```

```

;
; RESULT 3
;
; Sequence 7, Application US/08724095
;
; Patent No. 5688917
;
; GENERAL INFORMATION:
;
; APPLICANT: Warmke, Jeffrey W.
;
; APPLICANT: Hall, Linda
;
; APPLICANT: Feng, Gouping
;
; APPLICANT: Van der Ploeg, Leonardus
;
; TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
;
; TITLE OF INVENTION: PARA SODIUM CHANNEL
;
; NUMBER OF SEQUENCES: 7
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
;
; STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
;
; CITY: Rahway
;
; STATE: New Jersey
;
; COUNTRY: USA
;
; ZIP: 07065-0907
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: FASTseq, Version #1.ds
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/724,095
;
; FILING DATE:
;
; CLASSIFICATION: 536
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Hand, J. Mark
;
; REGISTRATION NUMBER: 36,545
;

```

QY	841	ATGAGATTATCTGACCAACATGTTCTCCCTGTGCGTGTGGCGTTATATGGGCGCTCAAGATCT	900
Dp	841	ATGAGATTATCTGACCAATGTTCTCCCTGTGCGTGTGGCGTTATATGGGCGCTCAAGATCT	900
QY	901	ATTATGGGCGTGTCAACCGAAGATGATCAACAAGAACTCCCGCTGGACGGTTCTGGGGCA	960
Dp	901	ATTATGGGCGTGTCAACCGAAGATGATCAACAAGAACTCCCGCTGGACGGTTCTGGGGCA	960
QY	961	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTGATATTCGAGG	1020
Dp	961	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAAATTGATATTCGAGG	1020
QY	1021	ACGAGGGCATCTCATTTCCGTTATGCGGCATATATCCGCTGCGGGGCATATCGACGACG	1080
Dp	1021	ACGAGGGCATCTCATTTCCGTTATGCGGCATATATCCGCTGCGGGGCATATCGACGACG	1080
QY	1081	ATTACGCTGCTGACGAGGGGTTTGGTCCGAATTCGAATTATAGCTACACGAGCTTCGATT	1140
Dp	1081	ATTACGCTGCTGACGAGGGGTTTGGTCCGAATTCGAATTATAGCTACACGAGCTTCGATT	1140
QY	1141	CGTTCCGATGGGGCTTCCGTGCCGCTTCCGGCTGATACACAGGACTTTCGGAGAGATC	1200
Dp	1141	CGTTCCGATGGGGCTTCCGTGCCGCTTCCGGCTGATACACAGGACTTTCGGAGAGATC	1200
QY	1201	TGTACACAGCTGATGTTGCGCGCGCCGACCAATGSCACATGCTGTTCTTTATATGATCA	1260
Dp	1201	TGTACACAGCTGATGTTGCGCGCGCCGACCAATGSCACATGCTGTTCTTTATATGATCA	1260
QY	1261	TCTTCCTTAGGTTCATTCTATCTGTGGAATTTGAATTTTGGCCATTGTGCCATGTGCTATG	1320
Dp	1261	TCTTCCTTAGGTTCATTCTATCTGTGGAATTTGAATTTTGGCCATTGTGTGCATGTGCTATG	1320
QY	1321	ACGAATTGCCAAGAGAGGCCGGAAGAAGAAAGGCTGCCGAAGAGGAGCGATACCTGTAG	1380
Dp	1321	ACGAATTGCCAAGAGAGGCCGGAAGAAGAAAGGCTGCCGAAGAGGAGCGATACCTGTAG	1380
QY	1381	CGAAGAAGAGCTGCGCGCGCCCAAGCGGCCAAGCTGAGAGCGGCGCAATGCGCAGGCTC	1440
Dp	1381	CGAAGAAGAGCTGCGCGCGCCCAAGCGGCCAAGCTGAGAGAGCGGCGCAATGCGCAGGCTC	1440
QY	1441	AGGACGACGCGGATGCGGCTGCGCGCGGAAGAGGCTGCACTGATCCGGAATATGGCCAGA	1500
Dp	1441	AGGACGACGCGGATGCGGCTGCGCGCGGAAGAGGCTGCACTGATCCGGAATATGGCCAGA	1500
QY	1501	GTCCGACGTAATTCCTTGATCAGCTATGAGCTATTTGTTGGCGGCGAGAAAGGCAACGATG	1560
Dp	1501	GTCCGACGTAATTCCTTGATCAGCTATGAGCTATTTGTTGGCGGCGAGAAAGGCAACGATG	1560
QY	1561	ACAACCAACAAAGAGAAGATGTCATTGCGAGCGCTGAGGTGAGTCCGAGTCCGATGAGCG	1620
Dp	1561	ACAACCAACAAAGAGAAGATGTCATTGCGAGCGCTGAGGTGAGTCCGAGTCCGATGAGCG	1620
QY	1621	TTTATACAAAGACACACAGACCTTATCCACACGACACCAAGCTTACCAAAGTTGCTAAAGTGA	1680
Dp	1621	TTTATACAAAGACACACAGACCTTATCCACACGACACCAAGCTTACCAAAGTTGCTAAAGTGA	1680
QY	1681	GACAGACATCTTATCTTATCCTTACCTGTTACCGTTTAAATACACGAGGGGATCAGCTAGTT	1740
Dp	1681	GACAGACATCTTATCTTATCCTTACCTGTTTAAATACATACGAGGGGATCAGCTAGTT	1740
QY	1741	CTCACAAATGACAGATACGGAACGGAACGTGCGCGCTTTGATATCCCGGTAGCGATCGTA	1800
Dp	1741	CTCACAAATGACAGATACGGAACGGAACGTGCGCGCTTTGATATCCCGGTAGCGATCGTA	1800
QY	1801	AGCCATTGCTATTTGTCAACATATCAGGATGCCACAGACACTTGGCTTATGCCACGACT	1860
Dp	1801	AGCCATTGCTATTTGTCAACATATCAGGATGCCACAGACACTTGGCTTATGCCACGACT	1860
QY	1861	CGAATGCGGTCAACCCCGATGTCCGAAGAAGATGGGGCCATCATATGTCGCCGTGTCTATG	1920
Dp	1861	CGAATGCGGTCAACCCCGATGTCCGAAGAAGATGGGGCCATCATATGTCGCCGTGTCTATG	1920
QY	1921	GCAATCTTAGGCTCCCGACATCTCATGTATACCTCGCATGATGCCGAATATTCGATTA	1980

Dp	1921	GCATCTTAGGCTCCCGACACTCATCGTATACCTTGCATCACTCCCGAATATCGTATACCT	1988
Qy	1981	CACATGGCGCATCTACTCGGCGGCATATGGCCGTCATATGGCGTGCAGCAATATGACAAAGAGA	2040
Dp	1981	CACATGGCGCATCTACTCGGCGGCATATGGCCGTCATATGGCGTGCAGCAATATGACAAAGAGA	2040
Qy	2041	GCAAAATTCGCGAACCGCAACACCGCAATCATATGATGGCGCCACCAATGGCGGCACCA	2100
Dp	2041	GCAAAATTCGCGAACCGCAACACCGCAATCATATGATGGCGCCACCAATGGCGGCACCA	2100
Qy	2101	CCTGCTTGGAGAACCAATTCACAAAGCTTCATATCGCGACTATGAAATTTGGCCGTGAGTGC	2160
Dp	2101	CCTGCTTGGAGAACCAATTCACAAAGCTTCATATCGCGACTATGAAATTTGGCCGTGAGTGC	2160
Qy	2161	CGGACGAAGCTGGCGAAAGATTAAACATCATATGACATCTTTATCGAGCCGCTCCAGACAC	2220
Dp	2161	CGGACGAAGCTGGCGAAAGATTAAACATCATATGACATCTTTATCGAGCCGCTCCAGACAC	2220
Qy	2221	AAACGGTGTGATATATGAAGATGTATGTCTCTGAATGACATCATCGAACAGCGCCGCTG	2280
Dp	2221	AAACGGTGTGATATATGAAGATGTATGTCTCTGAATGACATCATCGAACAGCGCCGCTG	2280
Qy	2281	GTCGGCACAGTCGGGGCAAGCGATATCGCGGTGTCTCCGTTACTATTTCCCAACAGAGACG	2340
Dp	2281	GTCGGCACAGTCGGGGCAAGCGATATCGCGGTGTCTCCGTTACTATTTCCCAACAGAGACG	2340
Qy	2341	ATGACAGAGATGGGCGCGACGTTCAAAGCAAGGCACTCGAAGTATCCTCAAGGCAACG	2400
Dp	2341	ATGACAGAGATGGGCGCGACGTTCAAAGCAAGGCACTCGAAGTATCCTCAAGGCAACG	2400
Qy	2401	ATGTGTATTTGTGTGTGGGACCTGTTCGTGGTGTGGTGTGAAATTTCAAGAGTGGTATTCG	2460
Dp	2401	ATGTGTATTTGTGTGTGGGACCTGTTCGTGGTGTGGTGTGAAATTTCAAGAGTGGTATTCG	2460
Qy	2461	TCAATGCTTTGGATATCCCTTCGTGAGCTCTTCATACAGCTGTGCAATTTGGTTCAAACGA	2520
Dp	2461	TCAATGCTTTGGATATCCCTTCGTGAGCTCTTCATACAGCTGTGCAATTTGGTTCAAACGA	2520
Qy	2521	TGTTTCATGGCAATGGATCACACGATATATGAACAGAGATGGAACGCGTGTCAAAGAGT	2580
Dp	2521	TGTTTCATGGCAATGGATCACACGATATATGAACAGAGATGGAACGCGTGTCAAAGAGT	2580
Qy	2581	GCAACTATATTTCTTCAACCGCCACTTTTGGCATCGAGGCCACCATGAAAGCTAATGGCCATGA	2640
Dp	2581	GCAACTATATTTCTTCAACCGCCACTTTTGGCATCGAGGCCACCATGAAAGCTAATGGCCATGA	2640
Qy	2641	GCCCCAAGTACTATTTCCAGAGAGGCTGGAAACATCTTCGATTCATTATCGTGGCCCTAT	2700
Dp	2641	GCCCCAAGTACTATTTCCAGAGAGGCTGGAAACATCTTCGATTCATTATCGTGGCCCTAT	2700
Qy	2701	GGCTATTTGGAACGTGGGACCTCGAGGGGTGCAAGGGTCTGCGTATTTGGTTCCTTTGCAT	2760
Dp	2701	GGCTATTTGGAACGTGGGACCTCGAGGGGTGCAAGGGTCTGCGTATTTGGTTCCTTTGCAT	2760
Qy	2761	TGCTGCGGTATTAACAACTGGCCAAAGCTTGGCCCAACTTAATTTATCTCATTTGCATTA	2820
Dp	2761	TGCTGCGGTATTAACAACTGGCCAAAGCTTGGCCCAACTTAATTTATCTCATTTGCATTA	2820
Qy	2821	TGGAGCGCACATGGGCGCTTTGGGTATCTGAACATTTGATCTTTGCATTAATCATCTTCA	2880
Dp	2821	TGGAGCGCACATGGGCGCTTTGGGTATCTGAACATTTGATCTTTGCATTAATCATCTTCA	2880
Qy	2881	TCTTTGGCGGTATGGGAATGCAACGTGTGGAAAGAAATTAATCATGATCACAAAGACCGCT	2940
Dp	2881	TCTTTGGCGGTATGGGAATGCAACGTGTGGAAAGAAATTAATCATGATCACAAAGACCGCT	2940
Qy	2941	TTTCGGATATGGGACCTGCGCGCTGGAACCTTCAACGACTTTATGCAACAGCTTCATATGATCG	3000
Dp	2941	TTTCGGATATGGGACCTGCGCGCTGGAACCTTCAACGACTTTATGCAACAGCTTCATATGATCG	3000
Qy	3001	TGTTTCGGGTCTCTGCGGAGATATGATCGATTCATATGAGGACTGCATGTATGCTGGCG	3060
Dp	3001	TGTTTCGGGTCTCTGCGGAGATATGATCGATTCATATGAGGACTGCATGTATGCTGGCG	3060



QY 5221 TGCGAAGTGGCCGCTGCTTCCATGCTGAGGAGGAGCCCAAGGCGCATTCGCACTGCG 5280  
DB 5221 TGCGAAGTGGCCGCTGCTTCCATGCTGAGGAGGAGCCCAAGGCGCATTCGCACTGCG 5280  
QY 5281 TCTTCGCGTGGCCATGCTGCTGCGCGCCCTGTTCAACATCTGCTGCTGCTGCTGCG 5340  
DB 5281 TCTTCGCGTGGCCATGCTGCTGCGCGCCCTGTTCAACATCTGCTGCTGCTGCTGCG 5340  
QY 5341 TCATGTTATCTTTGGCCATTTTGGCGAGTGTCTTTTCAATGCACTGAGAGAGAGAGCG 5400  
DB 5341 TCATGTTATCTTTGGCCATTTTGGCGAGTGTCTTTTCAATGCACTGAGAGAGAGAGCG 5400  
QY 5401 GCATTAAGAGCTTACAACTTCAAGACTTGGCCAGAGCATGATCTGCTCTTCAAGA 5460  
DB 5401 GCATTAAGAGCTTACAACTTCAAGACTTGGCCAGAGCATGATCTGCTCTTCAAGA 5460  
QY 5461 TGTGACGCTGAGCCGCTTGGAGTGTGTAAGTGAAGCCATTAATCAATGAGAGAGCATGCG 5520  
DB 5461 TGTGACGCTGAGCCGCTTGGAGTGTGTAAGTGAAGCCATTAATCAATGAGAGAGCATGCG 5520  
QY 5521 ATCCACCCGAGACGACGCAAAAGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGAATTA 5580  
DB 5521 ATCCACCCGAGACGACGCAAAAGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGAATTA 5580  
QY 5581 CGTTCTCTCTCATACCTAGTTATAGCTTTTGTATGTTATTAATATGTAATGCTGCG 5640  
DB 5581 CGTTCTCTCTCATACCTAGTTATAGCTTTTGTATGTTATTAATATGTAATGCTGCG 5640  
QY 5641 TCATTTCTGAGAACTATAGTGAAGCCACCGAGAGAGTGAAGAGGCTTAAACGAGAGCG 5700  
DB 5641 TCATTTCTGAGAACTATAGTGAAGCCACCGAGAGAGTGAAGAGGCTTAAACGAGAGCG 5700  
QY 5701 ACTACGACATGTAATGATGATCTGGGAGCAATTTGATCCGAGGCGACCCAGTACATAC 5760  
DB 5701 ACTACGACATGTAATGATGATCTGGGAGCAATTTGATCCGAGGCGACCCAGTACATAC 5760  
QY 5761 GCTATGATCAGCTGCGCAATTTCTGAGAGTACTGAGAGCCCGCGCTGAGATCCCAAG 5820  
DB 5761 GCTATGATCAGCTGCGCAATTTCTGAGAGTACTGAGAGCCCGCGCTGAGATCCCAAG 5820  
QY 5821 CGAACAGATACAGATCATATGATGAGCATATCCCATCTGTCGCGGTACCTCATGTA 5880  
DB 5821 CGAACAGATACAGATCATATGATGAGCATATCCCATCTGTCGCGGTACCTCATGTA 5880  
QY 5881 GCGTCGACATCTCTGAGCCCTTACGAAAGACTTTTGGCGGAGAGGCGCAATCCGATAG 5940  
DB 5881 GCGTCGACATCTCTGAGCCCTTACGAAAGACTTTTGGCGGAGAGGCGCAATCCGATAG 5940  
QY 5941 AGGAGACGCGTGAAGTGTGAGTGAAGGCGCCGCGGATTAACGAGGCGCTACGAGCCG 6000  
DB 5941 AGGAGACGCGTGAAGTGTGAGTGAAGGCGCCGCGGATTAACGAGGCGCTACGAGCCG 6000  
QY 6001 TCTCATCAACGCTGCGTGAAGGCTGAGAGTACTGCGCCCGGCTAATCCAGACGCGCT 6060  
DB 6001 TCTCATCAACGCTGCGTGAAGGCTGAGAGTACTGCGCCCGGCTAATCCAGACGCGCT 6060  
QY 6061 GCGGAAAGCACAAGGCGCGCGCGAGGAGGAGTGGTCTTTGAGAGCGGATACGATCATG 6120  
DB 6061 GCGGAAAGCACAAGGCGCGCGCGAGGAGGAGTGGTCTTTGAGAGCGGATACGATCATG 6120  
QY 6121 GCGATGCGGAGTATCCGAGTCCGCGGAGCCGCGCGCGGATTAAGAGCAGAGCGCGATG 6180  
DB 6121 GCGATGCGGAGTATCCGAGTCCGCGGAGCCGCGCGCGGATTAAGAGCAGAGCGCGATG 6180  
QY 6181 CGCCCGCTGCTGAGATGTAAGTGAACGCTTACGAGAGAGCTGCGATGCGGATG 6240  
DB 6181 CGCCCGCTGCTGAGATGTAAGTGAACGCTTACGAGAGAGCTGCGATGCGGATG 6240  
QY 6241 AGAGTATGTAATATGTCGCGGTGAGATGAGCGCGCGCGCGAGAGAGAGAGAGAGAG 6300  
DB 6241 AGAGTATGTAATATGTCGCGGTGAGATGAGCGCGCGCGAGAGAGAGAGAGAGAGAG 6300  
QY 6301 CGGCGCGCGCGGAGCAGAGCGCGGAGAGTCCCGAGAGCGGTAGCGCGGCGAGAGAG 6360

DB 6301 CGGCGCGCGCGGAGCAGAGCGCGGAGAGTCCCGAGCGGATGCGCGCGGAGAGAG 6360  
QY 6361 CGCGCTTCTGCTGAGAGAGCAGCGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420  
DB 6361 CGCGCTTCTGCTGAGAGAGCAGCGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420  
QY 6421 ACTGCGATGCGCGAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6480  
DB 6421 ACTGCGATGCGCGAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6480  
QY 6481 CCTCCAGATGACAGCGAGATTAAGCTCTAGA 6513  
DB 6481 CCTCCAGATGACAGCGAGATTAAGCTCTAGA 6513  
  
RESULT 4  
PCT-US95-14262-7  
Sequence 7, Application PC/TUS9514262  
GENERAL INFORMATION:  
APPLICANT: Warmke, Jeffrey W.  
APPLICANT: Van Der Ploeg, Leonardus  
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jack L. Tribble  
STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14262  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: 19338 PCT  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6513 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-14262-7  
  
Query Match 100.0%; Score 6513; DB 5; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 ATGTGCGAAGAAAAAAGAAATCCGATATGATGACGAGACGAGATGAAGTTC 240  
| | | | |  
Db 181 ATGTGCGAAGAAAAAAGAAATCCGATATGATGACGAGACGAGATGAAGTTC 240  
QY 241 CAAACCGGATCTCTACCTTGAACAGGGGTGCGCAATACCTGTTGATGACAGGGAGCT 300  
| | | | |  
Db 241 CAAACCGGATCTCTACCTTGAACAGGGGTGCGCAATACCTGTTGATGACAGGGAGCT 300  
QY 301 TCCCGCGGAATGAGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTA 360  
| | | | |  
Db 301 TCCCGCGGAATGAGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTA 360  
QY 361 TGAATTCGTAGTTGTAGCAAGAAAGAAATATTTTTCGCTTTTCTGCATCAAAAGCA 420  
| | | | |  
Db 361 TGAATTCGTAGTTGTAGCAAGAAAGAAATATTTTTCGCTTTTCTGCATCAAAAGCA 420  
QY 421 TGTGATGCTCCGATCCATTCATCCGATACGTGTGTGGCCATTTCATTCTAGTGATC 480  
| | | | |  
Db 421 TGTGATGCTCCGATCCATTCATCCGATACGTGTGTGGCCATTTCATTCTAGTGATC 480  
QY 481 CATTATTTTCCCTATTCATCATCAACCAATTCCTGTCATCTGATGATATATGC 540  
| | | | |  
Db 481 CATTATTTTCCCTATTCATCATCAACCAATTCCTGTCATCTGATGATATATGC 540  
QY 541 CGAACACGCCACGGTTGAGTCCACTGAGGTGATTTCAACCGAATCTACATTTGAAT 600  
| | | | |  
Db 541 CGAACACGCCACGGTTGAGTCCACTGAGGTGATTTCAACCGAATCTACATTTGAAT 600  
QY 601 CAGGTGTAAGGATGAGGACGAGGTTTCATTTTATGCGGTTTACGATCTTAGAGATG 660  
| | | | |  
Db 601 CAGGTGTAAGGATGAGGACGAGGTTTCATTTTATGCGGTTTACGATCTTAGAGATG 660  
QY 661 CATGAATGAGCTGAGCTTCTGATGATATGATGATGATGATGATGATGATGATGAT 720  
| | | | |  
Db 661 CATGAATGAGCTGAGCTTCTGATGATATGATGATGATGATGATGATGATGATGAT 720  
QY 721 TAGGATATCTAGACGCCCTGCGAAGCTTTAGGGGTGCGAGGCGCTTAAACGCTAGCA 780  
| | | | |  
Db 721 TAGGATATCTAGACGCCCTGCGAAGCTTTAGGGGTGCGAGGCGCTTAAACGCTAGCA 780  
QY 781 TTGTGCGAGCTTGAAGACCATCGTCCGCGCCGTCATCGATCGATGAGATCTGCGC 840  
| | | | |  
Db 781 TTGTGCGAGCTTGAAGACCATCGTCCGCGCCGTCATCGATCGATGAGATCTGCGC 840  
QY 841 ATGTGATTAATCTGACCATGTTCTCCCTGTGCGGTGCTGCGGTGATGAGTCT 900  
| | | | |  
Db 841 ATGTGATTAATCTGACCATGTTCTCCCTGTGCGGTGCTGCGGTGATGAGTCT 900  
QY 901 ATATGGGCGGTGCTGACCGAAGATGACCAAGAGTTCCGCTGAGCGTTCTGCGGCA 960  
| | | | |  
Db 901 ATATGGGCGGTGCTGACCGAAGATGACCAAGAGTTCCGCTGAGCGTTCTGCGGCA 960  
QY 961 ATCTGACCGACGAGACCTGAGATCATCAATCGCAATAGCTCCATTTGATTCGAGG 1020  
| | | | |  
Db 961 ATCTGACCGACGAGACCTGAGATCATCAATCGCAATAGCTCCATTTGATTCGAGG 1020  
QY 1021 ATCTGACCGACGAGACCTGAGATCATCAATCGCAATAGCTCCATTTGATTCGAGG 1080  
| | | | |  
Db 1021 ATCTGACCGACGAGACCTGAGATCATCAATCGCAATAGCTCCATTTGATTCGAGG 1080  
QY 1081 ATTAAGTGTGCTGACGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
| | | | |  
Db 1081 ATTAAGTGTGCTGACGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 CGTTGCGATGAGCTTTCTGTCGCGCTTCGCGCTGATGACACAGACTTCTGAGAGATC 1200  
| | | | |  
Db 1141 CGTTGCGATGAGCTTTCTGTCGCGCTTCGCGCTGATGACACAGACTTCTGAGAGATC 1200  
QY 1201 TGTACCACTGCTGTGCGCGCGCGCGACATGACATGACATGCTTTTATATATCA 1260  
| | | | |  
Db 1201 TGTACCACTGCTGTGCGCGCGCGCGACATGACATGACATGCTTTTATATATCA 1260  
QY 1261 TCTTCCAGAGTTCAATCTATCTTGATGATTTGATTTGGCCATTGTCATGTCGATG 1320  
| | | | |

Db 1261 TCTTCCAGAGTTCAATCTATCTTGATGATTTGATTTGGCCATTGTCATGTCGATG 1320  
QY 1321 ACGAATTTGCAAGGAAGGCGCAAGGAAGAGGCTCCGAGAGAGAGGCGATACGTGAAG 1380  
| | | | |  
Db 1321 ACGAATTTGCAAGGAAGGCGCAAGGAAGAGGCTCCGAGAGAGAGGCGATACGTGAAG 1380  
QY 1381 CGAAGAACTGCGCGCGCAAGGCGCAAGGAGAGGCGCAATGCGAGGCTC 1440  
| | | | |  
Db 1381 CGAAGAACTGCGCGCGCAAGGCGCAAGGAGAGGCGCAATGCGAGGCTC 1440  
QY 1441 AAGCAGCAGCGAGATGCGGCTGCGCGCAAGAGGCTGCACTGATCGGAAATGCGCAAG 1500  
| | | | |  
Db 1441 AAGCAGCAGCGAGATGCGGCTGCGCGCAAGAGGCTGCACTGATCGGAAATGCGCAAG 1500  
QY 1501 GTCCGACGATATCTTGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
| | | | |  
Db 1501 GTCCGACGATATCTTGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
QY 1561 ACAACAAAGAAAGAAAGATGCTCATTCGAGAGGCTGAGAGTGGAGTGGAGGCG 1620  
| | | | |  
Db 1561 ACAACAAAGAAAGAAAGATGCTCATTCGAGAGGCTGAGAGTGGAGTGGAGGCG 1620  
QY 1621 TTATACAAAGACACAGACCTACACACAGACACACACACACACACACACACACAC 1680  
| | | | |  
Db 1621 TTATACAAAGACACAGACCTACACACAGACACACACACACACACACACACACAC 1680  
QY 1681 GCAAGCATCTTATCTTACCTGATGATGATGATGATGATGATGATGATGATGATG 1740  
| | | | |  
Db 1681 GCAAGCATCTTATCTTACCTGATGATGATGATGATGATGATGATGATGATGATG 1740  
QY 1741 CTCACAAAGTACAGATGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
| | | | |  
Db 1741 CTCACAAAGTACAGATGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
QY 1801 AGCCATTTGATTTGTCACATATCAGATGATGATGATGATGATGATGATGATGATG 1860  
| | | | |  
Db 1801 AGCCATTTGATTTGTCACATATCAGATGATGATGATGATGATGATGATGATGATG 1860  
QY 1861 CGAATGCGTCAACCCCGATGCTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
| | | | |  
Db 1861 CGAATGCGTCAACCCCGATGCTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
QY 1921 GCAATCTAGGCTCCGACACTCATCTGATACCTCGATCAGTCCGAAATATGATAT 1980  
| | | | |  
Db 1921 GCAATCTAGGCTCCGACACTCATCTGATACCTCGATCAGTCCGAAATATGATAT 1980  
QY 1981 CACATGCGATCTTACTCGGCGGATGAGGCGGTCATGAGGCGTCAAGCAATGACCAAG 2040  
| | | | |  
Db 1981 CACATGCGATCTTACTCGGCGGATGAGGCGGTCATGAGGCGTCAAGCAATGACCAAG 2040  
QY 2041 GCAAAATTTGCGCAACCCGACACACAGAGATCAATCAATGAGGCGGCGGACCA 2100  
| | | | |  
Db 2041 GCAAAATTTGCGCAACCCGACACACAGAGATCAATCAATGAGGCGGCGGACCA 2100  
QY 2101 CCGTCTGACACCAATCAACCAAGCTGATCATGCACTACGAAATTTGCGCTGAGTGA 2160  
| | | | |  
Db 2101 CCGTCTGACACCAATCAACCAAGCTGATCATGCACTACGAAATTTGCGCTGAGTGA 2160  
QY 2161 CGAGAGAGCTGCGAAGATTAACATCATGACATCTTTTATCGAGCCGTCAGACAC 2220  
| | | | |  
Db 2161 CGAGAGAGCTGCGAAGATTAACATCATGACATCTTTTATCGAGCCGTCAGACAC 2220  
QY 2221 AAAGCGGTGATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
| | | | |  
Db 2221 AAAGCGGTGATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
QY 2281 GTGCGCACAGTCCGGGCAAGGATGCGGCTGCTCCGTTTACTATTTTCCAAAGAGAG 2340  
| | | | |  
Db 2281 GTGCGCACAGTCCGGGCAAGGATGCGGCTGCTCCGTTTACTATTTTCCAAAGAGAG 2340  
QY 2341 ATGACGAGATGAGGCGGAGCTTCAAGACAGGACCTGAAAGTATCTTAAAGGATCG 2400  
| | | | |

2341 ATGACGAGATGGGCGGACGTTCAAGAACAAGACCTCGAAGTATCTCAAGGCATCG 2400  
2401 ATGTTTGTGTGTGGGACCTGTGTGGGTTTGTGTAATTTTCAAGATGGGTATCGC 2460  
2401 ATGTTTGTGTGTGGGACCTGTGTGGGTTTGTGTAATTTTCAAGATGGGTATCGC 2460  
2461 TCATGCTTGTGATCCCTTCGTCGAGCTCTTCATCAGCTGTGCTGTGGTCAACAGA 2520  
2461 TCATGCTTGTGATCCCTTCGTCGAGCTCTTCATCAGCTGTGCTGTGGTCAACAGA 2520  
2521 TGTTCATGCAATGATCACCACGATATGAACAAGAGATGGAACGCGTGTCAAGATG 2580  
2521 TGTTCATGCAATGATCACCACGATATGAACAAGAGATGGAACGCGTGTCAAGATG 2580  
2581 GCACATATTTCTTCAACGCGCACCTTTGCTCAGAGCCACATGAACTAATGGCATGA 2640  
2581 GCACATATTTCTTCAACGCGCACCTTTGCTCAGAGCCACATGAACTAATGGCATGA 2640  
2641 GCCCAAGTACATTTTCAGAGAGGCTGGAACATCTTCGACTTATTCGTGGCCCTAT 2700  
2641 GCCCAAGTACATTTTCAGAGAGGCTGGAACATCTTCGACTTATTCGTGGCCCTAT 2700  
2701 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGGTCTGTCCGTATGCGTTCTTTGAT 2760  
2701 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGGTCTGTCCGTATGCGTTCTTTGAT 2760  
2761 TGTCTGCTGTATTTCAAACTGGCCAACTTTGGCCCACTTAATTACTCATTTGATTA 2820  
2761 TGTCTGCTGTATTTCAAACTGGCCAACTTTGGCCCACTTAATTACTCATTTGATTA 2820  
2821 TGGACGCAACCATGGGCGCTTTGGGATCTGACATTTGTACTTTGATTAATCACTTCA 2880  
2821 TGGACGCAACCATGGGCGCTTTGGGATCTGACATTTGTACTTTGATTAATCACTTCA 2880  
2881 TCTTTGCGGTGATGGAATGCACTGTCGAAAGATTAATCATGATCAACAAGACGCT 2940  
2881 TCTTTGCGGTGATGGAATGCACTGTCGAAAGATTAATCATGATCAACAAGACGCT 2940  
2941 TTTCCGATGGGACCTGCGGCTGGAACCTTCAACGATTTATGACACGCTTCAATGATG 3000  
2941 TTTCCGATGGGACCTGCGGCTGGAACCTTCAACGATTTATGACACGCTTCAATGATG 3000  
3001 TGTTCGCGGATGCTGCGGATGGAATGCACTGTCGAAAGATTAATCATGATCAACAAGACGCT 3060  
3001 TGTTCGCGGATGCTGCGGATGGAATGCACTGTCGAAAGATTAATCATGATCAACAAGACGCT 3060  
3061 ATGCTGCTGATCCCTTCTTCTTGGCCACCGTGTGATCGGAATCTTGTGATCTTA 3120  
3061 ATGCTGCTGATCCCTTCTTCTTGGCCACCGTGTGATCGGAATCTTGTGATCTTA 3120  
3121 ACCTTTCTTACGCTTGTGCTTGTGCAATTTGGCTCATCTAGCTTATCAGCGCCGATG 3180  
3121 ACCTTTCTTACGCTTGTGCTTGTGCAATTTGGCTCATCTAGCTTATCAGCGCCGATG 3180  
3181 CCGATACGATGCAATTAATTAAGCCGAGGCTTCAATGCAATTTGGCCGATTAATTAAGT 3240  
3181 CCGATACGATGCAATTAATTAAGCCGAGGCTTCAATGCAATTTGGCCGATTAATTAAGT 3240  
3241 GGGTTAAGCGTAAATGCTGATTTGTTCAAGTTAATACGTAACAATTTGAATCAAA 3300  
3241 GGGTTAAGCGTAAATGCTGATTTGTTCAAGTTAATACGTAACAATTTGAATCAAA 3300  
3301 TAAATGATCAACATCAAGGTGAGAGCAACAACGATCAATTTGAGGCAAGAGC 3360  
3301 TAAATGATCAACATCAAGGTGAGAGCAACAACGATCAATTTGAGGCAAGAGC 3360  
3361 ATGTTGACAAAGCACTGAGGCTGAGGCAACAACGATCAATTTGAGGCAAGAGC 3420  
3361 ATGTTGACAAAGCACTGAGGCTGAGGCAACAACGATCAATTTGAGGCAAGAGC 3420  
3421 AGGGATCAAGAGCAAGCACTGAGGCTGAGGCAACAACGATCAATTTGAGGCAAGAGC 3480  
3421 AGGGATCAAGAGCAAGCACTGAGGCTGAGGCAACAACGATCAATTTGAGGCAAGAGC 3480

3481 TACACGCGACATGAAAGCAACAAGCCGAAAGAAATCCAAATCTTAATTAACGCAAGA 3540  
3481 TACACGCGACATGAAAGCAACAAGCCGAAAGAAATCCAAATCTTAATTAACGCAAGA 3540  
3541 TGATTTGCACTCAATTAACCAACAAGCAATTAAGTGAACAGAGCTTAACCAATAG 3600  
3541 TGATTTGCACTCAATTAACCAACAAGCAATTAAGTGAACAGAGCTTAACCAATAG 3600  
3601 GTTTGTCTTACAGACGACGACCTGCAAGCAATTAATCAATATGTAAGCAATGAATC 3660  
3601 GTTTGTCTTACAGACGACGACCTGCAAGCAATTAATCAATATGTAAGCAATGAATC 3660  
3661 GTTTGTCTTACAGACGACGACCTGCAAGCAATTAATCAATATGTAAGCAATGAATC 3720  
3661 GTTTGTCTTACAGACGACGACCTGCAAGCAATTAATCAATATGTAAGCAATGAATC 3720  
3721 GCGACGCGACGAGAGGATTAAGTCTGACAGAGAACTGGAACGAGAGGCGCAATGCG 3780  
3721 GCGACGCGACGAGAGGATTAAGTCTGACAGAGAACTGGAACGAGAGGCGCAATGCG 3780  
3781 AGAGGCGCGCTGACGCGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3840  
3781 AGAGGCGCGCTGACGCGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3840  
3841 AATATTCAGATGATTTGCTGCGCCGATTCGATCTAATGAATTTCCATCTTACCGG 3900  
3841 AATATTCAGATGATTTGCTGCGCCGATTCGATCTAATGAATTTCCATCTTACCGG 3900  
3901 AGATGACTCGCGCTTGGCAAGATGAGGCAATTAACGACTGAAACTTTCAATTA 3960  
3901 AGATGACTCGCGCTTGGCAAGATGAGGCAATTAACGACTGAAACTTTCAATTA 3960  
3961 TGAAGATTAATTAATTTGAAACAGCTGTATCACTATGATTTAATGATGCTTACCT 4020  
3961 TGAAGATTAATTAATTTGAAACAGCTGTATCACTATGATTTAATGATGCTTACCT 4020  
4021 TGGCATTAAGAGATGATCTGCAACAAGACCAATCTGACAGATTTTAAATCTTA 4080  
4021 TGGCATTAAGAGATGATCTGCAACAAGACCAATCTGACAGATTTTAAATCTTA 4080  
4081 TGGACAGATTAATTAAGGATTAATTTCTTCTGAAATGTTATCAAGTGTGCGCTG 4140  
4081 TGGACAGATTAATTAAGGATTAATTTCTTCTGAAATGTTATCAAGTGTGCGCTG 4140  
4081 TGGACAGATTAATTAAGGATTAATTTCTTCTGAAATGTTATCAAGTGTGCGCTG 4140  
4081 TGGACAGATTAATTAAGGATTAATTTCTTCTGAAATGTTATCAAGTGTGCGCTG 4140  
4141 GCTTCAAGTGTACTTCAACAAGCGGTGCTGCTGATTTGCTGATTTGCTGAT 4200  
4141 GCTTCAAGTGTACTTCAACAAGCGGTGCTGCTGATTTGCTGATTTGCTGAT 4200  
4141 GCTTCAAGTGTACTTCAACAAGCGGTGCTGCTGATTTGCTGATTTGCTGAT 4200  
4201 CGCTTATCAACTTGTGCTTCACTTTGTTGAGAGCTGCTGATTTCAAGCTTCAAGCTA 4260  
4201 CGCTTATCAACTTGTGCTTCACTTTGTTGAGAGCTGCTGATTTCAAGCTTCAAGCTA 4260  
4261 TGGCAAGTAAAGGACCTGAGCACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320  
4261 TGGCAAGTAAAGGACCTGAGCACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320  
4321 TCGTGTAAATGCGCTGTAACGATTAACGCTCACTTCAATGCTGATTTGCTGCTG 4380  
4321 TCGTGTAAATGCGCTGTAACGATTAACGCTCACTTCAATGCTGATTTGCTGCTG 4380  
4321 TCGTGTAAATGCGCTGTAACGATTAACGCTCACTTCAATGCTGATTTGCTGCTG 4380  
4381 TAAATTTTGGCTAATTTTGGCCATAATGAGGTGACGCTTTTGTGCTGAAAAATTTTA 4440  
4381 TAAATTTTGGCTAATTTTGGCCATAATGAGGTGACGCTTTTGTGCTGAAAAATTTTA 4440  
4441 AGTSCAGACATGATGAGCAAGAGCTCAGCCAGAGATCAATCAAAATGCGATGCT 4500  
4441 AGTSCAGACATGATGAGCAAGAGCTCAGCCAGAGATCAATCAAAATGCGATGCT 4500  
4441 AGTSCAGACATGATGAGCAAGAGCTCAGCCAGAGATCAATCAAAATGCGATGCT 4500  
4441 AGTSCAGACATGATGAGCAAGAGCTCAGCCAGAGATCAATCAAAATGCGATGCT 4500  
4501 GCGAGACGAGAACTACACGTGGGTGAATTCAGCAATGAATTTGATCATGTAGTAAG 4560  
4501 GCGAGACGAGAACTACACGTGGGTGAATTCAGCAATGAATTTGATCATGTAGTAAG 4560

QY 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACTTCAAAGGCTGGATACAAATCATGAAGATG 4620  
 DB 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACTTCAAAGGCTGGATACAAATCATGAAGATG 4620  
 QY 4621 CTATCGATTCAGAGAGGAGGAGCAAGCAACCAATTCGTGAAACGAACATCTACATGATTT 4680  
 DB 4621 CTATCGATTCAGAGAGGAGGAGCAAGCAACCAATTCGTGAAACGAACATCTACATGATTT 4680  
 QY 4681 TATATTCGTATTCCTTCATCATATATTTGGATCCCTTTTTCACACTCAATCTGTTCAATGGTG 4740  
 DB 4681 TATATTCGTATTCCTTCATCATATATTTGGATCCCTTTTTCACACTCAATCTGTTCAATGGTG 4740  
 QY 4741 TTTATCTGATATTTTAAATGACAAAGAAAAGAGAGGTGATCATTAAGAAATGTTCA 4800  
 DB 4741 TTTATCTGATATTTTAAATGACAAAGAAAAGAGAGGTGATCATTAAGAAATGTTCA 4800  
 QY 4801 TGACAGAGATCAGAAAAAGTACTATATGCTATGAAAAAGATGGGCTTAAAAAAACAT 4860  
 DB 4801 TGACAGAGATCAGAAAAAGTACTATATGCTATGAAAAAGATGGGCTTAAAAAAACAT 4860  
 QY 4861 TAAAGCCATTCCTCAAGACCAAGGTGGGACCAAGCAATATGCTTTGAAATAGTAAACG 4920  
 DB 4861 TAAAGCCATTCCTCAAGACCAAGGTGGGACCAAGCAATATGCTTTGAAATAGTAAACG 4920  
 QY 4921 ATTAAGAAATTCGAT 4980  
 DB 4921 ATTAAGAAATTCGAT 4980  
 QY 4981 TCGATCGTACAGATGCGTGGGACCAAGTAAAGCGGCTTAAAGCTATCTCAATGCGATAT 5040  
 DB 4981 TCGATCGTACAGATGCGTGGGACCAAGTAAAGCGGCTTAAAGCTATCTCAATGCGATAT 5040  
 QY 5041 TCGATGATATATTCAGTTCGGAATGCTATTAATAAATATATTCGTTTACATATCAATAT 5100  
 DB 5041 TCGATGATATATTCAGTTCGGAATGCTATTAATAAATATATTCGTTTACATATCAATAT 5100  
 QY 5101 TTTATGAGCCATGGAATTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 DB 5101 TTTATGAGCCATGGAATTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 QY 5161 TACTTACGATATTTATGAGAGATGACTTCGTGCGCGACCTTCCTCCAGTGGTGCGTG 5220  
 DB 5161 TACTTACGATATTTATGAGAGATGACTTCGTGCGCGACCTTCCTCCAGTGGTGCGTG 5220  
 QY 5221 TGGCGAAAGTGGGCGCTGCTTCCTGACTGCTGTAAGGAGCAAGGCGATTCGACACTGC 5280  
 DB 5221 TGGCGAAAGTGGGCGCTGCTTCCTGACTGCTGTAAGGAGCAAGGCGATTCGACACTGC 5280  
 QY 5281 TCTTTCGCTTGGCGATGCTGCTGCGGCGCTTCCTTCATCATCTGCTGCTGCTGCTGCTG 5340  
 DB 5281 TCTTTCGCTTGGCGATGCTGCTGCGGCGCTTCCTTCATCATCTGCTGCTGCTGCTGCTG 5340  
 QY 5341 TCAATGTTCACTTTTCCCATTTTCCGCAATGCTGCTTCCTTCATGCAAGTGAAGAGAGAGCG 5400  
 DB 5341 TCAATGTTCACTTTTCCCATTTTCCGCAATGCTGCTTCCTTCATGCAAGTGAAGAGAGCG 5400  
 QY 5401 GCATTTAAGAGCTTACAACTTCAAGACCTTTGGCCAGAGCATGATCTCTCTCTTCA 5460  
 DB 5401 GCATTTAAGAGCTTACAACTTCAAGACCTTTGGCCAGAGCATGATCTCTCTCTTCA 5460  
 QY 5461 TGTGCAAGTCAAGCGGTTGGAGTGTGTATCGAGCGCATTTATCAATGAAGAGCATGCG 5520  
 DB 5461 TGTGCAAGTCAAGCGGTTGGAGTGTGTATCGAGCGCATTTATCAATGAAGAGCATGCG 5520  
 QY 5521 ATCCACCCGACAGAGCAAGAGCTATCCGCGCAATTTGGTTGACGAGCGTTGGAATTA 5580  
 DB 5521 ATCCACCCGACAGAGCAAGAGCTATCCGCGCAATTTGGTTGACGAGCGTTGGAATTA 5580  
 QY 5581 CGTTTCTCTCTCTACCTATGATTAAGCTTTTGAATGTTTAAATATATATGATGCTG 5640  
 DB 5581 CGTTTCTCTCTCTACCTATGATTAAGCTTTTGAATGTTTAAATATATATGATGCTG 5640  
 QY 5641 TCATTTCTGAGAACTATATATGTCAGGCAACGAGAGCTGCAAGAGGCTTAAACGAGACG 5700

DB 5641 TCATTTCTGAGAACTATATATGTCAGGCAACGAGAGCTGCAAGAGGCTTAAACGAGACG 5700  
 QY 5701 ACTACGACATGTAATAATGATCTGGCAGCAATTTGATTCGAGAGGCACTCAATATAC 5760  
 DB 5701 ACTACGACATGTAATAATGATCTGGCAGCAATTTGATTCGAGAGGCACTCAATATAC 5760  
 QY 5761 GCTATATATAGCTGTCCTGCAATTCCTGAGAGTATCGAGAGGCGGCTGAGATTCACAAAC 5820  
 DB 5761 GCTATATATAGCTGTCCTGCAATTCCTGAGAGTATCGAGAGGCGGCTGAGATTCACAAAC 5820  
 QY 5821 CGAACAGTACAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
 DB 5821 CGAACAGTACAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
 QY 5881 GCGTGCACATCTCTGACGCTTTCAGAAAGACTTCTTGGCGGAGAGGCAATCCGATAG 5940  
 DB 5881 GCGTGCACATCTCTGACGCTTTCAGAAAGACTTCTTGGCGGAGAGGCAATCCGATAG 5940  
 QY 5941 AGAGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
 DB 5941 AGAGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
 QY 6001 TCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6060  
 DB 6001 TCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6060  
 QY 6061 GCGGAAAGCAAGAGCGGCGGCGGAGAGAGTGGTCTTTGAGCCGATATAGGATCATG 6120  
 DB 6061 GCGGAAAGCAAGAGCGGCGGCGGAGAGAGTGGTCTTTGAGCCGATATAGGATCATG 6120  
 QY 6121 GCGATGCGGCTATCCGATGCGGAGGACCGGCGGCGGATGAAAGCAAGGACGCGGATG 6180  
 DB 6121 GCGATGCGGCTATCCGATGCGGAGGACCGGCGGCGGATGAAAGCAAGGACGCGGATG 6180  
 QY 6181 CGCCCGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
 DB 6181 CGCCCGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
 QY 6241 AGAGTATGTAATATGCTCGGCTGAGAGATGCAAGGCGGCGGATGCAAGGAGAGAGAG 6300  
 DB 6241 AGAGTATGTAATATGCTCGGCTGAGAGATGCAAGGCGGCGGATGCAAGGAGAGAGAG 6300  
 QY 6301 CGCGGCGGCGGCGGAG 6360  
 DB 6301 CGCGGCGGCGGCGGAG 6360  
 QY 6361 CGCGGCTTCTGCTGAG 6420  
 DB 6361 CGCGGCTTCTGCTGAG 6420  
 QY 6421 ACTGCGGATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
 DB 6421 ACTGCGGATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
 QY 6481 CCCTCCAGATGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540  
 DB 6481 CCCTCCAGATGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540

RESULT 5  
 PCT-US95-14378-7  
 ; Sequence 7, Application PC/TUS9514378  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warmke, Jeffrey W.  
 ; APPLICANT: Hall, Linda  
 ; APPLICANT: Feng, Gouping  
 ; APPLICANT: Van Der Ploeg, Leonardus  
 ; TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
 ; TITLE OF INVENTION: PARA SODIUM CHANNEL  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Roy D. Meredith

STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14378  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 19332 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6513 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-14378-7

Query Match 100.0%; Score 6513; DB 5; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACGTTGGCGCATAGACATGACGAGATTCGATCTGATCTGAGAGAAC 60  
DB 1 TCTAGACGTTGGCGCATAGACATGACGAGATTCGATCTGATCTGAGAGAAC 60  
QY 61 GCAGTTTGTTCCTTCCTTTACCCGCGAATCTGTCGAATCCAAACGACATTCGCG 120  
DB 61 GCAGTTTGTTCCTTCCTTTACCCGCGAATCTGTCGAATCCAAACGACATTCGCG 120  
QY 121 CTGAACATGAAAG 180  
DB 121 CTGAACATGAAAG 180  
QY 121 CTGAACATGAAAG 180  
DB 121 CTGAACATGAAAG 180  
QY 181 ATGTCGCAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGATC 240  
DB 181 ATGTCGCAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGATC 240  
QY 241 CACAAACCGGATCTACATCTGAAACAGGCTGTCATCTGTCATCTGTCATCTGTCAT 300  
DB 241 CACAAACCGGATCTACATCTGAAACAGGCTGTCATCTGTCATCTGTCATCTGTCAT 300  
QY 301 TCCCGCGGAGATTCGCTCCACTCTCTCGAGAGATTCGCTCCACTCCACTCCACTCC 360  
DB 301 TCCCGCGGAGATTCGCTCCACTCTCTCGAGAGATTCGCTCCACTCCACTCCACTCC 360  
QY 361 TGAATTCGTAAGTGAAG 420  
DB 361 TGAATTCGTAAGTGAAG 420  
QY 421 TGTGATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 480  
DB 421 TGTGATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 480  
QY 481 CATATTTTCCCTATTCATCTACACCAATTTCTGATCTGATCTGATCTGATCTGATCT 540  
DB 481 CATATTTTCCCTATTCATCTACACCAATTTCTGATCTGATCTGATCTGATCTGATCT 540  
QY 541 CGACAAAGCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
DB 541 CGACAAAGCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 601 CAGCTGTTAAAGTATGACAGAGATTCATTTATGCGCCGTTACGATCTTAGAGATG 660  
DB 601 CAGCTGTTAAAGTATGACAGAGATTCATTTATGCGCCGTTACGATCTTAGAGATG 660  
QY 661 CATGAAATTTGCTGAGCTTCGTAAGTATGATGATGATGATGATGATGATGATGATG 720  
DB 661 CATGAAATTTGCTGAGCTTCGTAAGTATGATGATGATGATGATGATGATGATGATG 720  
QY 721 TAGGTAATCTAGCAGAGCCCTGCGAAGTTTAGAGGTCGCGAGCGTTAAACCGTAGCA 780  
DB 721 TAGGTAATCTAGCAGAGCCCTGCGAAGTTTAGAGGTCGCGAGCGTTAAACCGTAGCA 780  
QY 781 TTGTGCGAGGCTTGAAGCAATCGTCGCGCCGTCATCGAATCGGTGAAGATCTGCGCG 840  
DB 781 TTGTGCGAGGCTTGAAGCAATCGTCGCGCCGTCATCGAATCGGTGAAGATCTGCGCG 840  
QY 841 ATGATATATCTGACCGCATGTTCTCCGTCGAGTTCGCGTTGATGAGGCGCTACAGATCT 900  
DB 841 ATGATATATCTGACCGCATGTTCTCCGTCGAGTTCGCGTTGATGAGGCGCTACAGATCT 900  
QY 901 ATATGAGGCGTCTGACCGAGAGATGATCAAGAAATTCGCGTGAACGTTCTGAGGCA 960  
DB 901 ATATGAGGCGTCTGACCGAGAGATGATCAAGAAATTCGCGTGAACGTTCTGAGGCA 960  
QY 961 ATCTGACCGAG 1020  
DB 961 ATCTGACCGAG 1020  
QY 1021 ACGAGGAGCATCTCATTTCCGTTATGCGGCAATATATCCGTCGAGGAGAGAGAGAGAG 1080  
DB 1021 ACGAGGAGCATCTCATTTCCGTTATGCGGCAATATATCCGTCGAGGAGAGAGAGAGAG 1080  
QY 1081 ATTAAGTGTGCTGACAGGAGGTTTGTCGAATCCGAATATAGGCTACACAGCTTCGATT 1140  
DB 1081 ATTAAGTGTGCTGACAGGAGGTTTGTCGAATCCGAATATAGGCTACACAGCTTCGATT 1140  
QY 1141 CGTTCCGATGAGGCTTTCTGTCGCGCTTCGCGGCTGATGACACAGAGCTTCGAGAGATC 1200  
DB 1141 CGTTCCGATGAGGCTTTCTGTCGCGCTTCGCGGCTGATGACACAGAGCTTCGAGAGATC 1200  
QY 1201 TGTAACAGCTGATGAGGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
DB 1201 TGTAACAGCTGATGAGGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
QY 1261 TCTTCTAGGTTCAATCTGATCTGTAATTTGATTTTGCCATTGTCATGTCGATG 1320  
DB 1261 TCTTCTAGGTTCAATCTGATCTGTAATTTGATTTTGCCATTGTCATGTCGATG 1320  
QY 1321 ACGAATTCGAAAG 1380  
DB 1321 ACGAATTCGAAAG 1380  
QY 1381 CGGAAGAGCTGCGCGCGCGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
DB 1381 CGGAAGAGCTGCGCGCGCGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
QY 1441 AGGAG 1500  
DB 1441 AGGAG 1500  
QY 1501 GTCCGAGGATTTCTTGAATCAAGCTATGAGCTATTTGTTGAGGAGAGAGAGAGAGAG 1560  
DB 1501 GTCCGAGGATTTCTTGAATCAAGCTATGAGCTATTTGTTGAGGAGAGAGAGAGAGAG 1560  
QY 1561 ACAACAACAAAGAGAGAGATGCTATTCGAGAGCTGAGAGTGAATCGAGTCTGAGAGG 1620  
DB 1561 ACAACAACAAAGAGAGAGATGCTATTCGAGAGCTGAGAGTGAATCGAGTCTGAGAGG 1620  
QY 1621 TTATACAAAGCAACAGACCTTACACAGACACCAAGCTTACCAAGTTCTGTAAGTGA 1680  
DB 1621 TTATACAAAGCAACAGACCTTACACAGACACCAAGCTTACCAAGTTCTGTAAGTGA 1680

QY	1681	GCACGACATCCTTATCTCTTACCTGTCCACCGCTTTAAACATACGACGAGGATACACGATGT	1740
Db	1681	GCACGACATCCTTATCTCTTACCTGTCCACCGCTTTAAACATACGACGAGGATACGATGAT	1740
QY	1741	CTCACAGTACACGATACGGAACGGAAGTGGCGCTTTGGTATACCGCGTAGCGATCGTA	1800
Db	1741	CTCACAGTACACGATACGGAACGGAAGTGGCGCTTTGGTATACCGCGTAGCGATCGTA	1800
QY	1801	AGCCATTGGTATTTGTCAACATATACGATATGCCCCACAGACCTTGCCCTATGCCGACGACT	1860
Db	1801	AGCCATTGGTATTTGTCAACATATACGATATGCCCCACAGACCTTGCCCTATGCCGACGACT	1860
QY	1861	CGAATGCCGATACCCCGATGTCCGAGAGAGATGGGGCCATCATATGTCGCCGTACTATG	1920
Db	1861	CGAATGCCGATACCCCGATGTCCGAGAGAGATGGGGCCATCATATGTCGCCGTACTATG	1920
QY	1921	GCAATCTAAGCTCCCGACACTCATGTATTAACCTTCGATCAAGTCCGATATTCGTATACCT	1980
Db	1921	GCAATCTAAGCTCCCGACACTCATGTATTAACCTTCGATCAAGTCCGATATTCGTATACCT	1980
QY	1981	CACATGGGAGATCTATCTGGGGGGGAGATGGCGGCTCATGGGCGTACAGACAATACCAAGAGA	2040
Db	1981	CACATGGGAGATCTATCTGGGGGGGAGATGGCGGCTCATGGGCGTACAGACAATACCAAGAGA	2040
QY	2041	GCAAAATTCGCGAACCCGCAACACACGCAATCAATCATGTGGGCGCCACCAATGGCGGCACCA	2100
Db	2041	GCAAAATTCGCGAACCCGCAACACACGCAATCAATCATGTGGGCGCCACCAATGGCGGCACCA	2100
QY	2101	CTGTCTGTGGACCAACCATACAAAGCTCGATCATGTGGCGCTACGAAATTTGGCTGGAGTGA	2160
Db	2101	CTGTCTGTGGACCAACCATACAAAGCTCGATCATGTGGCGCTACGAAATTTGGCTGGAGTGA	2160
QY	2161	CGGACGAAGCTGGCAAGATTAACATCATATGACATCCCTTTATGAGCCCGCTCCAGACAC	2220
Db	2161	CGGACGAAGCTGGCAAGATTAACATCATATGACATCCCTTTATGAGCCCGCTCCAGACAC	2220
QY	2221	AAACGGTGGTGTGATATGAAAGAATGTGATGTCTCGAATGACATATGAAACAGGCGGCTG	2280
Db	2221	AAACGGTGGTGTGATATGAAAGAATGTGATGTCTCGAATGACATATGAAACAGGCGGCTG	2280
QY	2281	GTGGGCAAGTTCGGGCAAGCATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGACG	2340
Db	2281	GTGGGCAAGTTCGGGCAAGCATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGACG	2340
QY	2341	ATGACGAGAGATGGGCGGACGTTCAAAAGCAACAGGCACTCGAAAGTATCTCAAAAGCATCG	2400
Db	2341	ATGACGAGAGATGGGCGGACGTTCAAAAGCAACAGGCACTCGAAAGTATCTCAAAAGCATCG	2400
QY	2401	ATGTGTTTGTGTGTGGGACGTGGCTGGATTGGTGAATTTCAAGAGTGGGATATCGC	2460
Db	2401	ATGTGTTTGTGTGTGGGACGTGGCTGGATTGGTGAATTTCAAGAGTGGGATATCGC	2460
QY	2461	TCATGCTCTTCGATCCCTTCGTGTGAGCTCTTCATACAGCTGTGCATTTGTGTCAACACGA	2520
Db	2461	TCATGCTCTTCGATCCCTTCGTGTGAGCTCTTCATACAGCTGTGCATTTGTGTCAACACGA	2520
QY	2521	TGTTATATGGCAATGATATCAACACGATATGAAACAAGAGATGGAACGCGTGTCAAGAGTG	2580
Db	2521	TGTTATATGGCAATGATATCAACACGATATGAAACAAGAGATGGAACGCGTGTCAAGAGTG	2580
QY	2581	GCAACTATTTCTTCAACCGGCACTTTGTCATGAGGCGCACCATGAGACTTAATGCGCATGA	2640
Db	2581	GCAACTATTTCTTCAACCGGCACTTTGTCATGAGGCGCACCATGAGACTTAATGCGCATGA	2640
QY	2641	GCCCCAAGTACATTTTCCAGAGGGCTGGAACATTTGACCTTATATCGTGGCCCAT	2700
Db	2641	GCCCCAAGTACATTTTCCAGAGGGCTGGAACATTTGACCTTATATCGTGGCCCAT	2700
QY	2701	CGCTATTGGAACTGGGAGCTCGAGGGTGTCAAGGTCGTGCGTATTTGCGTTCCTTTGCAT	2760
Db	2701	CGCTATTGGAACTGGGAGCTCGAGGGTGTCAAGGTCGTGCGTATTTGCGTTCCTTTGCAT	2760
QY	2761	TGCTGCGTATTTCAAACTGGCGAAAGCTTTGGCCCAACTTATTTACTCATTTTCGATTA	2820

Db	2761	TGCTGGGTGTAATTCAAACGCGCCAACTCTTGCCCACTTATATTAATCAATTCGATTA	2820
QY	2821	TGGAGCGACACATGGGCGCTTTGGGTAACTGCACTTTGTACTTTGCATTAATCATCTTCA	2880
Db	2821	TGGAGCGACACATGGGCGCTTTGGGTAACTGCACTTTGTACTTTGCATTAATCATCTTCA	2880
QY	2881	TCTTTGGGTGATGGGATATGCACTGTTGGGAAAGAAATTATCATGTATTCACAGACCGGT	2940
Db	2881	TCTTTGGGTGATGGGATATGCACTGTTGGGAAAGAAATTATCATGTATTCACAGACCGGT	2940
QY	2941	TTCCGAGTGGCGACCTGCGCGCTTGGAACCTTACACGACTTATAGCACAGCTTCATATCG	3000
Db	2941	TTCCGAGTGGCGACCTGCGCGCTTGGAACCTTACACGACTTATAGCACAGCTTCATATCG	3000
QY	3001	TGTTCCGGGTGCTCTGCGAGAAATGATATGATGTCATGTGGGACTGTCATAGTGGGGCG	3060
Db	3001	TGTTCCGGGTGCTCTGCGAGAAATGATATGATGTCATGTGGGACTGTCATAGTGGGGCG	3060
QY	3061	ATGTCCTGTCATCTCCCTTCTTCTGCGCCACCGTGTGCATCGGCAATCTGTGTACTTAA	3120
Db	3061	ATGTCCTGTCATCTCCCTTCTTCTGCGCCACCGTGTGCATCGGCAATCTGTGTACTTAA	3120
QY	3121	ACCTTTCTTACGCTTGCTTTGTGTCOAATTTGACTCATCTATACGCGCCGACTG	3180
Db	3121	ACCTTTCTTACGCTTGCTTTGTGTCOAATTTGACTCATCTATACGCGCCGACTG	3180
QY	3181	CCGATTAACGATAGGAATTAATAATGCGAGGCGCTTCAATCGAATGGCCGATTTAAAGTT	3240
Db	3181	CCGATTAACGATAGGAATTAATAATGCGAGGCGCTTCAATCGAATGGCCGATTTAAAGTT	3240
QY	3241	GGGTTAAGCGTAATATTTGCTGATTTGTTTCAAGTTAATACGTAACTAATTGACAAATCAA	3300
Db	3241	GGGTTAAGCGTAATATTTGCTGATTTGTTTCAAGTTAATACGTAACTAATTGACAAATCAA	3300
QY	3301	TAAATGATTCAAACCATCAGTGTGAGAGGACCAACCAAGATCACTGGATTTGGAGGAAAGC	3360
Db	3301	TAAATGATTCAAACCATCAGTGTGAGAGGACCAACCAAGATCACTGGATTTGGAGGAAAGC	3360
QY	3361	ATGATGACAACGAATCTGAGCTGGGCCACGACGAGATCCTCGCGCAGCGGCTCATCAAGA	3420
Db	3361	ATGATGACAACGAATCTGAGCTGGGCCACGACGAGATCCTCGCGCAGCGGCTCATCAAGA	3420
QY	3421	AGGCGATTCAGAGACGACGCAACTGGAAGTGTGCATCTGGGATTCGGATAGGAATTCACGA	3480
Db	3421	AGGCGATTCAGAGACGACGCAACTGGAAGTGTGCATCTGGGATTCGGATAGGAATTCACGA	3480
QY	3481	TACACGGCGACATGAAGAACCAACAGCGCGAAATCAATATCTTAATTAACGCAACGA	3540
Db	3481	TACACGGCGACATGAAGAACCAACAGCGCGAAATCAATATCTTAATTAACGCAACGA	3540
QY	3541	TGATTTGGCACTCAATTAACCAACGAACATTAAGCTGTGAAACACAGACTAAACCATAGAG	3600
Db	3541	TGATTTGGCACTCAATTAACCAACGAACATTAAGCTGTGAAACACAGACTAAACCATAGAG	3600
QY	3601	GTTTGTGCTTACAGAGACGACACTGCGACATTAATCTCAATGTGTAGCATTAAGATC	3660
Db	3601	GTTTGTGCTTACAGAGACGACACTGCGACATTAATCTCAATGTGTAGCATTAAGATC	3660
QY	3661	GACCATTCAGAGACGAGCCACAAGGCGACGCTCGAGACGATGGAGGGCGACGAGAGAC	3720
Db	3661	GACCATTCAGAGACGAGCCACAAGGCGACGCTCGAGACGATGGAGGGCGACGAGAGAC	3720
QY	3721	GCGACGCGCAGAAAGAGATTTAGGTCTCGACGAGAACTGTGACGAGAGGGCGAAATCGC	3780
Db	3721	GCGACGCGCAGAAAGAGATTTAGGTCTCGACGAGAACTGTGACGAGAGGGCGAAATCGC	3780
QY	3781	AGGAGGCGCCCTCGACGGTATATCAATTAATTCACACGAGAGATTAATCTCATG	3840
Db	3781	AGGAGGCGCCCTCGACGGTATATCAATTAATTCACACGAGAGATTAATCTCATG	3840
QY	3841	AATATCCAGCTGATTTGCTGCCGATTTGATCTATTAAGAAATTTCCATCTTACCGGTG	3900
Db	3841	AATATCCAGCTGATTTGCTGCCGATTTGATCTATTAAGAAATTTCCATCTTACCGGTG	3900

Dh 3841 AATAATCCAGCTGATGCTGCCCCGATGCTACTATAGAATAATTCGATCTTAGCCGGG 3900  
Qy 3901 ACGATGATCGCCCGCTTTCGCAAGATGGGGCAATTTACGACTGAAAATTTCATTTA 3960  
Db 3901 ACGATGATCGCCCGCTTTCGCAAGATGGGGCAATTTACGACTGAAAATTTCATTTA 3960  
Qy 3961 TTGAAAATTAATATTTTGAACAGCTGTATCATCATGATTTTAAATGAGTACCTAGCT 4020  
Db 3961 TTGAAAATTAATATTTTGAACAGCTGTATCATCATGATTTTAAATGAGTACCTAGCT 4020  
Qy 4021 TGGCAATTAAGATGTACATCTGCCCAAGAACCCATCTGAGAGATATTTATATCTATA 4080  
Db 4021 TGGCAATTAAGATGTACATCTGCCCAAGAACCCATCTGAGAGATATTTATATCTATA 4080  
Qy 4081 TGGACAGAAATTTTACGCTTATATCTTCTTGAAATGTATCAAGTGTGGCGCTCG 4140  
Db 4081 TGGACAGAAATTTTACGCTTATATCTTCTTGAAATGTATCAAGTGTGGCGCTCG 4140  
Qy 4141 GCTTCAAGATGTAATCTTCAACACGGGCTGTGGCTGATTTGCTGATTTGCTGAT 4200  
Db 4141 GCTTCAAGATGTAATCTTCAACACGGGCTGTGGCTGATTTGCTGATTTGCTGAT 4200  
Qy 4201 CGCTTATCACTCTGCTCTTCACTTGTGAGCTGTGTATTCAGACCTTCAAGACTA 4260  
Db 4201 CGCTTATCACTCTGCTCTTCACTTGTGAGCTGTGTATTCAGACCTTCAAGACTA 4260  
Qy 4261 TGGCAACCTTAAAGACACTGAGACCACTACGCTGCTCCGTAATGCAAGGCGATGAGG 4320  
Db 4261 TGGCAACCTTAAAGACACTGAGACCACTACGCTGCTCCGTAATGCAAGGCGATGAGG 4320  
Qy 4321 TCGTGTATATGCGCTGTGTAACAGCTATACGCTCATCTTCAATGTGCTATTTGCTGTC 4380  
Db 4321 TCGTGTATATGCGCTGTGTAACAGCTATACGCTCATCTTCAATGTGCTATTTGCTGTC 4380  
Qy 4381 TAATATATTTGGCTATATTTTGGCATATGAGTGTATACAGCTTTTGTGCTGAAAATATTTTA 4440  
Db 4381 TAATATATTTGGCTATATTTTGGCATATGAGTGTATACAGCTTTTGTGCTGAAAATATTTTA 4440  
Qy 4441 AGTCGAGGAGATGAAATGGCAAGAGCTCAGCCAGCAATCATACCAATTCGCATGCTCT 4500  
Db 4441 AGTCGAGGAGATGAAATGGCAAGAGCTCAGCCAGCAATCATACCAATTCGCATGCTCT 4500  
Qy 4501 GCGAGAGGAGAACTTACAGTGGGTGAATTCAGCAATGATTTGATCATGTAGGTAACG 4560  
Db 4501 GCGAGAGGAGAACTTACAGTGGGTGAATTCAGCAATGATTTGATCATGTAGGTAACG 4560  
Qy 4561 CGTATCTGTGCTTTTCCAGTGGCCACTTCAAGGCTGTGATACCAATTCATGAAACGATG 4620  
Db 4561 CGTATCTGTGCTTTTCCAGTGGCCACTTCAAGGCTGTGATACCAATTCATGAAACGATG 4620  
Qy 4621 CTATGATTCAGAGAGGTGACAAAGCAATTCGTGAACCGAACATCTACATGTATTT 4680  
Db 4621 CTATGATTCAGAGAGGTGACAAAGCAATTCGTGAACCGAACATCTACATGTATTT 4680  
Qy 4681 TATATTTGATTTCTTCAATATTTGATGATCTTTTCACTCAATCTGTGCTGATG 4740  
Db 4681 TATATTTGATTTCTTCAATATTTGATGATCTTTTCACTCAATCTGTGCTGATG 4740  
Qy 4741 TTATCATTTGATATTTTATGAGCAAAAGAAAAGAGAGCTGATCATTAAGATGTTCA 4800  
Db 4741 TTATCATTTGATATTTTATGAGCAAAAGAAAAGAGAGCTGATCATTAAGATGTTCA 4800  
Qy 4801 TGAAGAGATGAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAATAAACCAT 4860  
Db 4801 TGAAGAGATGAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAATAAACCAT 4860  
Qy 4861 TAAAGACATTCGAAGCAAGAGTGGGAGCAACAGCAATAGCTTTTAAATATGATGACG 4920  
Db 4861 TAAAGACATTCGAAGCAAGAGTGGGAGCAACAGCAATAGCTTTTAAATATGATGACG 4920  
Qy 4921 ATAAAGAAATTCGATATTAATCATTTATGTTATTCATTTGCTGAAACATGTTCAACGATGACCC 4980  
Db 4921 ATAAAGAAATTCGATATTAATCATTTATGTTATTCATTTGCTGAAACATGTTCAACGATGACCC 4980

Qy 4981 TCGATCGTACAGTCCGTCGAGCAAGTATTAACGGGCTTCATGACTATCTCAATGAGATAT 5040  
Db 4981 TCGATCGTACAGTCCGTCGAGCAAGTATTAACGGGCTTCATGACTATCTCAATGAGATAT 5040  
Qy 5041 TCGATGATATTTTCAAGTCCGAATGTCTATTAATAATATTCGCTTACGATATCACTATT 5100  
Db 5041 TCGATGATATTTTCAAGTCCGAATGTCTATTAATAATATTCGCTTACGATATCACTATT 5100  
Qy 5101 TTATTTAGCCATGAAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATG 5160  
Db 5101 TTATTTAGCCATGAAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATG 5160  
Qy 5161 TACTTAAAGATATTTTAAAGAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220  
Db 5161 TACTTAAAGATATTTTAAAGAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5220  
Qy 5221 TGGCAAAAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5280  
Db 5221 TGGCAAAAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5280  
Qy 5281 TCTTTCGCTTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5340  
Db 5281 TCTTTCGCTTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5340  
Qy 5341 TCAATGCTATCTTGGCCATTTTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5400  
Db 5341 TCAATGCTATCTTGGCCATTTTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5400  
Qy 5401 GCATTAACGAGCTGTAACAACTTCAAGACCTTTGGCCAGAGATATCTGCTCTTTCAGA 5460  
Db 5401 GCATTAACGAGCTGTAACAACTTCAAGACCTTTGGCCAGAGATATCTGCTCTTTCAGA 5460  
Qy 5461 TGTGAGCTGAGCCGCTTGGAGTGTGATCTGACGCCATTTATCATATGAGAGAGATGCG 5520  
Db 5461 TGTGAGCTGAGCCGCTTGGAGTGTGATCTGACGCCATTTATCATATGAGAGAGATGCG 5520  
Qy 5521 ATTCACCCGACAGGAGCAAGAGGCTATCCGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTG 5580  
Db 5521 ATTCACCCGACAGGAGCAAGAGGCTATCCGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTG 5580  
Qy 5581 CGTTTCTCTCTCATACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
Db 5581 CGTTTCTCTCTCATACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640  
Qy 5641 TCAATTCGAGAACTATAGTCAAGGCCACCGAGAGCTGCAAGAGGCTTAAACGACGAG 5700  
Db 5641 TCAATTCGAGAACTATAGTCAAGGCCACCGAGAGCTGCAAGAGGCTTAAACGACGAG 5700  
Qy 5701 ACTACGACATGATATGATGATCTGAGCAAGATTCGAGAGGCAACCCAGATACATAC 5760  
Db 5701 ACTACGACATGATATGATGATCTGAGCAAGATTCGAGAGGCAACCCAGATACATAC 5760  
Qy 5761 GCTATGATCACTGCTGCAATTTCTGAGACGTAAGAGCCCGCTGCAAGATTCACAAAC 5820  
Db 5761 GCTATGATCACTGCTGCAATTTCTGAGACGTAAGAGCCCGCTGCAAGATTCACAAAC 5820  
Qy 5821 CGAACAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
Db 5821 CGAACAGTACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5880  
Qy 5881 GCGTGCATCTCTGAGAGCCCTTACGAAAGACTTTTGGCGGAGAGGCAATCCGATAG 5940  
Db 5881 GCGTGCATCTCTGAGAGCCCTTACGAAAGACTTTTGGCGGAGAGGCAATCCGATAG 5940  
Qy 5941 AGGAGACGGGTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
Db 5941 AGGAGACGGGTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
Qy 6001 TCTCATCAACGCTGTGCGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
Db 6001 TCTCATCAACGCTGTGCGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 6060

QY 6061 GGCGAAGCACAAGCGCGCGCGAGAGAGTGGTCTTTGAGCCGGATACGGATCATG 6120  
 DB 6061 GGCGAAGCACAAGCGCGCGCGAGAGAGTGGTCTTTGAGCCGGATACGGATCATG 6120  
 QY 6121 GCGATGGCGGTATTCGGATGCGCGGAGACCCGCGCCCATTAAGACAGAGCGCGAGT 6180  
 DB 6121 GCGATGGCGGTATTCGGATGCGCGGAGACCCGCGCCCATTAAGACAGAGCGCGAGT 6180  
 QY 6181 CGCGCGGTGGTGAAGATGATAGTGTAAAGGTAAGTGAAGAGAGTGGCGATGCGATG 6240  
 DB 6181 CGCGCGGTGGTGAAGATGATAGTGTAAAGGTAAGTGAAGAGAGTGGCGATGCGATG 6240  
 QY 6241 AGAGTATGTAATAGTCCGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAG 6300  
 DB 6241 AGAGTATGTAATAGTCCGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAG 6300  
 QY 6301 CGCGCGGTGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6360  
 DB 6301 CGCGCGGTGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6360  
 QY 6361 CGCGCGGTGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6420  
 DB 6361 CGCGCGGTGGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6420  
 QY 6421 ACTGCGATGCGCGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6480  
 DB 6421 ACTGCGATGCGCGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6480  
 QY 6481 CCTCCAGATGCAAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6513  
 DB 6481 CCTCCAGATGCAAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 6513

## RESULT 6

US-08-793-24

Sequence 24 Application US/0808793

Patent No. 5858713

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS

TITLE OF INVENTION: AND USE THEREOF

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans &amp; Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,793

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,361

FILING DATE: 24-DEC-1996

CLASSIFICATION: 435

APPLICATION NUMBER: US 60/012,649

FILING DATE: 01-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Braman, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-263-1636

TELEFAX: 716-263-1600  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6519 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-793-24

Query Match 94.6%; Score 6163.8; DB 2; Length 6519;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 6339; Conservative 0; Mismatches 12; Indels 138; Gaps 3;

QY 24 ATGACAGAGATTCGAGTCTGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 83  
 DB 1 ATGACAGAGATTCGAGTCTGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
 QY 84 CGCGAATCATTTGGTGAAGATGAGACAGAGATTCGAGATGAGAGAGAGAGAGAGAGAG 143  
 DB 61 CGCGAATCATTTGGTGAAGATGAGACAGAGATTCGAGATGAGAGAGAGAGAGAGAGAG 120  
 QY 144 CTGGAAG 203  
 DB 121 CTGGAAG 180  
 QY 204 GAATTCGATATGATGAG 263  
 DB 181 GAATTCGATATGATGAG 240  
 QY 264 CAGGTGTGCAATACCTGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
 DB 241 CAGGTGTGCAATACCTGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 324 CCTCTGAGAGATTCGATTCCTACTACAGATTCCTACTACAGATTCCTACTACAGATTC 383  
 DB 301 CCTCTGAGAGATTCGATTCCTACTACAGATTCCTACTACAGATTCCTACTACAGATTC 360  
 QY 384 GGAAGAGATATTTTGGCTTTTCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443  
 DB 361 GGAAGAGATATTTTGGCTTTTCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 QY 444 CCGATACGTCGTGAGCAATTTACATTTAGTGCATCATTTATTTTCCCTATTCATCATC 503  
 DB 421 CCGATACGTCGTGAGCAATTTACATTTAGTGCATCATTTATTTTCCCTATTCATCATC 480  
 QY 504 ACCACAAATTCGTCAATCGCATTCCTGATGATGATGATGATGATGATGATGATGATG 563  
 DB 481 ACCACAAATTCGTCAATCGCATTCCTGATGATGATGATGATGATGATGATGATGATG 540  
 QY 564 ACTGAGGTGATTCACCGGATCTCAATTTGATGATGATGATGATGATGATGATGATGATG 623  
 DB 541 ACTGAGGTGATTCACCGGATCTCAATTTGATGATGATGATGATGATGATGATGATGATG 600  
 QY 624 GATTTCATTTTATGCGCGTTTACGATCTTGAAGATGATGATGATGATGATGATGATGATG 683  
 DB 601 GATTTCATTTTATGCGCGTTTACGATCTTGAAGATGATGATGATGATGATGATGATGATG 660  
 QY 684 GTATATGATTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
 DB 661 GTATATGATTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
 QY 744 ACGTTTATGAGGTGAG 803  
 DB 721 ACGTTTATGAGGTGAG 780  
 QY 804 GTGCGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
 DB 781 GTGCGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 QY 864 TCCCTGTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 923  
 DB 841 TCCCTGTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

QY 924 TGCATCAAGAGTTCCCGCTGGAGCGTTCTGGGGCAATCTGACCGAGAGAACTGGGAC 983  
Db 901 TGCATCAAGAGTTCCCGCTGGAGCGTTCTGGGGCAATCTGACCGAGAGAACTGGGAC 960  
QY 984 TATCACAATCGCAATAGCTCCAAATTGGATTCGAGAGACGAGGCAATCTCAATTCCTGTA 1043  
Db 961 TATCACAATCGCAATAGCTCCAAATTGGATTCGAGAGACGAGGCAATCTCAATTCCTGTA 1020  
QY 1044 TGGCGCAATATATCCGGTGGCGGGCAATGCGACGATTAAGTGTGCTGACAGGGGTTT 1103  
Db 1021 TGGCGCAATATATCCGGTGGCGGGCAATGCGACGATTAAGTGTGCTGACAGGGGTTT 1080  
QY 1104 GGTCCGAATCCGAATTAATGCTACACGAGCTTCGATTCGATGGGCTTTCCTGTC 1163  
Db 1081 GGTCCGAATCCGAATTAATGCTACACGAGCTTCGATTCGATGGGCTTTCCTGTC 1140  
QY 1164 GCTTTCGGCTGATGACACAGGACTTCTGGAGAGATCTGACAGCTGTGTTGCGGCGC 1223  
Db 1141 GCTTTCGGCTGATGACACAGGACTTCTGGAGAGATCTGACAGCTGTGTTGCGGCGC 1200  
QY 1224 GCGGAGCCATGAGCAATGCTGTTCTTAATGATCATCTTCTAGGTTCAATTCATT 1283  
Db 1201 GCGGAGCCATGAGCAATGCTGTTCTTAATGATCATCTTCTAGGTTCAATTCATT 1260  
QY 1284 GTGAATTTGATTTTGGCCATTTGTCATGTCGATGACGAAATTCGAAAGAGAGCGGAA 1343  
Db 1261 GTGAATTTGATTTTGGCCATTTGTCATGTCGATGACGAAATTCGAAAGAGAGCGGAA 1320  
QY 1344 GAAGAAAGAGCTGCGAAG 1403  
Db 1321 GAAGAAAGAGCTGCGAAG 1380  
QY 1404 GCGGCAAGCTGAG 1463  
Db 1381 GCGGCAAGCTGAG 1440  
QY 1464 GCGGCAAGAGCTGAG 1523  
Db 1441 GCGGCAAGAGCTGAG 1500  
QY 1524 TATGAGCTATTTTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583  
Db 1501 TATGAGCTATTTTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
QY 1584 ATTGAGAGCTGAG 1643  
Db 1561 ATTGAGAGCTGAG 1620  
QY 1644 ACCAGAGCAACAG 1703  
Db 1621 ACCAGAGCAACAG 1680  
QY 1704 GGTTCACGTTTAAATATAG 1763  
Db 1681 GGTTCACGTTTAAATATAG 1740  
QY 1764 GAGAGTGGCGCTTGGTATATCCGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823  
Db 1741 GAGAGTGGCGCTTGGTATATCCGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1824 CAGAGATCCCAAG 1883  
Db 1801 CAGAGATCCCAAG 1860  
QY 1884 GAAGAGATGGGAG 1943  
Db 1861 GAAGAGATGGGAG 1920  
QY 1944 TCGATATCTTCGATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2003  
Db 1921 TCGATATCTTCGATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980

QY 2004 ATGGCCGTCATGGGCGTCAG 2063  
Db 1981 ATGGCCGTCATGGGCGTCAG 2040  
QY 2064 CGCAATCAATCAGTGGGCGGCGCAGCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2123  
Db 2041 CGCAATCAATCAGTGGGCGGCGCAGCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
QY 2124 CTGATCATGAG 2183  
Db 2101 CTGATCATGAG 2160  
QY 2184 CATATGACATCTTTATGAG 2243  
Db 2161 CATATGACATCTTTATGAG 2220  
QY 2244 GTGATGCTCTGATATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2303  
Db 2221 GTGATGCTCTGATATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
QY 2304 GCGGCTGTCTCCGTTTAACTTTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2363  
Db 2281 GCGGCTGTCTCCGTTTAACTTTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
QY 2364 AAGAGCAAGGAG 2423  
Db 2341 AAGAGCAAGGAG 2400  
QY 2424 TGTGAGGTTTGTGTAATTTAG 2483  
Db 2401 TGTGAGGTTTGTGTAATTTAG 2460  
QY 2484 GAGCTCTTCAATCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2543  
Db 2461 GAGCTCTTCAATCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520  
QY 2544 GATATGAAAG 2603  
Db 2521 GATATGAAAG 2580  
QY 2604 TTTGCAATGAG 2663  
Db 2581 TTTGCAATGAG 2640  
QY 2664 GGTGGAACATCTTCAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2723  
Db 2641 GGTGGAACATCTTCAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2700  
QY 2724 GGTGTCAG 2783  
Db 2701 GGTGTCAG 2760  
QY 2784 AAGCTTGGCCCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2843  
Db 2761 AAGCTTGGCCCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2820  
QY 2844 GGTATCTGACATTTGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2903  
Db 2821 GGTATCTGACATTTGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2880  
QY 2904 CTGTTTGGAG 2963  
Db 2881 CTGTTTGGAG 2940  
QY 2964 TGGAACTTCAAG 3023  
Db 2941 TGGAACTTCAAG 3000  
QY 3024 TGGATGAGTCAATGAG 3083  
Db 3001 TGGATGAGTCAATGAG 3060  
QY 3084 TTGGCAACGGTGTATGAG 3143

Db 3037 TTGGCCACGGTGTCTCGGCATCTTGTGTACTTAACCTTTCTTACCTTGTCTTTTG 3096  
Qy 3144 TCCAAATTTTGGCTCATCTAGCTTATGAGGCGGACCTGCGATACATAGATAGATAAATA 3203  
Db 3097 TCCAAATTTTGGCTCATCTAGCTTATGAGGCGGACCTGCGATACATAGATAGATAAATA 3156  
Qy 3204 GCCGAGGCTTCAATGCAATTTGGCCGATTTAAAAGTTGGTTAAGGTAAATTTGCTGAT 3263  
Db 3157 GCCGAGGCTTCAATGCAATTTGGCCGATTTAAAAGTTGGTTAAGGTAAATTTGCTGAT 3216  
Qy 3264 TGTTTAAGTTAATAGTAAACAATTTGACAAATCAATTAAGTATGACACATGAGTGAG 3323  
Db 3217 TGTTTAAGTTAATAGTAAACAATTTGACAAATCAATTAAGTATGACACATGAGTGAG 3269  
Qy 3324 AGGACCAACGATGATGATTTGGAGCAAGACATGCTGACAAAGACTGAGCTG 3383  
Db 3270 -----AGACATGCTGACAAAGACTGAGCTG 3297  
Qy 3384 GGCACGACGAGATCTCTGCGACGCTCTCATCAAGAGGGGATCAAGAGCAGACGCA 3443  
Db 3298 GGCACGACGAGATCTCTGCGACGCTCTCATCAAGAGGGGATCAAGAGCAGACGCA 3357  
Qy 3444 CTGAGAGTGGCCATCGGGGATGCGATGGAATTCACGATACAGGCGACATGAAGAACAC 3503  
Db 3358 CTGAGAGTGGCCATCGGGGATGCGATGGAATTCACGATACAGGCGACATGAAGAACAC 3417  
Qy 3504 AAGCCGACGAATTCAAATCTTAATTAACGACAGATGATTTGGCAATCAATTAACAC 3563  
Db 3418 AAGCCGACGAATTCAAATCTTAATTAACGACAGATGATTTGGCAATCAATTAACAC 3452  
Qy 3564 CAAGACATAGCTGGAACAGAGCTAACCATAAGAGTTTGTCTTACAGACGACGAC 3623  
Db 3453 -----GACAGACGAC 3462  
Qy 3624 ACTGCCAGCATTAATCATATGTGTAGCCATTAAGATGACCATTTCAAGACGAGACGAC 3683  
Db 3463 ACTGCCAGCATTAATCATATGTGTAGCCATTAAGATGACCATTTCAAGACGAGACGAC 3522  
Qy 3684 AAGGGGACGCGCAGACGATGAGAGGGGAGAGAAAGCGCAGCAAGAGAGATTTA 3743  
Db 3523 AAGGGGACGCGCAGACGATGAGAGGGGAGAGAAAGCGCAGCAAGAGAGATTTA 3582  
Qy 3744 GGTCTGACGAGAACTGGAAGAGAGGGGAAATGAGAGAGGGCCGCTCGACGAGAT 3803  
Db 3583 GGTCTGACGAGAACTGGAAGAGAGGGGAAATGAGAGAGGGCCGCTCGACGAGAT 3642  
Qy 3804 ATCATTAATTCATGACACAGACGAGATATCTCGATGATATTCAGCTGATGCTGCC 3863  
Db 3643 ATCATTAATTCATGACACAGACGAGATATCTCGATGATATTCAGCTGATGCTGCC 3702  
Qy 3864 GATTCGTATATAGAAATTTCCGATTTTACCGGTGACGATACCTGCGCTTCTGCAA 3923  
Db 3703 GATTCGTATATAGAAATTTCCGATTTTACCGGTGACGATACCTGCGCTTCTGCAA 3762  
Qy 3924 GATTCGGGCAATTAAGCATGAAACCTTTCATTTAATGAATAAATTTTGAACA 3983  
Db 3763 GATTCGGGCAATTAAGCATGAAACCTTTCATTTAATGAATAAATTTTGAACA 3822  
Qy 3984 GCTGTTATCACTATGATTTTAAAGATAGCTTGGCATTTAGAGATGATACATCTG 4043  
Db 3823 GCTGTTATCACTATGATTTTAAAGATAGCTTGGCATTTAGAGATGATACATCTG 3882  
Qy 4044 CCAAAAGACCCATGACGAGATTTTAACTATATGACAGAAATATTTAGGTTAA 4103  
Db 3883 CCAAAAGACCCATGACGAGATTTTAACTATATGACAGAAATATTTAGGTTAA 3942  
Qy 4104 TTTCTTCTGGAATTTAATCAAGTGTGCGCTGCGCTTCAAGGTACTTCAACAAC 4163  
Db 3943 TTTCTTCTGGAATTTAATCAAGTGTGCGCTGCGCTTCAAGGTACTTCAACAAC 4002  
Qy 4164 GCGTGTGTGGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4223

Db 4003 GCGTGTGTGGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4062  
Qy 4224 CTTGTTGAGCTGTGTGTATTTCAAGCTTTCAAGACTATGCAAGCTTAAAGACACTGAG 4283  
Db 4063 CTTGTTGAGCTGTGTGTATTTCAAGCTTTCAAGACTATGCAAGCTTAAAGACACTGAG 4122  
Qy 4284 CCACTACGTCATGCTCCGTTATGACAGGCGATGAGGGTGTGTAAATGCGCTGAGACA 4343  
Db 4123 CCACTACGTCATGCTCCGTTATGACAGGCGATGAGGGTGTGTAAATGCGCTGAGACA 4182  
Qy 4344 GCTATACGTCATGCTCCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 4403  
Db 4183 GCTATACGTCATGCTCCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 4242  
Qy 4404 ATATAGGCTGTACGCTTTTGTGTAATAATTTTAAAGTGGAGACATGAAATGGCAG 4463  
Db 4243 ATATAGGCTGTACGCTTTTGTGTAATAATTTTAAAGTGGAGACATGAAATGGCAG 4302  
Qy 4464 AAGCTCAGCAGAGATCATCAATGCAATGCAATGCGATGCGAGAGAGACATACAGTGG 4523  
Db 4303 AAGCTCAGCAGAGATCATCAATGCAATGCAATGCGATGCGAGAGAGACATACAGTGG 4362  
Qy 4524 GTGAATTCAGCATGATTTTGCATCATGATGATGATGATGATGATGATGATGATGATGAT 4583  
Db 4363 GTGAATTCAGCATGATTTTGCATCATGATGATGATGATGATGATGATGATGATGATGAT 4422  
Qy 4584 GGCACCTTCAAAAGCTGTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4643  
Db 4423 GGCACCTTCAAAAGCTGTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4482  
Qy 4644 AAGCAACGAATTCGTGAACGAACATCTACATGATTTTAAATTTGCTTTCATCAT 4703  
Db 4483 AAGCAACGAATTCGTGAACGAACATCTACATGATTTTAAATTTGCTTTCATCAT 4542  
Qy 4704 TTTGATCTTTTTCACACTCAATCTGTCATTTGTTATCATGATTAATTAATGAG 4763  
Db 4543 TTTGATCTTTTTCACACTCAATCTGTCATTTGTTATCATGATTAATTAATGAG 4602  
Qy 4764 CAAAAGAAAAAGCAGTGTGATTTAGAAATGTTCAATGACAGATCAAGAAAGTAC 4823  
Db 4603 CAAAAGAAAAAGCAGTGTGATTTAGAAATGTTCAATGACAGATCAAGAAAGTAC 4662  
Qy 4824 TATATGCTATGAAAAAAGTGGCTCTTAAAAACATTTAAAGCCATTCGAAGCCAG 4883  
Db 4663 TATATGCTATGAAAAAAGTGGCTCTTAAAAACATTTAAAGCCATTCGAAGCCAG 4722  
Qy 4884 TGGCGACCAAGCAATAGCTTTTGAATATGTAACGATTAAGAAATTCATATATCAT 4943  
Db 4723 TGGCGACCAAGCAATAGCTTTTGAATATGTAACGATTAAGAAATTCATATATCAT 4782  
Qy 4944 ATGTTATGATTTGATGTAACATGTTCAACATGACCTCGATGTTACGATGCTGCGAC 5003  
Db 4783 ATGTTATGATTTGATGTAACATGTTCAACATGACCTCGATGTTACGATGCTGCGAC 4842  
Qy 5004 ACGTATTAAGCGGCTCTTACATATCTCAATGCGATATTCGTATTTTCAAGTTCCGA 5063  
Db 4843 ACGTATTAAGCGGCTCTTACATATCTCAATGCGATATTCGTATTTTCAAGTTCCGA 4902  
Qy 5064 TGTCTATTAATAATTTCCGTTTACATATCTCAATTTTATTTAGGACATGAAATTAATT 5123  
Db 4903 TGTCTATTAATAATTTCCGTTTACATATCTCAATTTTATTTAGGACATGAAATTAATT 4962  
Qy 5124 GATGTATGTTGTATTTTATTCATATAGGCTTGTATGATGATGATGATGATGATGATGAT 5183  
Db 4963 GATGTATGTTGTATTTTATTCATATAGGCTTGTATGATGATGATGATGATGATGATGAT 5022  
Qy 5184 TACTTGTGTGCGACCTGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 5243  
Db 5023 TACTTGTGTGCGACCTGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 5082  
Qy 5244 CCACTGTGTAAGGAGCCCAAGGCAATTCGACATCTGCTTGTGCTTGTGCTGCTGCTG 5303  
Db 5083 CCACTGTGTAAGGAGCCCAAGGCAATTCGACATCTGCTTGTGCTTGTGCTGCTGCTG 5142





Db 2278 AAAGCAAGGCACTGGAAGTGAATCCTCAAGGCAATGATGTGTTGTGTGGAGCTGT 2337  
Qy 2424 TGCTGGGTTTGGTTGAATTTTCAGAGATGGGTAATGGCTCATGTCTTGATCCCTTCGTG 2483  
Db 2338 TGCTGGGTTTGGTTGAATTTTCAGAGATGGGTAATGGCTCATGTCTTGATCCCTTCGTG 2397  
Qy 2484 GAGCTCTTCATCACTGCTGATGCTTGTGTCACAGATGTTGATGGCAATGGATCAACC 2543  
Db 2398 GAGCTCTTCATCACTGCTGATGCTTGTGTCACAGATGTTGATGGCAATGGATCAACC 2457  
Qy 2544 GATATGAACAGAGATGGAAGCGCTGTCTCAAGATGGCAATATTTCTTCAACGCCAC 2603  
Db 2458 GATATGAACAGAGATGGAAGCGCTGTCTCAAGATGGCAATATTTCTTCAACGCCAC 2517  
Qy 2604 TTTGCAATCGAGGCCACATGAAGCTAATGGCATGAGCCCAAGTACTATTTCCAGAG 2663  
Db 2518 TTTGCAATCGAGGCCACATGAAGCTAATGGCATGAGCCCAAGTACTATTTCCAGAG 2577  
Qy 2664 GAGCTGGAACATCTTGCATCTATATCGTGGCCCTATGCTATTGGAACTGGGACTCGAG 2723  
Db 2578 GAGCTGGAACATCTTGCATCTATATCGTGGCCCTATGCTATTGGAACTGGGACTCGAG 2637  
Qy 2724 GGTGTCCAGGGTCTGTCCGTAATGGCTTCTTTCGATTGCTGCTGTAATTCAACTGGCC 2783  
Db 2638 GGTGTCCAGGGTCTGTCCGTAATGGCTTCTTTCGATTGCTGCTGTAATTCAACTGGCC 2697  
Qy 2784 AAGCTTTGGCCCACTTAATTTACTCATTTTCGATTATGGAACGCAACATGGGCGCTTGG 2843  
Db 2698 AAGCTTTGGCCCACTTAATTTACTCATTTTCGATTATGGAACGCAACATGGGCGCTTGG 2757  
Qy 2844 GGTATCTGACATTTGTACTTGTGCTATTCATCTTTCGATGGGATGGAATGCA 2903  
Db 2758 GGTATCTGACATTTGTACTTGTGCTATTCATCTTTCGATGGGATGGAATGCA 2817  
Qy 2904 CTGTTCGGAAAGATTAATCATGATCAAGAGACGCTTTCGGATGGGACCTGGCGGC 2963  
Db 2818 CTGTTCGGAAAGATTAATCATGATCAAGAGACGCTTTCGGATGGGACCTGGCGGC 2877  
Qy 2964 TGGAACTTCAACGCTTTATGACAGCTTTCATGATTCGTTTCCGGTCTCTGGCGAAG 3023  
Db 2878 TGGAACTTCAACGCTTTATGACAGCTTTCATGATTCGTTTCCGGTCTCTGGCGAAG 2937  
Qy 3024 TGAATCGAGTCCATGTGGGACGTCGATGATGCGGCGATGTCGATGATCCCTTCTTC 3083  
Db 2938 TGAATCGAGTCCATGTGGGACGTCGATGATGCGGCGATGTCGATGATCCCTTCTTC 2997  
Qy 3084 TTTGGCCACGTTGTTCATCGGCAATCTTGTGTACTTAACTTTTCTTACCTTGTCTTTC 3143  
Db 2998 TTTGGCCACGTTGTTCATCGGCAATCTTGTGTACTTAACTTTTCTTACCTTGTCTTTC 3057  
Qy 3144 TCCAAATTTGGCTCATCTAGCTTATCAGCGCGGATGCGGATTAAGATTAAGATTAATA 3203  
Db 3058 TCCAAATTTGGCTCATCTAGCTTATCAGCGCGGATGCGGATTAAGATTAAGATTAATA 3117  
Qy 3204 GCCAGAGGCTTCAATCGAATTTGGCGGATTTAAAGTTGGTTAAAGCGTAATATTGCTGAT 3263  
Db 3118 GCCAGAGGCTTCAATCGAATTTGGCGGATTTAAAGTTGGTTAAAGCGTAATATTGCTGAT 3177  
Qy 3264 TGTTCAGATTAAATCGTAACAAATTGAACAAATCAATTAAGTATCAACCATCAAGTAG 3323  
Db 3178 TGTTCAGATTAAATCGTAACAAATTGAACAAATCAATTAAGTATCAACCATCAAGTAG 3230  
Qy 3324 AGGACCAACGATCACTGATTTGGAGCGAAGGCTGTGTGACACGAACTGGAGCTG 3383  
Db 3231 -----AGGACCAACGATCACTGATTTGGAGCGAAGGCTGTGTGACACGAACTGGAGCTG 3258  
Qy 3384 GGGCAAGAGATCTTCGCGGACGCGCTCATCAAGAGGGGATCAAGAGACAGCGCA 3443  
Db 3259 GGGCAAGAGATCTTCGCGGACGCGCTCATCAAGAGGGGATCAAGAGACAGCGCA 3318  
Qy 3444 CTGAGAGTGTGCATCGGAGATCGATGGAATTTCAAGATCAAGCGGACATGAAGAAC 3503  
Db 3319 CTGAGAGTGTGCATCGGAGATCGATGGAATTTCAAGATCAAGCGGACATGAAGAAC 3378

Qy 3504 AAGCGAAGAAATCCAAATATCTAAATACGCAAGATGATTTGGCACTCAATTAACAC 3563  
Db 3379 AAGCGAAGAAATCCAAATATCTAAATACGCAAC----- 3413  
Qy 3564 CAAGCAATTAAGCTGGAACACGAGCTAAACATAGAGTTGTCTTCAAGACGAGAC 3623  
Db 3414 -----GAGCAACAC 3423  
Qy 3624 ACTGCAGCAATTAATCTCATATGTAAGCCATAAGATTCAGCAATTCAGAGACGAGCCAC 3683  
Db 3424 ACTGCAGCAATTAATCTCATATGTAAGCCATAAGATTCAGCAATTCAGAGACGAGCCAC 3483  
Qy 3684 AAGGCAAGCGCGGACGATGGAAGGCGGACGAGGAGAGAGAGAGAGATTTA 3743  
Db 3484 AAGGCAAGCGCGGACGATGGAAGGCGGACGAGGAGAGAGAGAGATTTA 3543  
Qy 3744 GGTCTGACGAGGAATCTGGAAGAGAGGCGAATGCGAGAGGCGCGCTGACGCTGAT 3803  
Db 3544 GGTCTGACGAGGAATCTGGAAGAGAGGCGAATGCGAGAGGCGCGCTGACGCTGAT 3603  
Qy 3804 ATCATTTATTCATGCAACAGAGAGATTAATCTCATATGTAATTCAGCTGATTTGCTGCC 3863  
Db 3604 ATCATTTATTCATGCAACAGAGAGATTAATCTCATATGTAATTCAGCTGATTTGCTGCC 3663  
Qy 3864 GATTGCTATTAAGAAATTTCCGATCTTACCGGTGACGATGACTCGCCGTTCTGGCA 3923  
Db 3664 GATTGCTATTAAGAAATTTCCGATCTTACCGGTGACGATGACTCGCCGTTCTGGCA 3723  
Qy 3924 GGAATGGGCAATTAACGACTGAAATCTTCAATTAATTAAGAAATTAATTTGAAACA 3983  
Db 3724 GGAATGGGCAATTAACGACTGAAATCTTCAATTAATTAAGAAATTAATTTGAAACA 3783  
Qy 3984 GCTGTATCACTATGATTTTAATGATAGTACTTACCTTGGCATTAAGATGATCATCTG 4043  
Db 3784 GCTGTATCACTATGATTTTAATGATAGTACTTACCTTGGCATTAAGATGATCATCTG 3843  
Qy 4044 CCAAGAAAGCCCAATCGAGAGATTTTAATCTATATGACAGAAATTTTAAGCTTATA 4103  
Db 3844 CCAAGAAAGCCCAATCGAGAGATTTTAATCTATATGACAGAAATTTTAAGCTTATA 3903  
Qy 4104 TTTCTTCTGGAATGTTAATCAATGTTGGCGCTCGGCTTCAAGTGTACTTCAACCAAC 4163  
Db 3904 TTTCTTCTGGAATGTTAATCAATGTTGGCGCTCGGCTTCAAGTGTACTTCAACCAAC 3963  
Qy 4164 GCGTGTGTGGCTGATTTTGTGATGTCATGATGCTTATCAACTTGTGCTTCA 4223  
Db 3964 GCGTGTGTGGCTGATTTTGTGATGTCATGATGCTTATCAACTTGTGCTTCA 4023  
Qy 4224 CTGTGGAAGCTGTGTATTAAGCTTCAAGCTATGCAACGTTAAGAGACTGAGA 4283  
Db 4024 CTGTGGAAGCTGTGTATTAAGCTTCAAGCTATGCAACGTTAAGAGACTGAGA 4083  
Qy 4284 CCACTAGGTCGATGTCGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4343  
Db 4084 CCACTAGGTCGATGTCGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4143  
Qy 4344 GCTATACCGTCCATCTTCAATGTCATTTGGTGTCTAATATTTTGGCTAATTTTGGCC 4403  
Db 4144 GCTATACCGTCCATCTTCAATGTCATTTGGTGTCTAATATTTTGGCTAATTTTGGCC 4203  
Qy 4404 ATATAGGCTGTACAGCTTTTGTCTGGAATAATTTTAAGTCCGAGACATGAATGCGACG 4463  
Db 4204 ATATAGGCTGTACAGCTTTTGTCTGGAATAATTTTAAGTCCGAGACATGAATGCGACG 4263  
Qy 4464 AAGCTCAGCAGAGATCATACCAATTCGCAATGCTGCGAGAGCGGAACTACACGTGG 4523  
Db 4264 AAGCTCAGCAGAGATCATACCAATTCGCAATGCTGCGAGAGCGGAACTACACGTGG 4323  
Qy 4524 GTGAATTCAGCAATGAAATTTGATCATGTAGGTAACCGGATCTGTGCTTTTCAAGTG 4583  
Db 4324 GTGAATTCAGCAATGAAATTTGATCATGTAGGTAACCGGATCTGTGCTTTTCAAGTG 4383

QY 4584 GCGACCTTCAAGGCTGGATTAACAATCAGATGCTATGCTTCAAGAGAGTGGAC 4643  
 DB 4384 GCGACCTTCAAGGCTGGATTAACAATCAGATGCTATGCTTCAAGAGAGTGGAC 4443  
 QY 4644 AACCAACCAATTCGTGTAAGCAACATCTACATGATATTTATTTCTTCATCATTA 4703  
 DB 4444 AACCAACCAATTCGTGTAAGCAACATCTACATGATATTTATTTCTTCATCATTA 4503  
 QY 4704 TTTGATCTTTTTCACATCACTCAATCTGTCATGTTGTTATCATGTAATTTTAAATGAG 4763  
 DB 4504 TTTGATCTTTTTCACATCACTCAATCTGTCATGTTGTTATCATGTAATTTTAAATGAG 4563  
 QY 4764 CAAAAGAAAAAAGAGAGTGAATGATTAAGAAATGTCATGACAGAAATGCAAAAAAGTAC 4823  
 DB 4564 CAAAAGAAAAAAGAGAGTGAATGATTAAGAAATGTCATGACAGAAATGCAAAAAAGTAC 4623  
 QY 4824 TATATGCTATGAAAAAAGAGTGGCTCTAATAAAAAACATTAAGCCATTCAGAACCAAG 4883  
 DB 4624 TATATGCTATGAAAAAAGAGTGGCTCTAATAAAAAACATTAAGCCATTCAGAACCAAG 4683  
 QY 4884 TGGCGACCAAGCAATGATCTTTGAAATGTAACCGATTAAGAAATTCGATATATCAT 4943  
 DB 4684 TGGCGACCAAGCAATGATCTTTGAAATGTAACCGATTAAGAAATTCGATATATCAT 4743  
 QY 4944 ATGTTATTCATGCTGTCGATGATGTCATGATGACATGACCTGATGTTACGATGCTGGAC 5003  
 DB 4744 ATGTTATTCATGCTGTCGATGATGTCATGATGACATGACCTGATGTTACGATGCTGGAC 4803  
 QY 5004 ACCTATTAACCGGCTCTAGATCTATCTCAATGCAATTCGATATTTTCACTTCGAA 5063  
 DB 4804 ACCTATTAACCGGCTCTAGATCTATCTCAATGCAATTCGATATTTTCACTTCGAA 4863  
 QY 5064 TGTCTATTAATAAATATTCGCTTACATGATATCATTTTATTTGAGCCATGAAATTTAT 5123  
 DB 4864 TGTCTATTAATAAATATTCGCTTACATGATATCATTTTATTTGAGCCATGAAATTTAT 4923  
 QY 5124 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5183  
 DB 4924 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4983  
 QY 5184 TACTTGTGTGCGGACCTCTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5243  
 DB 4984 TACTTGTGTGCGGACCTCTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5043  
 QY 5244 CGACTGTGTGAAGGAGCGCAAGGGGATTCGACACTGCTCTTCGCGTGTGCGATGTCGTG 5303  
 DB 5044 CGACTGTGTGAAGGAGCGCAAGGGGATTCGACACTGCTCTTCGCGTGTGCGATGTCGTG 5103  
 QY 5304 CCGGCGCTGTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5363  
 DB 5104 CCGGCGCTGTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5163  
 QY 5364 GCGATGTCGTTCTTCATGACAGTGAAGAGAGAGCGGCAATTAACGATCTCAACTTC 5423  
 DB 5164 GCGATGTCGTTCTTCATGACAGTGAAGAGAGAGCGGCAATTAACGATCTCAACTTC 5223  
 QY 5424 AAGACCTTTGGCGAAGACATGATCTGCTCTTCATGATGTCGATGACCGGTTGGAT 5483  
 DB 5224 AAGACCTTTGGCGAAGACATGATCTGCTCTTCATGATGTCGATGACCGGTTGGAT 5283  
 QY 5484 GGGTATCTGACCGCATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5543  
 DB 5284 GGGTATCTGACCGCATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5343  
 QY 5544 TATCCGGGCAATTCGTCGACGACCGTGTGAATTAAGTTTCTCTCATACCTAGTT 5603  
 DB 5344 TATCCGGGCAATTCGTCGACGACCGTGTGAATTAAGTTTCTCTCATACCTAGTT 5403  
 QY 5604 ATAAAGCTTTTGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5661  
 DB 5404 ATAAAGCTTTTGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5461

RESULT 8  
 US-08-808-793-1  
 ; Sequence 1, Application US/08080793  
 ; Patent No. 5858713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soderlund, David M.  
 ; APPLICANT: Ingles, Patricia J.  
 ; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
 ; TITLE OF INVENTION: AND USE THEREOF  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/808,793  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/034,361  
 ; FILING DATE: 24-DEC-1996  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/012,649  
 ; FILING DATE: 01-MAR-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Braham, Susan J.  
 ; REGISTRATION NUMBER: 34,103  
 ; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 716-263-1636  
 ; TELEFAX: 716-263-1600  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6318 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-808-793-1  
 Query Match 68.3%; Score 4447.8; DB 2; Length 6318;  
 Best Local Similarity 82.0%; Pred. No. 0;  
 Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;  
 QY 24 ATGACGAGAAGATTCGACATCGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 83  
 DB 1 ATACAGAGAGATTCGACATCGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
 QY 84 CGGAAATCAATGTTGTCGAAATCGAACACGCAATTCGCTGAACATGAAAAAGAGAGAG 143  
 DB 61 CGGAAATCAATGTTGTCGAAATCGAACACGCAATTCGCTGAACATGAAAAAGAGAGAG 117  
 QY 144 CTGGAAGAAAG 203  
 DB 118 CTGGAAGAAAG 148  
 QY 204 GAATTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263  
 DB 149 -AGATTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207  
 QY 264 CAGGAGTGTCCATATCACTGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
 DB 208 CAGGAGTGTCCATATCACTGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267

324 CCTCTGAGGATATCGATCCCTACTACAGCAATGTACTGATGGTGTGAAGCAA 383  
268 CCTCTGAGGATATCGATCCCTACTACAGCAATGTACTGATGGTGTGAAGCAA 327  
384 GAAAAAGATATTTTTCGCTTTTCTGATCAAAAGCAATGTGAGCTCGATCCATTCAT 443  
328 GAAAAAGATATTTTTCGCTTTTCTGATCAAAAGCAATGTGAGCTCGATCCATTCAT 387  
444 CGATACGTGCTGAGGATTTACATCTAGTGCATCCATTTATTTTCCCTATTCATC 503  
388 CGATACGTGCTGAGGATTTACATCTAGTGCATCCATTTATTTTCCCTATTCATC 447  
504 ACCAATATTTCTGATCACTGATCCCTGATGATTAATGCGCAAGCCGAGCTGATGCC 563  
448 ACCAATATTTCTGATCACTGATCCCTGATGATTAATGCGCAAGCCGAGCTGATGCC 507  
564 ACTGAGGATATTTACCGGAACTTCAACATTTGATCACTGATTAATGATGAGCA 623  
508 ACAGAGGATATTTACCGGAACTTCAACATTTGATCACTGATTAATGATGAGCA 567  
624 GATTTCATTTATGCGCGTTTACGATCTTGAAGATGCAATGGAATTTGCTGATCTGTA 683  
568 GATTTCATTTATGCGCGTTTACGATCTTGAAGATGCAATGGAATTTGCTGATCTGTA 627  
684 GAAATAGCTTATGCTTATGATGCAATGGAATTTGATGATTAATGATGATGATGATG 743  
628 GAAATAGCTTATGCTTATGATGCAATGGAATTTGATGATTAATGATGATGATGATG 687  
744 ACATTTAGGATGCTGAGCGCTTAAACCGTATGCTGATGCTGATGCTGATGCTGATG 803  
688 ACATTTAGGATGCTGAGCGCTTAAACCGTATGCTGATGCTGATGCTGATGCTGATG 747  
804 GTGCGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 863  
748 GTGCGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 807  
864 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923  
808 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867  
924 TGCATCAAGAAATTTCCGCTGAGCGTTCTGCGGCAATCTGACCGACGAGAACTGGAGC 983  
868 TGCATCAAGAAATTTCCGCTGAGCGTTCTGCGGCAATCTGACCGACGAGAACTGGAGC 927  
984 TATACAAATGCGCAATGCTCCAAATTTGATTTCCAGAGGAGGAGGATCTCAATTTCCGTTA 1043  
928 TATACAAATGCGCAATGCTCCAAATTTGATTTCCAGAGGAGGAGGATCTCAATTTCCGTTA 987  
1044 TGCAGCAATATATCCGCTGAGCGGCAATGCGACGATTAATGCTGCTGCTGCTGCTGCTG 1103  
988 TGCAGCAATATATCCGCTGAGCGGCAATGCGACGATTAATGCTGCTGCTGCTGCTGCTG 1047  
1104 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1163  
1048 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1107  
1164 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1223  
1108 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1167  
1224 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1283  
1168 GGTCCGAATCCGAATTTATGCTGACACGATTTGATTTGCTGCTGCTGCTGCTGCTGCTG 1227  
1284 GTGATTTGATTTTGGCATTGTTGCAATGCTGATGCAATTTGCAAAAGGAGGAGGAGG 1343  
1228 GTGATTTGATTTTGGCATTGTTGCAATGCTGATGCAATTTGCAAAAGGAGGAGGAGG 1287  
1344 GAAAGAGGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1403  
1288 GAAAGAGGCTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1347

1404 GCGGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1463  
1348 GCGGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1407  
1464 GCGGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1523  
1408 GCGGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1467  
1524 TATGAGCTATTTTGGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1583  
1468 TATGAGCTATTTTGGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1527  
1584 ATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1643  
1528 ATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1587  
1644 ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1703  
1588 ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1644  
1704 GATTTCATTTTATGCTGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1763  
1645 GATTTCATTTTATGCTGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1704  
1764 GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1823  
1705 GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1764  
1824 CAGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1883  
1765 CAGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1824  
1884 GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1943  
1825 GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1884  
1944 TCGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2003  
1885 TCGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1944  
2004 ATGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2063  
1945 ATGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2004  
2064 CGCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2123  
2005 CGCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2064  
2124 CTGAT-----CATGCGAGCTAGCAAAATTTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 2168  
2065 CCGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2124  
2169 GCTGCGAAGATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2228  
2125 GCTGCGAAGATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2184  
2229 GTTATATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2288  
2185 GTTATATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244  
2289 AGTGGGCAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2348  
2245 AGTGGGCAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280  
2349 GATGGGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2408  
2281 GATGGGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340  
2409 TGTGTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2468  
2341 TGTGTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
2469 TTGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2528

Db 2401 TTGATTCATTTGTTGAGCTCTTCTTATTAACCTGTGATTTGGTCAATACGATGTTTATG 2460  
Qy 2529 GCATGATCACCACGATATGAAACAAGATGAAAGCGTGTCAAGATGGCAACTAT 2588  
Db 2461 GCATGATCATACGACATGAATCCGGAATAGAGAGTGTGAAAGATGGTAACTAT 2520  
Qy 2589 TTCTTACCGCCACCTTTGGCATGAGGCAACATGAGTAAATGGCCATGAGCCCAAG 2648  
Db 2521 TTCTTACCGCCACCTTTGGCAATGGAACGACATGAACTGATGGCCATGAGCCCAAG 2580  
Qy 2649 TACTATTTCCAGAGGGCTGGAACATCTTCACTTCACTTATCGTGGCCATGCTATTTG 2708  
Db 2581 TACTATTTCCAGAGGGCTGGAACATCTTCACTTCACTTATCGTGGCCATGCTATTTG 2640  
Qy 2709 GAATGGGCTGAGGGGTGTCCAGGGGCTGTGGGTGTGGAAGTTTTCGTTTGGCTTGGT 2700  
Db 2641 GAATGGGCTGAGGGGTGTCCAGGGGCTGTGGGTGTGGAAGTTTTCGTTTGGCTTGGT 2700  
Qy 2769 GTATTTCAATCTGGCCAAAGTCTTGGCCCAACTTAATTTACTCATTTTGGATTTAGGAGCC 2828  
Db 2701 GTATTTCAATTTGGCAAAATATGAGCCCACTCAATTTACTCATTTTGGATTTAGGAGCC 2760  
Qy 2829 ACATGAGGCGCTTGGGTATCTGACATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2888  
Db 2761 ACATGAGGCGCTTGGGTATCTGACATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2820  
Qy 2889 GTATGAGGAATGCACTGTTCCGAAAGAAATTAATCATGATCAAGAGCCGCTTCCGAT 2948  
Db 2821 GTATGAGGAATGCACTTTCGGAAGAACTATATTTGACCAAGATCCGCTTCAAGGAC 2880  
Qy 2949 GGGGACCTGGCGGCTGGAACTTCAACGATTTATGACAGCTTCATGATTCGTTCCGG 3008  
Db 2881 CATGAATTCACCGCGCTGGAACCTTCAACGATTCATGACAGCTTCATGATTCGTTCCGG 2940  
Qy 3009 GTGCTCGCGAGAAATGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 3068  
Db 2941 GTGCTCGCGAGAGTGTGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 3000  
Qy 3069 TGCATTCCTTCTTCTTGGCCACCGCTTGTGATGCGCAATCTTGTGATCTTAACTTTTC 3128  
Db 3001 TGCATTCCTTCTTCTTGGCCACCGCTTGTGATGCGCAATCTTGTGATCTTAACTTTTC 3060  
Qy 3129 TTAGCGCTGTTTGTTCATTTTGTGCTCATCTAGCTTACAGCGCCGATCGCGCATAC 3188  
Db 3061 TTAGCTTGTCTTTGTTCATTTTGTGCTCATCTAGCTTACAGCGCCGATCGCGCATAC 3120  
Qy 3189 GATACGAATAAATAGCCGAGGCTTCAATCGAATTTGCGCATTTAAAGTTGGTTAG 3248  
Db 3121 GATACGAATAAATAGCGAGGCTTCAATCGAATTTGCTGTTTAAAGATCGGTTGAAA 3180  
Qy 3249 CGTAAATTTGCTGATTTGTTCAAGTTAAATCGTAAACAATTTGACAAATTAAGTAT 3308  
Db 3181 CGTAAATTTGCTGATTTGTTAAATCGTAAACAATTTGACAAATTAAGTAT 3240  
Qy 3309 CATCCATCAGGTAGAGACCAACGATCAGTTGATTTGAGCGAAGGATGATGAC 3368  
Db 3241 CATCCATC-----AGAACATTTGGGAT 3261  
Qy 3369 AAGCACTGAGCTGGGCAACAAGATCTTCCGACGCTCATCAAGAGGGATC 3428  
Db 3262 AAGCACTGAGCTGGGCTGATGAGCAATCATGGCGATGGCTTGAATCAAAAAGGATG 3321  
Qy 3429 AAGGAGCAAGCACTGAGAGTGGCATGGGAGATGATGATTTCAAGATTCACGCGC 3488  
Db 3322 AAGGAGCAAGCACTGAGAGTGGCATGGGAGATGATGATTTCAAGATTCACGCGC 3381  
Qy 3489 GATACGAAGAACAAGCGAGAAATCAAAATTAATAAAGCAAGATGATTTGCG 3548  
Db 3382 GATACGAAGAACAAGCGAGAAATCAAAATTAATAAAGCAAGATGATTTGCG 3441  
Qy 3549 AACTCAATTAACAACAAGCAATAGACTGAAACAAGCTTAAACATAGAGTTTGTCC 3608

Db 3442 AACTCAATTAACAACAAGCAATAGACTGAAATGAGCTAAACCATAGAGTTTGTCC 3501  
Qy 3609 TTACAGAGAGAGCACTGTGCGACATTAATCTATATGATGATTAAGATGACCATTC 3668  
Db 3502 ATACAGAGAGAGCACTGTGCGACATTAATCTATATGATGATTAAGATGACCATTC 3561  
Qy 3669 AAGGAGCAAGCAAGAGGCGAGCGCGAGATGAGGCGAGAGGAGGAGGAGGAGGAGGAGG 3728  
Db 3562 AAGGAGCAAGCAAGAGGCGAGCGCGAGATGAGGCGAGAGGAGGAGGAGGAGGAGGAGG 3621  
Qy 3729 AGCAAGAGATTTAGTGTCTGACGAGAACTGACGAGAGGCGCAATGCGAGAGGCG 3788  
Db 3622 AGCAAGAGAGCACTGTGCGACATGAGAACTGACGAGAGGCGCAAGGCGAGGCGAGGCG 3681  
Qy 3789 CGCTGAGAGGATATCATTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3845  
Db 3682 CAGCTGAGAGGATATCATTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3741  
Qy 3846 CAGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3905  
Db 3742 CAGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3801  
Qy 3906 GACTGCGCTTCTGCGAGAGATGCGGCAATTAAGACTGAAACCTTTCAATTAATTGA 3965  
Db 3802 GACTGCGCTTCTGCGAGAGATGCGGCAATTAAGACTGAAACCTTTCAATTAATTGA 3861  
Qy 3966 AATTAATTTTGAACACGCTGTATCACTATGATTTTATAGTGTAGCTTGGCA 4025  
Db 3862 AATTAATTTTGAACACGCTGTATCACTATGATTTTATAGTGTAGCTTGGCA 3921  
Qy 4026 TTGAAGATGATACCTGCGACAAAGACCATCTGAGATTTTATATATATGAGAC 4085  
Db 3922 TTGAAGATGATACCTGCGACATGACATGACATGACATGACATGACATGACATGACATGAC 3981  
Qy 4086 AGAATATTTACGTTAAATTTCTTGAAGATTTATCAAGTGTGGCGCTCGCTTC 4145  
Db 3982 AGAATATTTACGTTAAATTTCTTGAAGATTTATCAAGTGTGGCGCTCGCTTC 4041  
Qy 4146 AAGTGTACTTCAACCAACGCGGTGTGTGCTGATTTGATGATGATGATGATGATGATGATG 4205  
Db 4042 AAGTGTACTTCAACCAACGCGGTGTGTGCTGATTTGATGATGATGATGATGATGATGATG 4101  
Qy 4206 ATCACTGCTGCTTCACTTGTGAGGCTGTGATTAAGACCTTCAAGATATGCA 4265  
Db 4102 ATCACTGCTGCTTCACTTGTGAGGCTGTGATTAAGACCTTCAAGATATGCA 4161  
Qy 4266 ACCTTAAGAGACTGAGACCACTAGTGCATGTCCGATGAGAGGCAATGAGGCTGTC 4325  
Db 4162 ACCTTAAGAGACTGAGACCACTAGTGCATGTCCGATGAGAGGCAATGAGGCTGTC 4221  
Qy 4326 GTTAATGCGGTGTACAGCTATACGTCATCTTCAATGTGCTATTTGGTGTCTAAT 4385  
Db 4222 GTTAATGCGGTGTACAGCTATACGTCATCTTCAATGTGCTATTTGGTGTCTAAT 4281  
Qy 4386 TTTTGGCTAATTTTGGCTAATGAGTGTACAGCTTTTGTGGAATAATTTTAAAGTGC 4445  
Db 4282 TTTTGGCTAATTTTGGCTAATGAGTGTACAGCTTTTGTGGAATAATTTTAAAGTGC 4341  
Qy 4446 GAGGACATGATGAGCAAGGCTGAGCAGAGATCATACCAATGCGAATGCTGCGAG 4505  
Db 4342 AAGAGATGATGATGAGCAAGGCTGAGCAGAGATCATACCAATGCGAATGCTGCGAG 4401  
Qy 4506 AGGAGAACTACACGAGGAGTGAATGAGCAATGATTTGATGATGATGATGATGATGATG 4565  
Db 4402 AGGAGAACTACACGAGGAGTGAATGAGCAATGATTTGATGATGATGATGATGATGATG 4461  
Qy 4566 CTGTGCTTTTCCAGATGCGCACTTCAAGGCTGATCAATTCATGAGATGCTATC 4625  
Db 4462 CTGTGCTTTTCCAGATGCGCACTTCAAGGCTGATCAATTCATGAGATGCTATC 4521  
Qy 4626 GATTCACGAGAGTGAACAAGCAATTTGTAACCAACATCTTCAATGATTTATAT 4685  
Db 4522 GATTCACGAGAGTGAACAAGCAATTTGTAACCAACATCTTCAATGATTTATAT 4581

[illegible]

OY 5766 GATCAGCTGTCCGAATTCCTGGACGTACTGGAGACCCTCCCTGGAGATCCAAACGGAAC 5825  
 Db 5662 GACCAAGCTGTCCGAATTTCTGGAAGTGTCTGGAGCCCGCTGCAGATCCAAAGCCGAAC 5721  
 OY 5826 AAGTACAAAGATCATATCGATGGACATACCCATCTGTCTGCGGTGACCTCATGTACTGCTC 5885  
 Db 5722 AAGTCAAAATCATATTCGATGGACATGCGCATATGTCTGGGGCGACATGTATGTCTGTGTG 5781  
 OY 5886 GACATCCCTGACAGCCCTTATCGAAGAAGCTTTTGGCGCGGAAGGGCAATCCGATAGAGAG 5945  
 Db 5782 GATATATTGATGCTCCCTGACCAAGGACTTTCTTTGGCGCAAGGGTATACCGATCGAGAG 5841  
 OY 5946 ACGGTGAGATTGTGAGATAGACGCGCCCGCCCGATACCGAAGGCTTACGAGCCCGTCTCA 6005  
 Db 5842 ACGGTGAAATTGTGAGATAGACGCGCGGACCGGACACCGAGGGCTTATGATCCGGTGTG 5901  
 OY 6006 TCAACGCTGTGGCCCTCAGCGTGAAGAGATCTGCGCCCGCTTAATCCAGACGCTTGCGCA 6065  
 Db 5902 TCAACACTGTGGCCGCGCAGGTGAGAGATCTGCGCCAGCTGAATACAGATGCTGTGGCG 5961  
 OY 6066 AAGCAACAAGCGCGCGCGAGGAGAGTGGGTCTTTGAGCCGGATACGATCATGCGAT 6125  
 Db 5962 CGTTACAGAGATGCG-----CAACCACGAGAGGTGAT 5994  
 OY 6126 GCGCGTATCCGATATCCGGGAGACC CGCGCCCGATGAAGCAACGAGCGCGATGCGCCC 6185  
 Db 5995 GAGGCGGAGCGGCGCTGTGCGCAGAAATGGTCTGAAGCGGTGAGGGTGAAGAGGACAGC 6054  
 OY 6186 GGTGTGAGATGATGATGTTAAAGGTTACTGCAAGAGAGCTGCGGATGCCCATGAGAGT 6245  
 Db 6055 GCGCGCGCGCGCGATGATGTGTGCTCAGACAGAGGACAAACGCGCGCGGAGGCC 6114  
 OY 6246 AATGTAATAGTCCGGGTGAGGATGCAGCGCGCGCGCGCAGCAGCAGCAGCAGCGCG 6305  
 Db 6115 ACATCACCT-----CAAGTCCAGATGCGCGGAGACAGATGGTGCAGC 6159  
 OY 6306 GCGCGCGGCAAGCAGACGCGCGGAAAGTCCCGAGCGGGTATGCGCGCGGAGCAGACCGC 6365  
 Db 6160 GTGCGCGGCGCCCTTATGTCCGGCTGTATTATGTGCGGCAAGTATGCGCGCCAAAGGCC 6219  
 OY 6366 GTTCTCGTGAAGAGCAGCGGTTCTGTGAGAAAGCGCAGCAGAGGTGTATCCACTCG 6425  
 Db 6220 GTACTGTCGAAGAGATGTTTTTTTTCACAAAAAGGTCATTAAGTTTATATACACTCG 6279  
 OY 6426 CGATGCGCGAGCATCAGTCCGCGACGCGCGGATGTCTGA 6464  
 Db 6280 AGATGCGCGAGCATTAACATCCAGAGCGCAGATGTCTGA 6318

```

RESULT 9
US-08-772-512A-1
: Sequence 1, Application US/08772512A
: Patent No. 6022705
: GENERAL INFORMATION:
: APPLICANT: Soderlund, David M.
: APPLICANT: Knipple, Douglas C.
: APPLICANT: Ingles, Patricia J.
: TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
: TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
: TITLE OF INVENTION: FLIES
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
: STREET: P. O. Box 1051, Clinton Square
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30

```

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/772,512A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/608,618  
;; FILING DATE: 01-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Braham, Susan J.  
;; REGISTRATION NUMBER: 34,103  
;; REFERENCE/DOCKET NUMBER: 19603/601 (CRPD-1657)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 716-263-1636  
;; TELEFAX: 716-263-1600  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6318 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; US-08-772-512A-1  
  
Query Match 68.3%; Score 4447.8; DB 3; Length 6318;  
Best Local Similarity 82.0%; Pred. No. 0;  
Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;  
  
QY 24 ATGACGAAAGATTCCGACTCGATATCTGAGAGAAAGCGATTGTTCCGCTTACC 83  
DB 1 ATGACGAAAGATTCCGACTCGATATCTGAGAGAAAGCGATTGTTCCGCTTACC 60  
QY 84 CGGATTCATTTGGTGAATCGAACAAGCATTCGCGTGAACATGAAAAAGAGAG 143  
DB 61 CGGATTCATTTGGTGAATCGAACAAGCATTCGCGTGAACATGAAAAAGAGAG 117  
QY 144 CTGGAAGAAG 203  
DB 118 CTGGAAGAAG 148  
QY 204 GAATTCGATATGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 149 -AGATCGATATGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
QY 264 CAGGAGTGCATATCTGTTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 208 CAGGAGTGCATATCTGTTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267  
QY 324 CCTCTGAGAGATATCGATCCCTAATAAGCAATGTAATGATTCGATGTAAGCAAA 383  
DB 268 CCTCTGAGAGATATCGATCCCTAATAAGCAATGTAATGATTCGATGTAAGCAAA 327  
QY 384 GGAAGAATTTTGGCTTTTCTGATCAAAAGCAATGTAATGTAATGTAATGTAAT 443  
DB 328 GGAAGAATTTTGGCTTTTCTGATCAAAAGCAATGTAATGTAATGTAATGTAAT 387  
QY 444 CGCATAGCTGCTGAGCATTTACATTTAGTGCATTCATTTTCCCTATTCATCAGC 503  
DB 388 CGCATAGCTGCTGAGCATTTACATTTAGTGCATTCATTTTCCCTATTCATCAGC 447  
QY 504 ACCACAATTCGTCACATCGCATCTGATGATAAGCCGCAACGCCACGTTGAGTCC 563  
DB 448 ACCACAATTCGTCACATCTAATTTAATTAATGATATGCGCAACGCCACGTTGAGTCC 507  
QY 564 ACTGAGTATATTCACCGCAATCTACATTTGAAATCAGCTTTAAAGATGAGACGA 623  
DB 508 ACTGAGTATATTCACCGCAATCTACATTTGAAATCAGCTTTAAAGATGAGACGA 567  
QY 624 GGTTCATTTATGCGCGTTTATGTAATCTTAGAGATGATGATGATGATGATGATG 683  
DB 568 GGTTCATTTATGCGCGTTTATGTAATCTTAGAGATGATGATGATGATGATGATG 627  
QY 684 GTAATAGCTTTAGCTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 743

DB 628 GTAATAGCTTTAGCTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 687  
QY 744 AGCTTTAGGTCCTCGAGAGCGCTTAAACCGTACCATGTCGAGGCTTGAAGCAATC 803  
DB 688 ACATTTAGGTCCTCGAGAGCGCTTAAACCGTACCATGTCGAGGCTTGAAGCAATC 747  
QY 804 GTGCGCGCGTCATCGAATCGGTGAAAGATCTGCGGATGATTAATCTGACCAATGTC 863  
DB 748 GTGCGCGCTGATGTAATCTGTAATAAATCTACGGAGATGATTAATTTGACCAATGTT 807  
QY 864 TCCCTGTGCTGTTGCGTTGATGAGGCTTACAGATCTATATGCGGCTGTCACCGAAG 923  
DB 808 TCCCTGTGCTGTTGCGGCTGATGAGGCTTACAGATCTATATGCGGCTGTCACCAAG 867  
QY 924 TGCATCAAAAGTATCCCGTGAAGCGTTCCTGAGGCAATCTGACGAGCAATCTGGAGC 983  
DB 868 TGCATCAAAAGTATCCCGTGAAGCGTTCCTGAGGCAATCTGACGAGCAATCTGGAGC 927  
QY 984 TATCACAATCGCAATAGCTTCAATTTGATTTCCGAGAGAGAGGATCTCATTTCCGTTA 1043  
DB 928 CTACACAAATAGCAAGATTCATTTGTTAGGAGAAAGATGAGGAGTATATCCGCTG 987  
QY 1044 TCGGCAATATATCCGTCGCGGCAATGCGACAGCAATTAATGCTGCTGCAAGGCTTT 1103  
DB 988 TCGGCAATATATCCGTCGCGGCAATGCGGCAATGCGGCAATTAATGCTGCTGCAAGGCTTT 1047  
QY 1104 GGTCCGAATCCGAATTAATGCTTACACAGCTTGATGCTGCGAGAGAGGCTTTCTGCTC 1163  
DB 1048 GGTCCGAATCCGAATTAATGCTTACACAGCTTGATGCTGCGAGAGAGGCTTTCTGCTC 1107  
QY 1164 GCTTCCGCTGATGACACAGGATCTTGGAGAGATCTGTACAGCTGTGTTGCGGCTC 1223  
DB 1108 GGTTCGCTCATGACCAAGATTTCTGGAGAGATCTGTACAGCTGTGCGGCTC 1167  
QY 1224 GCGGCAATGCGACATGCTGTTTATGATGATCATCTTCTGATGATTTATCTT 1283  
DB 1168 GCTGAGCCTGCGACATGTTGTTTATGATGATCATCTTCTGATGATTTATCTT 1227  
QY 1284 GTGAATTTGATTTGGCTGATTTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1343  
DB 1228 GTGAATTTGATTTGGCTGATTTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1287  
QY 1344 GAAGAAGAGCTGCCAG 1403  
DB 1288 GAAGAAGAGCTGCCAG 1347  
QY 1404 GCGGCAATGCGACATGCTGTTTATGATGATCATCTTCTGATGATTTATCTT 1463  
DB 1348 GCGGCAATGCGAG 1407  
QY 1464 GCCGAAGAGGCTGCACTGATCCGAAATGCGCAAGATGCGACGATTTCTTGCATCAGC 1523  
DB 1408 GCGGCTGCGGCACTGATCCGAAATGCGCAAGATGCGACGATTTCTTGCATCAGC 1467  
QY 1524 TATGACTATTTGTTGGCGGCAAGAGGCAACGATGACCAACAAAGAAAGATGTC 1583  
DB 1468 TATGACTATTTGTTGGCGGCAAGAGGCAACGATGACCAACAAAGAAAGATGTC 1527  
QY 1584 ATTGAGAGGCTGAGGATGAGTGCAGTGGGTGAGGCTTATCAAAAGCAACACAGACCT 1643  
DB 1528 ATTGAGAGGCTGAGGATGAGTGCAGTGGGTGAGGCTTATCAAAAGCAACACAGACCT 1587  
QY 1644 ACCACAGCACACCAAGCTACCAAGTTCGTAAGTGAAGACGACATCTTATCTTACCT 1703  
DB 1588 ACCACAGCACCC---GTAATAAGTCCGTAAGTGAAGACGACATCTTATCTTACCT 1644  
QY 1704 GGTTCACGTTTAACTATACGAGGAGATCAAGTTCACAGAGTACACAGTACGGAAC 1763  
DB 1645 GGTTCACATTTAACTATACGAGGAGATCAAGTTCACAGAGTACACAGTACGGAAC 1704  
QY 1764 GGAAGTGGCGCTTGTGATACCGGCTAGAGATCGTAACCATTTGATTTGCAATAT 1823  
DB 1705 GGAAGTGGCGCTTGTGATACCGGCTAGAGATCGTAACCATTTGATTTGCAATAT 1764

1824 CAGATGCGCAGACCACTTGCCCTATGCGACGACTCGAATGCCGTCACCCCGATGCC 1883  
1765 CAGATGCGCAGACCACTTGCCCTATGCGACGACTCGAATGCCGTCACCCCGATGCC 1824  
1884 GAAGAGATGGGGCCATCATGATGCGCCGATGATGCAATGCAATGCAATGCAATGCA 1943  
1825 GAAGAGATGGGGCCATCATGATGCGCCGATGATGCAATGCAATGCAATGCAATGCA 1884  
1944 TCGATATCTTGCACTGATGCGCCGATGATGCAATGCAATGCAATGCAATGCAATGCA 2003  
1885 TCATATACCTGCACTGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1944  
2004 ATGGCGCGATGGGGCGTGAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2063  
1945 ATGGCGCGATGGGGCGTGAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2004  
2064 CGCAATCAATGATGCGCGCAGCAATGCGCGCAGCAATGCGCGCAGCAATGCGCGCAG 2123  
2005 CGCAATCAATGATGCGCGCAGCAATGCGCGCAGCAATGCGCGCAGCAATGCGCGCAG 2064  
2124 CTCGAT-----CATGCGACTGCAAAATGCGCGCGCGCGCGCGCGCGCGCGCGCG 2168  
2065 CCCGATGCGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2124  
2169 GCTGGCAAGATTTAAACATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2228  
2125 GCTGGCAAGATTTAAACATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2184  
2229 GTTGATATGAAAGATGATGATGCGCGCGCAGCAATGCAATGCAATGCAATGCAATGCA 2288  
2185 GTAGCATGAAAGATGATGATGCGCGCGCAGCAATGCAATGCAATGCAATGCAATGCAAT 2244  
2289 AGTGGGCGAAGCGATGCG 2348  
2245 AGTGGGCGAAGCGATGCG 2280  
2349 GATGGCGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2408  
2281 GATGGCGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2340  
2409 TGTGATGCGAAGCGATGCG 2468  
2341 TGTGATGCGAAGCGATGCG 2400  
2469 TTGATGCGCGAAGCGATGCG 2528  
2401 TTGATGCGCGAAGCGATGCG 2460  
2529 GCATGATGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2588  
2461 GCATGATGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2520  
2589 TTGATGCGCGAAGCGATGCG 2648  
2521 TTGATGCGCGAAGCGATGCG 2580  
2649 TACTATGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2708  
2581 TACTATGCGAAGCGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2640  
2709 GAATGCGCGAAGCGATGCG 2768  
2641 GAATGCGCGAAGCGATGCG 2700  
2769 GTATGCGCGAAGCGATGCG 2828  
2701 GTATGCGCGAAGCGATGCG 2760  
2829 ACCATGCGCGAAGCGATGCG 2888  
2761 ACCATGCGCGAAGCGATGCG 2820

2889 GTGATGGGATGCAATGCG 2948  
2821 GTGATGGGATGCAATGCG 2880  
2949 GCGGATGCG 3008  
2881 CATGATGCG 2940  
3009 GTGCTGCGCGAAGCGATGCG 3068  
2941 GTGCTGCGCGAAGCGATGCG 3000  
3069 TGCATGCG 3128  
3001 TGCATGCG 3060  
3129 TTAGGCTGCG 3188  
3061 TTAGGCTGCG 3120  
3189 GATGATGCG 3248  
3121 GATGATGCG 3180  
3249 GGTATATGCG 3308  
3181 GGTATATGCG 3240  
3309 CAACATGCG 3368  
3241 CAACATGCG 3261  
3369 AACGATGCG 3428  
3262 AACGATGCG 3321  
3429 AAGGATGCG 3488  
3322 AAGGATGCG 3381  
3489 GACATGCG 3548  
3382 GACATGCG 3441  
3549 AACTGATGCG 3608  
3442 AACTGATGCG 3501  
3609 TTAAGATGCG 3668  
3502 TTAAGATGCG 3561  
3669 AAGGATGCG 3728  
3562 AAGGATGCG 3621  
3729 AGGATGCG 3788  
3622 AGGATGCG 3681  
3789 CCGCTGCG 3845  
3682 CCGCTGCG 3741  
3846 CCGCTGCG 3905  
3742 CCGCTGCG 3801  
3906 GACTGCG 3965  
3802 GACTGCG 3861  
3966 AATAATGCG 4025

Db	3862	AAATAATTTTGGAAACCGCAGTTATCTGATTTTAAATGAGTAGCTTGGCC	3921
OY	4026	TTAAGATGTACATCTGCCA CAAGA CCACTG CAGATATTTATCTATATGAC	4085
Db	3922	TTAGAAGATGTCAATTTACCCGATCGACCTGTCA TGCAGATATACGTACTACATGAC	3981
OY	4086	AGAAATTTTACGATATATCTCTCTGGAAATGTAAATCAAGTGGTGGCCTGGCTTC	4145
Db	3982	AGCATTTTACGGTGATATCTTTTGGAGATGTGATCAATATGTTGGCCTGGCTTT	4041
OY	4146	AAAGTGTACTTCA CCAACGCGTGTTGGCTCAATTTTGATTTGTCATGTA TCGCTT	4205
Db	4042	AAGGTTTACTTCA CCAATGCCGTGGTGGCTGATTTGATGTGATCTCATTCGCTT	4101
OY	4206	ATCAACTTCGTGCTTCACTTGTTGGAGCTGTGATTTCAAGCTTCAACATATGCGA	4255
Db	4102	ATAAATTTGGTGGCCGTTTGGTGGGCTTAAATATATAGCCGTTTATGATCAATGGC	4161
OY	4266	ACGTTAAGACCTGAGACCACTACGTCGACATGTCCTCCGTATG CAGGGCATGAGGTCGTG	4325
Db	4162	ACACTGGCGCCCTTAAGGCCATTTGGTGCTGTCTCTAATGGAAGGATATGAAGTTGTC	4221
OY	4326	GTTATATGCGCTGTGTACAACTATACCGTTCATCTTCAATGTGTCTATTTGGTGTCTATA	4385
Db	4222	GTTAATGGCGCTGTTCAGACTATACCGTCAATCTTCAATGTGTCTATTTGGTGTCTATA	4281
OY	4386	TTTGGCTCAATTTTGGCCATATGGGTGTACAGCTTTTGGCTGGAATAATTTTAAAGTGC	4445
Db	4282	TTTTGGCTATTTTGGCCATATATGGAGTACAGCTTTTGGCTGGAATAATTTTAAAGTGC	4341
OY	4446	GAGGATGAAATGGCAGAGCTACGCCAGATCATACCAATTCGCAATGCTCGCAG	4505
Db	4342	AAAGTGTGTAATGACATGTGCTGAGCATTAATCAATCCGAATCGTAAATGCTCGCAGAA	4401
OY	4506	AGCGGAATCTACAGTGGGTGAATTCAGCAATGATTTGCATATGTGTGTAAAGCGCAT	4565
Db	4402	AGTGAATCTACAGTGGGAATTTGGCAATGAATCTTCAATGTGTGTAAATGCGCAT	4461
OY	4566	CTGTGCTCTTTTCCAAGTGGCCACTTCAAGGCTGTGATCAAAATCATGAAAGATGCTATC	4625
Db	4462	CTGTGTCTATTTCAAGTGGCCACTTTTAAAGGCTGTGATCCAGATTTATGAAGATGCTATC	4521
OY	4626	GATTCACGAGGTGTGACAAAGCAACCAATTTGTGAATGAACATCTAATGTATTTATAT	4685
Db	4522	GATTCACGAGGTGTGACAAAGCCGATCCGAGAAACCAATCTAATGTATTTATAT	4581
OY	4686	TTGCTATCTTCATCATATTTTGGATCTCTTTTTCACATCACTCATCTGTCATTTGCTTATC	4745
Db	4582	TTGCTATCTTCATCATATTTTGGATCAATTTTTCACATCACTCATCTGTCATTTGCTTATC	4641
OY	4746	ATTGATTAATTTTATGACAAAAGAAAAAGCAGGTGATCATTTGAATGTTCATGACA	4805
Db	4642	ATTGATTAATTTTATGACAAAAGAAAAAGCAGGTGATCATTTGAATGTTCATGACA	4701
OY	4806	GAAATGTCAAAAAGTACTATATATGCTATGAAAAAGATGGGCTCTAAAAAAACAATTAAA	4865
Db	4702	GAAATGTCAAAAAGTACTATATATGCTATGAAAAAGATGGGCTCTAAAAAAACAATTAAA	4761
OY	4866	GCCATTTCAAGACCAAGGTGGCGACCAAGCAATATGCTTTGAATGTAAACCGATAG	4925
Db	4762	GCCATTTCAAGACCAAGGTGGCGACCAAGCAATATGATTCGAAATGTGTAAACAGATAAA	4821
OY	4926	AAATTCGATTAATCATATATGTATTTCAATTTGGTCTGAACATGTTCAACATGACCTCGAT	4985
Db	4822	AAATTCGATTAATCATATATGTATTTCAATTTGGTCTTAACATGTTTCAACATGACCTCGAT	4881
OY	4986	CGTTACGATGCGTCGACACGTAATACCGGTCCTGACATATCTCAATGCGATATTCGTA	5045
Db	4882	CGTTACGATGCGCTCCGAGGCGTAACAACATGTCCGCAAAATCTCAATGGGATTTGCTA	4941
OY	5046	GTTATTTTCAAGTCCGATATGCTATTAATAATTTGCTTACGATATCACTATTTATTT	5105

[illegible]



QY 1464 GCCGAAAGAGCTGCTGATCGGAATGGCCAAAGTCCGACTATCTTGATCAAC 1523  
 DB 1408 GCCGTCGCGCAGCTCTGATCCCGAGATGGCAAGATCCGATCTTGATCAAC 1467  
 QY 1524 TATGACTATTTTGGCGCGGAAGGGCAAGATGACAAACAAGAGAGATGTC 1583  
 DB 1468 TATGAATCTTTGGCGCGGAAGGGCAAGATGACAAACAAGAGAGATGTC 1527  
 QY 1584 ATTCGAGGCGTGAAGTGGAGTGGAGTGGAGTGGATTAACAAGACACGACCT 1643  
 DB 1528 ATACGAGGCGTGAAGTGGAGTGGAGTGGAGTGGATTAACAAGACACGACCT 1587  
 QY 1644 ACCAGACACACCAAGCTACCAAGTTCGTAAGTGAACAAGACATCTTATCTTACCT 1703  
 DB 1588 ACCAGACACACCTGCTACTAAAGTCCGTAAGTGAACAAGACATCTTATCTTACCT 1644  
 QY 1704 GGTTCACCGTTTAACATACGACGAGGATCACTTATCTTCAACAAGTACAGATACGGAAC 1763  
 DB 1645 GGTTCACCGTTTAACATACGACGAGGATCACTTATCTTCAACAAGTACAGATACGGAAC 1704  
 QY 1764 GGAAGTGGCGCTTGGTATACCGGTAAGGATCGTAAGTGGATTTGATTTGATAT 1823  
 DB 1705 GGGCGTGGAGCTTTGGTATACCGGTAAGGATCGTAAGTGGATTTGATTTGATAT 1764  
 QY 1824 CAGGATGCGCAGACGATCTTCCCTTATGCGACGATCGATGCTGACCCGATGTC 1883  
 DB 1765 CAGGATGCGCAGACGATCTTCCCTTATGCGACGATCGATGCTGACCCGATGTC 1824  
 QY 1884 GAGGAAATGGGCGCATGATGCGGCTGATGAGGCAATGATGAGGCTCCGACACTA 1943  
 DB 1825 GAGGAAATGGGCGCATGATGCGGCTGATGAGGCAATGATGAGGCTCCGACACTA 1884  
 QY 1944 TCGTATACCTCGGATGCTCCGATATCGTATACCTCAATGAGGCAATCTTACCTGCGG 2003  
 DB 1885 TCGTATACCTCGGATGCTCCGATATCGTATACCTCAATGAGGCAATCTTATGAGG 1944  
 QY 2004 ATGGCGGTCATGGGCTGACGACATGACCAAGAGACAAATGGGCAACCGCACCA 2063  
 DB 1945 ATGGCGGTCATGGGCTGACGACATGACCAAGAGACAAATGGGCAACCGCACCA 2004  
 QY 2064 CGCAATCAATCAGTGGGCGCACCAATGCGGACCACTGTCGACCAATCAATCAAG 2123  
 DB 2005 CGCAATCAATCAGTGGGCGCACCAATGCGGACCACTGTCGACCAATCAATCAAG 2064  
 QY 2124 CTCGAT-----CATCGCACTACGAAATGGCCTGAGTGCACGACGAA 2168  
 DB 2065 CCGGATGCGCAATCAAGAGACAAAGGATTAAGAAATGGGTCAGGATTAACAGACGA 2124  
 QY 2169 GCTGGCAAGTTAAACATCAATGACATCTTTTATGAGCCGCTCCAGACAAACGCTG 2228  
 DB 2125 GCTGGCAAGTTAAACATCAATGACATCTTTTATGAGCCGCTCCAGACAAACGCTG 2184  
 QY 2229 GTTGATATGAAGATGATGCTGCTGAATGATCAATGACAGGCGCTGGTCGCGAC 2288  
 DB 2185 GTTGATATGAAGATGATGCTGCTGAATGATCAATGACAGGCGCTGGTCGCGAC 2244  
 QY 2289 AGTGGGCAAGCATCGCGGTCTCTCGTTTACTATTTCCAAAGAGACGATGACGAG 2348  
 DB 2245 AGTGGGTCTAGTGAAGAGT-----GAGGACGATGACGAA 2280  
 QY 2349 GATGGGCGGACGTTCAAGACAGGACCTGAAAGTATCTTCAAGGACATGATGTTT 2408  
 DB 2281 GATGGTCCGACATTCAGGACATCGCCGTGAATACATCTTAAAGGACATGAAATCTTT 2340  
 QY 2409 TGTGTGGAGTCTGCTGGGTTTGGTGAATTTGAGAGTGGGATGCTCATGCTC 2468  
 DB 2341 TGTGTGGAGTCTGCTGGGTTTGGTGAATTTGAGAGTGGGATGCTCATGCTC 2400  
 QY 2469 TTGATCCCTTGGTGAAGTCTTATCAACGCTGACATTTGGTCAACAGATGTTCAAG 2528  
 DB 2401 TTGATCCCTTGGTGAAGTCTTATCAACGCTGACATTTGGTCAACAGATGTTTATG 2460

QY 2529 GCATGATACACCAAGATATGAACAAGAGATGAACCGGTGCTCAAGTGGCAATAT 2588  
 DB 2461 GCCATGATACACCAAGATATGAACAAGAGATGAACCGGTGCTCAAGTGGCAATAT 2520  
 QY 2589 TTCTTCAACCGCACCTTTGCTGACGAGGACCAATGAAGTATGCGCATGAGCCCAAG 2648  
 DB 2521 TTCTTCAACCGCACCTTTGCTGACGAGGACCAATGAAGTATGCGCATGAGCCCAAG 2580  
 QY 2649 TACTATTTCAAGAGGCTGGAACATCTTCACTTATGATGATGCTGCTTATG 2708  
 DB 2581 TACTATTTCAAGAGGCTGGAACATCTTCACTTATGATGATGCTGCTTATG 2640  
 QY 2709 GAACTGGGACCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 2768  
 DB 2641 GAACTGGGACCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 2700  
 QY 2769 GTATTCAACTGCGCAAGCTTGGCCCACTTAATTTACTATTTGATTTGATGAGGAC 2828  
 DB 2701 GTATTCAACTGCGCAAGCTTGGCCCACTTAATTTACTATTTGATTTGATTTGAGG 2760  
 QY 2829 ACCATGGGCGCTTGGGATATGACATTTGATCTTGGATTAATCACTTTCG 2888  
 DB 2761 ACATGGGCGCTTGGGATATGACATTTGATCTTGGATTAATCACTTTCG 2820  
 QY 2889 GTATGGGAAATGCACTGTTGGGAAAGATTAATGATCAAGAGACGCTTCCGAT 2948  
 DB 2821 GTATGGGAAATGCACTGTTGGGAAAGATTAATGATCAAGAGACGCTTCCGAT 2880  
 QY 2949 GGGGACCTGCGCGCTGGAATCTTACCGACTTATGACAGGCTTCAATGATGCTGCTG 3008  
 DB 2881 CATGATTTACCGGCTGGAATCTTACCGACTTATGACAGGCTTCAATGATGCTGCTG 2940  
 QY 3009 GTGCTGCTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3068  
 DB 2941 GTGCTGCTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000  
 QY 3069 TGCATTCCTTCTTCTTGGGCAACGCTGATGATGATGATGATGATGATGATGATGATG 3128  
 DB 3001 TGCATTCCTTCTTCTTGGGCAACGCTGATGATGATGATGATGATGATGATGATGATG 3060  
 QY 3129 TTAGCCTTCTTCTTCTTGGGCAACGCTGATGATGATGATGATGATGATGATGATGATG 3188  
 DB 3061 TTAGCCTTCTTCTTCTTGGGCAACGCTGATGATGATGATGATGATGATGATGATGATG 3120  
 QY 3189 GATGCAATTAATTAAGGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATG 3248  
 DB 3121 GATGCAATTAATTAAGGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATG 3180  
 QY 3249 CGTATATTTGCTGATTTGTTCAAGTTAATGATTAATGATTAATGATTAATGATTAATG 3308  
 DB 3181 CGTATATTTGCTGATTTGTTCAAGTTAATGATTAATGATTAATGATTAATGATTAATG 3240  
 QY 3309 CAACCATCAAGTGAAGAGACCAACAGATCAATGATGATTTGAGCGAAGACATGATGAC 3368  
 DB 3241 CAACCATC-----AGAACATGCGCAT 3261  
 QY 3369 AACGAATGAGTGGGCGCACGACGATCTTCCGACGCGCTCATCAAGAGGAGATC 3428  
 DB 3262 AACGAATGAGTGGGCGCACGACGATCTTCCGACGCGCTCATCAAGAGGAGATC 3321  
 QY 3429 AAGGACAGCGCACTGAGGCTGCGATCGGGGATCGAGTGAATTTCAAGATACAGCG 3488  
 DB 3322 AAGGACAGCGCACTGAGGCTGCGATCGGGGATCGAGTGAATTTCAAGATACAGCG 3381  
 QY 3489 GACATGAAGAACCAAGCGCAAGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 3548  
 DB 3382 GATATGAAGAACCAAGCGCAAGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 3441  
 QY 3549 AACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3608  
 DB 3442 AACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3501  
 QY 3609 TTACAGAGAGACAGCACTGCGACGATTAATCAATGATGATGATGATGATGATGATGATG 3668

Db 3502 ATACAGACGATGACATCCGACGATTAATCATATGTTAGCCATTAAGAAATCGACCATTC 3561  
Qy 3669 AAGACGAGACCCACAGAGGCGCCGCGAGACGATGAGGGCGAGAGAGCGCGACCC 3728  
Db 3562 AAGACGAGACCCACAGAGGCGCCGCGAGACGATGAGGGCGAGAGAGCGCGACCC 3621  
Qy 3729 AGCAAGAGGATTAAGTCTGACGAGGAACTGACGAGGAGGGGAGTGGAGAGAGGGC 3788  
Db 3622 AGCAAGAGGACCTCGGCTCGACGAGGAACTGACGAGGAGGGCGAGGAGGAGGCGC 3681  
Qy 3789 CCGCTCGACGCTGATATCATTTATTCATG---ACACGACGAGATATATCTGATGATAT 3845  
Db 3682 CAGCTGATGATGATCATTTATCATTCATGCGGAAAACGACGAGATATGACGACATAT 3741  
Qy 3846 CCAAGTATGCTGCGCCGATTCGATCTATTAAGAAATTCGATCTTACCGGTCGAT 3905  
Db 3742 CCGGCGGATGTTCCCGGATCCGATCTATTAAGAAATTCGATCTTACCGGTCGAT 3801  
Qy 3906 GACTCGCGCTCTGCGACGATGAGGAGGAAATTAACGACGAAATCTTTCATTAATGA 3965  
Db 3802 GACTCGCGCTCTGCGACGATGAGGAGGAAATTAACGACGAAATCTTTCATTAATGA 3861  
Qy 3966 AATAAATTTTGAACAGCTGTTATCACTATGATTTTATGATGATGATGATGATGAT 4025  
Db 3862 AATAAATTTTGAACAGCTGTTATCACTATGATTTTATGATGATGATGATGATGAT 3921  
Qy 4026 TTGAAGATGATCATCTGCGACAAAGACCATCTGACGATATTTATCTATATAGAC 4085  
Db 3922 TTGAAGATGATCATCTGCGACCATCTGATGACGATATCTGATCTATCATAGAC 3981  
Qy 4086 AGAATTTTATGATTTATTTCTTCTGGAATTTTATCAAGTGTGTGGCTGCGCTTC 4145  
Db 3982 AGAATTTTATGATTTATTTCTTCTGGAATTTTATCAAGTGTGTGGCTGCGCTTC 4041  
Qy 4146 AAGATGATCTTCAACAGCGGCTGTTGCTGATTCGATTTGATGATGATGATGAT 4205  
Db 4042 AAGATGATCTTCAACAGCGGCTGTTGCTGATTTGATGATGATGATGATGATGAT 4101  
Qy 4206 ATCAACTCTGTTGCTTCACTGTTGAGCTGTTGATTTCAAGCTTCAAGATATGCA 4265  
Db 4102 ATCAACTCTGTTGCTTCACTGTTGAGCTTCAAGCTTCAAGATATGCAATGCGC 4161  
Qy 4266 ACGTTAAGACATGACGACCTACAGCTACGCTGCTGCTGCTGCTGCTGCTGCTG 4325  
Db 4162 ACGTTAAGACATGACGACCTACAGCTACGCTGCTGCTGCTGCTGCTGCTGCTG 4221  
Qy 4326 GTTAATGCTGTTGACAGCTATACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 4385  
Db 4222 GTTAATGCTGTTGACAGCTATACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 4281  
Qy 4386 TTTTGGCTAATTTTGGCATATGAGTGTATACGCTTTTGGTGAATAATTTTAAAGTC 4445  
Db 4282 TTTTGGCTAATTTTGGCATATGAGTGTATACGCTTTTGGTGAATAATTTTAAAGTC 4341  
Qy 4446 GAGACATGATGACGAGAGCTGACGACGATCATACCAATTCGATGCTGCGAG 4505  
Db 4342 AAGATGATGATGACGAGAGCTGACGACGATCATACCAATTCGATGCTGCGAG 4401  
Qy 4506 AGGAGAACTACAGCTGAGTGAATTCAGCATGAAATTCGATGCTGAGTGAAGCGAT 4565  
Db 4402 AGTGAATGATGACCTGAGGAAATTCGCAATGAACTTCGATGCTGAGTGAAGCGAT 4461  
Qy 4566 CTGCTGCTTTTCAAGTGGCACCTTCAAGGCTGATACAAATCATGAGAGTCTATC 4625  
Db 4462 CTGCTGCTTTTCAAGTGGCACCTTCAAGGCTGATACAAATCATGAGAGTCTATC 4521  
Qy 4626 GATTTCAGAGGCTGAGACGAAACCAATTCGTAAGCAACATCTACATGATTTATAT 4685  
Db 4522 GATTTCAGAGGCTGAGACGAAACCAATTCGTAAGCAACATCTACATGATTTATAT 4581  
Qy 4686 TTGCTATCTTCATATTTGATGCTTTTCACTGATCTGCTGCTGCTGCTATC 4745

Db 4582 TTGCTATCTTCATATTTGATGCTTTTCACTGATCTGCTGCTGCTGCTATC 4641  
Qy 4746 ATTGATTAATTTTATGACAAAGAAAGAGAGAGTGTGATTAAGAAATGTTATGCA 4805  
Db 4642 ATTGATTAATTTTATGACAAAGAAAGAGAGTGTGATTAAGAAATGTTATGCA 4701  
Qy 4806 GAGATGAGAAAGTACTATATGCTATGAAAGAAAGTGGCTCTAAAGAAACATTAAG 4865  
Db 4702 GAGATGAGAAAGTACTATATGCTATGAAAGAAAGTGGCTCTAAAGAAACATTAAG 4761  
Qy 4866 GCAATTCAGAGACCAAGTGGCGACCAAGCAATGCTTTGAAATAGTAACGATTAAG 4925  
Db 4762 GCAATTCAGAGACCAAGTGGCGACCAAGCAATGATTAAGAAATGTTATGCAATTA 4821  
Qy 4926 AATTCGATTAATCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4985  
Db 4822 AATTCGATTAATCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4881  
Qy 4986 CGTTACGATGCTGGGACAGTATTAAGCGGCTCTAGCTATCTCAATGCAATTTGTA 5045  
Db 4882 CGTTACGATGCTGGGACAGTATTAAGCGGCTCTAGCTATCTCAATGCAATTTGTA 4941  
Qy 5046 GTTATTTTCAAGTTCGATGCTATTTAAATATTCGTTTACGATATCACTATTTAT 5105  
Db 4942 GTTATTTTCAAGTTCGATGCTATTTAAATATTCGTTTACGATATCACTATTTAA 5001  
Qy 5106 GAGCATGGAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
Db 5002 GAGCATGGAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
Qy 5166 AGGATATTTATGAGAGTACTTGTGTCGCGACCCGCTGCGAGGAGTGTGGGCG 5225  
Db 5062 AGGATATTTATGAGAGTACTTGTGTCGCGACCCGCTGCGAGGAGTGTGGGCG 5121  
Qy 5226 AAGTGGGCGTGTCTTTCGACTGCTGTAAGGAGGACCAAGGATTCGACACTCTTC 5285  
Db 5122 AAGTGGGCGTGTCTTTCGACTGCTGTAAGGAGGACCAAGGATTCGACACTCTTC 5181  
Qy 5286 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTG 5345  
Db 5182 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTG 5241  
Qy 5346 TTCAATCTTGGCATTTTCCGATGCTGCTTCTTATGACGAGGAGGAGGAGGAGG 5405  
Db 5242 TTCAATCTTGGCATTTTCCGATGCTGCTTCTTATGATGATGATGATGATGATG 5301  
Qy 5406 AACAGCTGTAACACTTCAAGACCTTGGCGAGAGATGATGCTGCTTCTGATGCTG 5465  
Db 5302 AACAGCTGTAACACTTCAAGACCTTGGCGAGAGATGATGATGATGATGATGAT 5361  
Qy 5466 ACGTCAAGCGGTTGGATGCTGTAAGGAGGATGATGATGATGATGATGATGATGAT 5525  
Db 5362 ACGTCAAGCGGTTGGATGCTGTAAGGAGGATGATGATGATGATGATGATGATGAT 5421  
Qy 5526 CCGGACGAGCAAAAGCTATCCGCGCAATTTGGTTCAGGAGCCTGTTGAATAAGCT 5585  
Db 5422 CCGGACGAGCAAAAGCTATCCGCGCAATTTGGTTCAGGAGCCTGTTGAATAAGCT 5481  
Qy 5586 CTCTCTCATACCTAGTTATTAAGCTTTTGAATGATTAATGATGATGATGATGATGAT 5645  
Db 5482 CTCTCTCATACCTAGTTATTAAGCTTTTGAATGATTAATGATGATGATGATGATGAT 5541  
Qy 5646 CTGAGAACTATATGACGCGACCGAGAGCGTGAAGAGGCTTAACGAGAGGACTAC 5705  
Db 5542 CTGAGAACTATATGACGCGACCGAGAGGATGATGATGATGATGATGATGATGAT 5601  
Qy 5706 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5765  
Db 5602 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5661  
Qy 5766 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5825  
Db 5662 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5721

QY 5826 AAGTACAGATCATATGATGACATACCATCTGTCCGGTGAAGCTCATGTACTGCTC 5885  
 DB 5722 AAGTACAAATCATATGATGACATCCGATATGTCCGGGCGACATGATGTACTGTG 5781  
 QY 5886 GACATCTCGAGCCCTTTCGAAAGCTTCTTTCGGCGGAAAGGCAATCCGATAGAGAG 5945  
 DB 5782 GATATATGAGATCCCTGACCAAGACCTTCTTTCGGCGGAAAGGCAATCCGATAGAGAG 5841  
 QY 5946 ACAGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 DB 5842 ACAGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 QY 6006 TCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6065  
 DB 5902 TCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5961  
 QY 6066 AAGCACAAGGCG 6125  
 DB 5962 CGTTACAGATGATGCTC-----CCACCCCGAGAGGCTGAT 5994  
 QY 6126 GCGCGTATCCGATCCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6185  
 DB 5995 GAGGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6054  
 QY 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
 DB 6055 GCG 6114  
 QY 6246 AATGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6305  
 DB 6115 AATGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6159  
 QY 6306 GCG 6365  
 DB 6160 GTCGGCG 6219  
 QY 6366 GTTCTGTGAGAGCG 6425  
 DB 6220 GTTCTGTGAGAGCG 6279  
 QY 6426 CGATCG 6484  
 DB 6280 AGATCCCGAGCATATCATTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6318

RESULT 11  
 US-08-808-793-2  
 ; Sequence 2, Application US/0808793  
 ; Patent No. 5858713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soderlund, David M.  
 ; APPLICANT: Ingles, Patricia J.  
 ; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
 ; TITLE OF INVENTION: AND USE THEREOF  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/808,793  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,361  
 FILING DATE: 24-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/012,649  
 FILING DATE: 01-MAR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Braman, Susan J.  
 REGISTRATION NUMBER: 34,103  
 REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 716-263-1636  
 TELEFAX: 716-263-1600  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6315 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-808-793-2

Query Match 68.1%; Score 4434.2; DB 2; Length 6315;  
 Best Local Similarity 81.8%; Pred. No. 0;  
 Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;

QY 24 ATGACAGAAATTCGACTGATATCTGAGAGAAAGCAGATTGTCCTGCTTACC 83  
 DB 1 ATGACAGAAATTCGACTGATATCTGAGAGAAAGCAGATTGTCCTGCTTACC 60  
 QY 84 CCGGATCATTTGGTGAATTCGAAACCAACCTTCCCGTGAACATGAAAGAGAGAG 143  
 DB 61 CCGGATCATTTGGTGAATTCGAAACCAACCTTCCCGTGAACATGAAAGAGAG 117  
 QY 144 CTGGAAGAAAG 203  
 DB 118 CTGGAAGAAAG 148  
 QY 204 GAAATCGATATGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
 DB 149 -GATACGATATGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
 QY 264 CAGGGTGCCTATACCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 323  
 DB 208 CAGGGTGCCTATACCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 267  
 QY 324 CCTCTGAGAGATATGATCCCTTACTACAGCAATGTAAGTCAATTCGATGTAAGCAAA 383  
 DB 268 CCTCTGAGAGATATGATCCCTTACTACAGCAATGTAAGTCAATTCGATGTAAGCAAA 327  
 QY 384 GGAAGAAATATTTTGTGCTTTTCTGATCAAAAAGCATGTGATGATGATGATGATGAT 443  
 DB 328 GGAAGAAATATTTTGTGCTTTTCTGATCAAAAAGCATGTGATGATGATGATGATGAT 387  
 QY 444 CGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503  
 DB 388 CGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447  
 QY 504 ACCACAATTCGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 563  
 DB 448 ACCACAATTCGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 507  
 QY 564 ACTGAGGTATATTCACCGGAATCTACCAATTCGATGATGATGATGATGATGATGATGAT 623  
 DB 508 ACTGAGGTATATTCACCGGAATCTACCAATTCGATGATGATGATGATGATGATGATGAT 567  
 QY 624 GGTTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683  
 DB 568 GGTTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627  
 QY 684 GTATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743

Dh 628 GTATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTAATCTGCAGCTTTTGA 687  
Qy 744 ACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCATTTGCGAGGCTTGAAGCATC 803  
Db 688 ACATTTTGGGTACGCGAGCTCTGAAAACCGTAGCATTTGCGAGGCTTGAAGCATC 747  
Qy 804 GTGGGCGCGGTATCGATCGGTGAAGATCTGGCGCATGTATATCTGACCATGTC 863  
Db 748 GTGGGTGCTGTATGTAATCTGTAAATAATCTACGCAATGTATATTTTACAAATGTT 807  
Qy 864 TCCCTGTGCGGTGTCGCGTGTATGCGCTTACAGATCTATATGCGGTGCTCACCGAGAG 923  
Db 808 TCCCTGTGCGGTGTCGCGTGTATGCGCTTACAGATCTATATGCGGTGCTCACCGAGAG 867  
Qy 924 TGCATCAAGAGTTCCCGCTGGAAGGTTCTGGGGCATCTGACCGAGAGACTGGGAC 983  
Db 868 TGCATTAACGATTCCTCCCTGAGCGGAGTTGGGGCATCTGACCGAGAGACTGGGTT 927  
Qy 984 TATCACATCGCAATGCTCCAAATTGATTCGAGAGAGAGGAGATCTCAATTCCTGTTA 1043  
Db 928 CTACACATAGCAACAGTTTCAATTTGTTTACGAGAGAGAGTGGCGAGTCAATTCGAGT 987  
Qy 1044 TCGCGCAATATATCCGCTGCGGGCAATGCGACGATTAAGTGTGCTGCGAGGGTTT 1103  
Db 988 TCGCGGAATGTATCCGCTGCGGACCAATGCGCGAAGTTAGTCTGCTGCGAGGGCTTC 1047  
Qy 1104 GGTCCGAATCCGAATTTATGCTACACAGCTTCGATTCGATTCGATTCGATTCGATTC 1163  
Db 1048 GGGCCCAATCCCAATGACATGACACAGCTTCGATTCGATTCGATTCGATTCGATTC 1107  
Qy 1164 GCTTCGCGGTATGACACAGAGCTTCGAGAGAGTCTGACAGCTGCTGTTGCGGCGC 1223  
Db 1108 GCGTTTGTCTCATGACCCAGATTTCTGAGAGAGTCTGATACAGAGCTGCTGAGACA 1167  
Qy 1224 GCGGACCATAGCAATGCTGTTCTTATATGATCAATCTTCTAGGTTCAATCTTATCTT 1283  
Db 1168 GCTGACCCCTGCGACATGTTGTTCTTATATGATCAATCTTCTAGGTTCAATCTTATCTT 1227  
Qy 1284 GTGAATTTGATTTGGGCAATTTGTCATGTCATGATGCAATTTGCAAGAGAGCGGGA 1343  
Db 1228 GTGAATTTGATTTGGGCAATTTGTCATGTCATGATGCAATTTGCAAGAGAGCGGGA 1287  
Qy 1344 GAAGAGAGGCTGCGAAGAGAGAGGCGATGATGAGAGAGAGAGGCTGCGGCGCAAA 1403  
Db 1288 GAAGAGAGGCTGCGAAGAGAGAGGCGATGATGAGAGAGAGAGGCGGCGCAAG 1347  
Qy 1404 GCGGCAAGCTGAGAGAGCGGCGCAATGCGAGGCTGAGAGAGCGGATGCGGCTGCC 1463  
Db 1348 GCGGCAAGCTGAGAGAGCGGCGCAATGCGAGGCTGAGAGAGCGGATGCGGCTGCC 1407  
Qy 1464 GCGGAGAGGCTGCACTGCAATCGGAATGCGCAAGAGTCCGATTTCTTGCATCAGC 1523  
Db 1408 GCGGCTGCGGCACTGCAATCGGAATGCGCAAGAGTCCGATTTCTTGCATCAGC 1467  
Qy 1524 TATGAGGTAATTTGTTGGGCGGAGAGAGGCGCAAGATGACAAACAAAGAGAGATGCC 1583  
Db 1468 TATGAGGTAATTTGTTGGGCGGAGAGAGGCGCAAGATGACAAACAAAGAGAGATGCC 1527  
Qy 1584 ATTGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1643  
Db 1528 ATTGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1587  
Qy 1644 ACCGACAGACCAAGTCAAAAGTTCTTAAAGTGAAGAGACATCTTATCTTACT 1703  
Db 1588 ACCGACAGACCAAGTCAAAAGTTCTTAAAGTGAAGAGTGAAGTGAAGTGAAGTGAAG 1644  
Qy 1704 GGTTCACCGTTTAAATATGAGAGAGGAGATCAAGTATCTTCAAGATGAGAGAG 1763  
Db 1645 GGTTCACCGTTTAAATATGAGAGAGGAGATCAAGTATCTTCAAGATGAGAGAG 1704  
Qy 1764 GAGAGTGGCGCTTTGATATACCGGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1823  
Db 1705 GAGAGTGGCGCTTTGATATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1764

Qy 1824 CAGATGCCAGAGCACTTGCCCTATGCGAGAGACTGAAATGCGGTCACCCGAGATGCC 1883  
Db 1765 CAGATGCCAGAGCACTTGCCCTATGCGAGAGACTGAAATGCGGTCACCAATATGCC 1824  
Qy 1884 GAAGAGATGGGCGCATATATGATGCCGATGATGATGATGATGATGATGATGATGATGAT 1943  
Db 1825 GAAGAGATGGGCGCATATATGATGCCGATGATGATGATGATGATGATGATGATGATGAT 1884  
Qy 1944 TCGTATACCTGCAATGCTCCGAAATGCTATATCTGATGATGATGATGATGATGATGATG 2003  
Db 1885 TCGTATACCTGCAATGCTCCGAAATGCTATATCTGATGATGATGATGATGATGATGATG 1944  
Qy 2004 ATGGCGGCTATGGGCGTCAAGAGATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063  
Db 1945 ATGGCGGCTATGGGCGTCAAGAGATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2004  
Qy 2064 CGCAATCAATCAGTGGGCGGCGCAATGAGGCGGCGCACTGTCTGACACCAATCACAG 2123  
Db 2005 CGCAATCAATCAGTGGGCGGCGCAATGAGGCGGCGCACTGTCTGACACCAATCACAG 2064  
Qy 2124 CTGAT-----CATGCGACTACGAAATTTGCGCTGAGTGCAGGAGCA 2168  
Db 2065 CCCGATCCCAATCAAG 2124  
Qy 2169 GCTGGCAAGTTAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2228  
Db 2125 GCTGGCAAGTTAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2184  
Qy 2229 GTTATATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2288  
Db 2185 GTTATATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244  
Qy 2289 AGTGGGCAAGCGATGCGGCTGCTCGGTTACTATTTCCCAAGAGAGAGAGAGAGAGAG 2348  
Db 2245 AGTGGGCAAGCGATGCGGCTGCTCGGTTACTATTTCCCAAGAGAGAGAGAGAGAGAG 2280  
Qy 2349 GATGGGCGGAGCTTCAAG 2408  
Db 2281 GATGGGCGGAGCTTCAAG 2340  
Qy 2409 TGTGTGAGGAGCTGTTGCTGGGTTTGGTGAATTTTCAAGAGAGAGAGAGAGAGAGAGAG 2468  
Db 2341 TGTGTGAGGAGCTGTTGCTGGGTTTGGTGAATTTTCAAGAGAGAGAGAGAGAGAGAGAG 2400  
Qy 2469 TTTGATCCCTTCTGAGAGCTTTTCAATGATGATGATGATGATGATGATGATGATGATG 2528  
Db 2401 TTTGATCCCTTCTGAGAGCTTTTCAATGATGATGATGATGATGATGATGATGATGATG 2460  
Qy 2529 GCATGATCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2588  
Db 2461 GCATGATCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520  
Qy 2589 TTTTTCACCGGCACTTTGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2648  
Db 2521 TTTTTCACCGGCACTTTGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Qy 2649 TACTATTTCAAGAGAGGCTGGAACATCTTCAATGATGATGATGATGATGATGATGATG 2708  
Db 2581 TACTATTTCAAGAGAGGCTGGAACATCTTCAATGATGATGATGATGATGATGATGATG 2640  
Qy 2709 GAACTGGAGCTCAGAGGCTGTCAGAGGCTGTCAGAGGCTGTCAGAGGCTGTCAGAGG 2768  
Db 2641 GAACTGGAGCTCAGAGGCTGTCAGAGGCTGTCAGAGGCTGTCAGAGGCTGTCAGAGG 2700  
Qy 2769 GTATTCAAACTGGGCAAGCTTGGGCGGCACTTAATTTACTGATTTGATTTAGTGGAGCG 2828  
Db 2701 GTATTCAAACTGGGCAAGCTTGGGCGGCACTTAATTTACTGATTTGATTTAGTGGAGCG 2760  
Qy 2829 ACATGGGCGCTTTGGGTAATCTGACATTTGATCTTTCATATCATCTTCTTGGC 2888  
Db 2761 ACATGGGCGCTTTGGGTAATCTGACATTTGATCTTTCATATCATCTTCTTGGC 2820

QY 2889 GTGATGGGAATGCACTGTTCCGAAAGATATCATGATCAAGAGACCGCTTCCGAT 2948  
DB 2821 GTGATGGGAATGCACTTTCGAAAGAACTATATGACCAAGATGCTTCAAGAGAC 2880  
QY 2949 GGGACCTCGCGGCTGGAACTTACCGACTTATGACAGCTTCAATGATCGTTCGCG 3008  
DB 2881 CATGAATTCACCGGCTGGAACTTACCGACTTATGACAGCTTCAATGATCGTTCGCG 2940  
QY 3009 GTGCTCTGCGGAATGATCGATCGATGCGGATGCGATGATCGTGGCGGATGCTCG 3068  
DB 2941 GTGCTCTGCGGAATGATCGATCGATGCGGATGCGATGATCGTGGCGGATGCTCG 3000  
QY 3069 TCGATTCCTTCTTCTTGGCGACCGTTCATGCGGAATCTTGTGCTACTTAACTTTTC 3128  
DB 3001 TGTATACCTTCTTCTTGGCGACCGTTCATGCGGAATCTTGTGCTACTTAACTTTTC 3060  
QY 3129 TTAGCTTCTTCTTCTTGGCGACCGTTCATGCGGAATCTTGTGCTACTTAACTTTTC 3188  
DB 3061 TTAGCTTCTTCTTCTTGGCGACCGTTCATGCGGAATCTTGTGCTACTTAACTTTTC 3120  
QY 3189 GATAGCAATTAATGACCGGAGCTTCAATCGAATGCGGATGCGGATGCGGATGCG 3248  
DB 3121 GATAGCAATTAATGACCGGAGCTTCAATCGAATGCGGATGCGGATGCGGATGCG 3180  
QY 3249 CGTAAATGCTGATGCTTCAATGATTAATGCAATGCAATGCAATGCAATGCAATG 3308  
DB 3181 CGTAAATGCTGATGCTTCAATGATTAATGCAATGCAATGCAATGCAATGCAATG 3240  
QY 3309 CAACCATGAGTGGAGAGCAACAACGATGATGATGATGATGATGATGATGATGATG 3368  
DB 3241 CAACCATGAGTGGAGAGCAACAACGATGATGATGATGATGATGATGATGATGATG 3261  
QY 3369 AACGAACTGAGTGGAGAGCAACAACGATGATGATGATGATGATGATGATGATGATG 3428  
DB 3262 AATGAACTGAGTGGAGAGCAACAACGATGATGATGATGATGATGATGATGATGATG 3321  
QY 3429 AAGGAGCAGACGCACTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3488  
DB 3322 AAGGAGCAGACGCACTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3381  
QY 3489 GACATGAGAGCAACGAGCGGAGAGATGCAATATCTAATTAACGAACTGATGATG 3548  
DB 3382 GATGAGAGCAACGAGCGGAGAGATGCAATATCTAATTAACGAACTGATGATGATG 3441  
QY 3549 AACTCAATTAACGAACTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3608  
DB 3442 AACTCAATTAACGAACTGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3501  
QY 3609 TTAACGAGAGCAGACCTGCGAGCTTAATCTCATATGATGAGCAATGAGATGAG 3668  
DB 3502 AATACGAGAGCAGACCTGCGAGCTTAATCTCATATGATGAGCAATGAGATGAG 3561  
QY 3669 AAGGAGCAGAGCAGCAAGGAGCAGCGGAGAGTGGAGAGTGGAGAGTGGAGAG 3728  
DB 3562 AAGGAGCAGAGCAGCAAGGAGCAGCGGAGAGTGGAGAGTGGAGAGTGGAGAG 3621  
QY 3729 AAGGAGCAGAGTGAATGATCTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3788  
DB 3622 AAGGAGCAGAGTGAATGATCTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3681  
QY 3789 CCGCTGAGAGTGAATGATCTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3845  
DB 3682 CAGCTGAGAGTGAATGATCTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3741  
QY 3846 CAGCTGAGTGTGCTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3905  
DB 3742 CCGGCGGAGCTGTTTCCCGAGCTGCTACGAGAGTGGAGAGTGGAGAGTGGAG 3801  
QY 3906 GACTGCGCTGTTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3965  
DB 3802 GACTGCGCTGTTGCGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAG 3861  
QY 3966 AATTAATATTTTGAACAGCTGTTATCACTGATGATTTAATGATGATGATGATG 4025

DB 3862 AATTAATATTTTGAACAGCTGTTATCACTGATGATTTAATGATGATGATGATG 3921  
QY 4026 TTAGAAGATGATCATCTGCGCAAGAGCCATCTGAGAGATTTTATATATATGAG 4085  
DB 3922 TTAGAAGATGATCATTTACCGATCTGCGCAAGAGATTTTATATATATGAG 3981  
QY 4086 AATTAATTTTACGTTATATTTCTTGGAGATGTTAATCAAGTGGTGGCTGCGCTTC 4145  
DB 3982 AAGATATTTTACGTTATATTTCTTGGAGATGTTAATCAAGTGGTGGCTGCGCTTC 4041  
QY 4146 AAGATATTTTACGTTATATTTCTTGGAGATGTTAATCAAGTGGTGGCTGCGCTTC 4205  
DB 4042 AAGATATTTTACGTTATATTTCTTGGAGATGTTAATCAAGTGGTGGCTGCGCTTC 4101  
QY 4206 ATCAATTTCTGTTCTTCACTTGGAGAGTGGATGATGATGATGATGATGATGATG 4265  
DB 4102 AATTAATTTGCTTGGCTTGGAGAGTGGATGATGATGATGATGATGATGATGATG 4161  
QY 4266 AAGTAAAGAGCTGAGACCACTAGTGGAGATGATGATGATGATGATGATGATGATG 4325  
DB 4162 AAGTAAAGAGCTGAGACCACTAGTGGAGATGATGATGATGATGATGATGATGATG 4221  
QY 4326 GTTAATGCGTGGTCAAGCTTACCTGATGATGATGATGATGATGATGATGATGATG 4385  
DB 4222 GTTAATGCGTGGTCAAGCTTACCTGATGATGATGATGATGATGATGATGATGATG 4281  
QY 4386 TTTTGGCTAATTTTTCGATTAATGAGTGGATGATGATGATGATGATGATGATGATG 4445  
DB 4282 TTTTGGCTAATTTTTCGATTAATGAGTGGATGATGATGATGATGATGATGATGATG 4341  
QY 4446 GAGGACATGATGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATGATG 4505  
DB 4342 AAGGAGTGGATGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATGATG 4401  
QY 4506 AAGGAGTGGATGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATGATG 4565  
DB 4402 AAGGAGTGGATGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATGATG 4461  
QY 4566 CTGTCCTTTTTCGAGTGGAGCCTTCAAGAGTGGATGATGATGATGATGATGATG 4625  
DB 4462 CTGTCCTTTTTCGAGTGGAGCCTTCAAGAGTGGATGATGATGATGATGATGATG 4521  
QY 4626 GATTCAGAGAGTGGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATG 4685  
DB 4522 GATTCAGAGAGTGGAGACCAAGTGGATGATGATGATGATGATGATGATGATGATG 4581  
QY 4686 TTTGATTTCTTCAATATTTGATGATGATGATGATGATGATGATGATGATGATGATG 4745  
DB 4582 TTTGATTTCTTCAATATTTGATGATGATGATGATGATGATGATGATGATGATGATG 4641  
QY 4746 AATTAATTTTATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4805  
DB 4642 AATTAATTTTATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4701  
QY 4806 GAAAGATGAG 4865  
DB 4702 GAAAGATGAG 4761  
QY 4866 GCAATTTCCAGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4925  
DB 4762 GCAATTTCCAGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4821  
QY 4926 AATTTGAT 4985  
DB 4822 AATTTGAT 4881  
QY 4986 CGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5045  
DB 4882 CGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4941  
QY 5046 GTTATTTTCAAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5105



QY	24	ATGACAGAAAGTTCCGACTCGATATCTGAGAGAAAGACGATTTGTTCCGTCCTTAC	83
Db	1	ATGACAGAAAGTTCCGACTCGATATCTGAGAGAAAGACGATTTGTTCCGTCCTTAC	60
QY	84	CGCAGATCATTTGGTGGCAATGGAACAACGATTTCCCTGAACATGAAAGCAGAGAG	143
Db	61	CGCAGATCATTTGGTGGCAATGGAACAACGATTTCCCTGAACATGAAAGCAGAGAG	117
QY	144	CTGGAAAGAAAGAGCCGAGGAGAGGTGCGCGATATGGTGCAGAGAAACAAAAA	203
Db	118	CTGGAAAGAAAGAGCCGAGGAGAGGTGCGCGATATGGTGCAGAGAAACAAAAA	148
QY	204	GAATTCGATATGATGACGAGAGAGAGATGAAAGTCCACAACCGATTCCTACCTTGA	263
Db	149	-AGATACGATATGATGACGAGAGAGAGATGAAAGTCCACAACCGATTCCTACCTTGA	207
QY	264	CAGGATGGCAATATCCGTTGATTTGAGGAGGACGTTCCCGCGGAAATTTGGCTCCACT	323
Db	208	CAGGATGGCTATATCCGTTGATTTGATGAGGAGGACGTTCCCGCGGAAATTTGGCTCCACT	267
QY	324	CCTCTCGAGATATCGATCCCTACTACAGCAATGTACTGACATTTGATTTGTAAGCAA	383
Db	268	CCTCTCGAGATATCGATCCCTACTACAGCAATGTACTGACATTTGATTTGTAAGCAA	327
QY	384	GGAAGAAGATATTTTTCGTTTCTGTCATCAAAACGATATGAGAGTCCGATCCATCAAT	443
Db	328	GGAAGAAGATATTTTTCGTTTCTGTCATCAAAACGATATGAGAGTCCGATCCATCAAT	387
QY	444	CGATATCGCTGCTGAGCCATTTACATTTGATGATCCATTAATTTTCCATTCATCATC	503
Db	388	CGATATCGCTGCTGAGCCATTTATATTTTATGATCCATCCCTGTTTGGTATTCATATC	447
QY	504	ACCACAATTCCTGTCACACTGACCTCTGATGATTAATGCGACACAGCCACGGTTGAGTCC	563
Db	448	ACCACTATTTCTAACTAATTTGATTTATTAATGATTAATGCGACACAGCCACGGTGAATCC	507
QY	564	ACTGAGGTGATATTCACCGGAAATCTACACATTTGAATAGCGTTAAAGATGAGGACGA	623
Db	508	ACAGAGGTGATATTCACCGGAAATCTACACATTTGAATAGCGTTAAAGATGAGGACGA	567
QY	624	GGTTTCATTTTATGCGCGTTTACGATCTTATAGAGATGATGAAATTTGGCTGACCTTGTA	683
Db	568	GGTTTCATTTTATGCGCGTTTACGATCTTATAGAGATGATGAAATTTGGCTGACCTTGTA	627
QY	684	GTAATAGCTTTAGCTTATGTGACCATGCGGTATGATTTTGGTAAATCTAGCAGCCCTGCGA	743
Db	628	GTAATAGCTTTAGCTTATGTGACCATGCGGTATGATTTTGGTAAATCTAGCAGCTTGAGA	687
QY	744	ACGTTTATGGGTGCTCGGACCGTTTAAACCGTAGCATTTGGTCCAGGCTTAAAGCATC	803
Db	688	ACATTTATGGGTGCTCGGACCGTTTAAACCGTAGCATTTGGTCCAGGCTTAAAGCATC	747
QY	804	GTGCGGCGCGTATCGAATCGGTGGAAGATCTGCGCGATGTGATTAATCTGACCATGTTC	863
Db	748	GTGCGGTGCTATGATGAATCTGTAAAAATCTACCGCATGTGATTAATTTTGAATGTTT	807
QY	864	TCCCTGTGCGTGTGCGCGTTGATGAGGCTTACAGATCTTATATGCGGTGCTCACCGAGAG	923
Db	808	TCCCTGTGCGTGTGCGCGCTAGTATGAGGCTTACAAATCTATATGCGGTGCTTAAACAAAG	867
QY	924	TGCATCAAGAAAGTTCCCGTGGACGGTTCCTGCGGCAATCTGACCGAGAACTGGAC	983
Db	868	TGCATTTAAACGAATCCCCCTGACCGCAGTTGGGGCAATCTGACCGAGAAACCTGGTTT	927
QY	984	TATTCAGATCGAATATGCGAATTTGATTTGATTCGAGAGAGAGGGGATCTCATTTCCGTTA	1043
Db	928	CTACACATATGACAAGTTCCATTTGGTTTACGAGAAACGATGGCGAATCATATCCGATG	987
QY	1044	TGCGGCAATATATCCGATGCGGAGGCAATGCGACGATTAAGTGTGCTGACAGGGGTTT	1103
Db	988	TGCGGAAATGATATCCGATGCGGAGCAATGCGCGAAGATTAAGTGTGCTGACAGGGGCTTC	1047
QY	1104	GGTCCGAAATCGAATTAATGCTACACAGCTTCGATTTGCTTCCGATGGGCTTTTCTGTGCC	1163

Db	1048	GGCCCAATCCCACTACACTACACCAAGTTTCAGCTCATTCGGTTGGGCTTTCCTGTGC	1107
Oy	1164	GCCTTCGGGTGATGACACAGACCTTCGGAGATCTGACAGCGGTGGCGGCGC	1223
Db	1108	GCGTTTGCTCATGACCCAAAGATTTCTGGAGAGATCTGATCAGCACGTGTGCAAGCA	1167
Oy	1224	GCCGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCTAGGTTCAATCTT	1283
Db	1168	GCTGACCCCTGGACATGTTGTTCTTTATAGTCATCATCTTCTAGGTTCAATCTT	1227
Oy	1284	GTGAATTTGATTTTGGCCATTTGTCGCATGTCTGATACCAATTTGCAAAAGAGCCGAA	1343
Db	1228	GTGAATTTGATTTTGGCCATTTGTCGCATGTCTTATGACCAATTTGCAAAAGAGCCGAA	1287
Oy	1344	GAAGAAGGGCTGCGAAGAGAGAGCCGATCGTGAACGGAGAAGCTGCGCGCCAAA	1403
Db	1288	GAAGAAGGGCTGCGAAGAGAGAGCCGATCCGAGAGCTGAAGAAGCGGACGACCAAG	1347
Oy	1404	GCGGCCAAGCTGAGAGAGCGGGCCCATGTCGACGAGCTCAGACAGACGGATGCGGCTGCC	1463
Db	1348	GCGGCCAAGCTGAGAGAGCGGGCCCATGTGACAGCTCMAACGGCTCAGAGTGCACGAT	1407
Oy	1464	GCCGAAGAAGCTGACATGCAATCCGGAATGAGCCAAAGAGTCCGAGTATTCGTGATGAGC	1523
Db	1408	GCCCTCGCGAGCTGTGCATCCGAAATGGCAAAAGTCCACAGTACTCTTGATTAAGC	1467
Oy	1524	TATAGCTATTTTGTGGCGGCGAGAGAGGACGATGACAAACAAGAGAGATGTCC	1583
Db	1468	TATGAATGTTTGTGGCGGCGAGAGAGGACGATGACAAACAAGAGAGATGTGC	1527
Oy	1584	ATTGCGAGCTGTGAGGTGAGTCCGATCCGTGAGCGCTTATACAAACAACCGACACT	1643
Db	1528	ATTAGCGAGCTGTGAGGTGAGTCCGTGAGCGCTTATACAAACAACCGACACT	1587
Oy	1644	ACCACAGACACCAAGCTACCAAAAGTTCTGTAAGTGCACGACATCCTTATCCTTA	1703
Db	1588	ACCACAGACACCAAGCTACCAAAAGTTCTGTAAGTGCACGACATCCTTATCCTTA	1644
Oy	1704	GATTACCCGTTTAACATACGAGGGGATCACGTAGTTCTCACAGTACAGATCCGAGAC	1763
Db	1645	GATTACCCGTTTAACATACGAGGGGATCACGTAGTTCTCACAGTACAGATCCGAGAT	1704
Oy	1764	GAGGTGGCGCTTTGGTATACCGGATAGCATGTGAGCCATTTGATTTGTCAACATAT	1823
Db	1705	GAGGTGGCGCTTTGGTATACCGGATAGCATGTGAGCCATTTGATTTGTCAACATAT	1764
Oy	1824	CAGATGCCAGACGACCTTGCCCTATGCGACGACTCGAATGCCGTGACCCCGATGTC	1883
Db	1765	CAGATGCCAGACGACCTTTGCCCTATGCGATGACTCGAATGCCGTGACCCCGATGTC	1824
Oy	1884	GAAGAATGGGGCCATCATATGTGCCCGGTATCATAGGCAATCMAAGTCCCGACACTCA	1943
Db	1825	GAAGAATGGGGCCATCATATGTGTCACAGCCATCATATGTGAATTTAGTTCTGACACTCT	1884
Oy	1944	TGCTATACCTGCAATGCTCCGAATATCGTATACCTTCACATGGCGATCTTACTCGCGGC	2003
Db	1885	TGCTATACCTGCAATGCTCCGAATATCGTATACCTTCACATGGGATTTATGGGTGC	1944
Oy	2004	ATGCGCTCATGGGCGCTGACGACATGACCAAGAGACCAATTGGCGTACCCGACACCA	2063
Db	1945	ATGCGCGCATATGGGCGCGACGACATGACCAAGAGACCAATTGGCGTACCCGACACCA	2004
Oy	2064	CGCAATCAATCAGTGGGCGCACCAATGGCGGACCACTGTCTGGAACACCAATACCAAG	2123
Db	2005	CGCAATCAATCAGTGGTGTGTCGACCAATGGTGCAGTATTAAGCGCGGTGGTGCAT	206
Oy	2124	CTCGAT-----CATGCGACTACGAATTTGGCTTGGATGACGAGCA	2168
Db	2065	CCCGATGCCAATCAACAAGAAACAAGGATTTATGAATGGGTGAGGATTAATACAGCAAA	2124
Oy	2169	GCTGCAAGATTTAAATCATGACAAATCCTTTATCGAGCCGTCGAGCAAAAGGTG	2228

Db 2125 GCTGGCAAAATATTAACACGACGACATCTTTTATTCGAGCCGCTCCAAACTCAACAGATG 2184  
Qy 2229 GTTATATGAAAGATGATGATGCTCTGATATCATTCGAAACAGGCGCGCTGCTGGAC 2288  
Db 2185 GTAAACATGAAAGATGATGATGCTCTTAAATGATATCATTTGAAACAGGCGCTGGACAT 2244  
Qy 2289 AGTGGGCGACGATGCGGCTGCTCGTTACTATTTCCAAACAGAGAGATGACAG 2348  
Db 2245 AGTGTGCTAGTGAACGAGT-----GAGACGATGACGAA 2280  
Qy 2349 GATGGGCGGACGTTCAAGAAGACCTCGAAGTATCTCAAGGCGATGATGTTT 2408  
Db 2281 GATGGTCCCATTCGAGGACATGCGCTCGAATATCTTAAAGGATGGAATCTTT 2340  
Qy 2409 TGTGTGGGACGTTGCTGGGTTTGGTGAATTTCCAGAGTGGGATTCGCTCATGTC 2468  
Db 2341 TGTGTATGGGACGTTGTTGGGTTGGTAAATTTCCAGAAATGGGCTCTCTTTATGTCG 2400  
Qy 2469 TTGATCCCTCGTGGAGCTCTTGAATCAAGCTGTCATGTTGTCGAAACAGATGTTGATG 2528  
Db 2401 TTGATCCATTCGTGGAGCTCTTCAATTAACCTGTATGTTGTCATTAATGATGTTGATG 2460  
Qy 2529 GCAATGATCAACGATATGAACAGAGATGAAACGCTGCTCAAGAGTGGCACTAT 2588  
Db 2461 GCAATGATCAATCAAGATATGAAATCCGGAATTTGAGAGAGTGTGAAAGTGTATCTAT 2520  
Qy 2589 TTCTTCAACGCGACCTTTGCAATGAGGCAACATGAAGTATGAGCCATGAGCCCAAG 2648  
Db 2521 TTCTTCAACGCGACCTTTGCAATGAGGCAACATGAAGTATGAGCCATGAGCCCAAG 2580  
Qy 2649 TACTATTTCCAGAGAGGCTGGAACATCTTGCATCTTATCGTGGCCCTATCGTATATG 2708  
Db 2581 TACTATTTCCAGAGAGGCTGGAACATCTTGCATCTTATCGTGGCCCTATCGTATATG 2640  
Qy 2709 GAATGGGACCTGAGAGGCTGTCAGAGGCTGTCACGATATGCGTTCCCTTCAATGTCGATG 2768  
Db 2641 GAATGGGACCTGAGAGGCTGTCAGAGGCTGTCACGATATGCGATATGCGTTCCCTTCAATGTCGATG 2700  
Qy 2769 GTATTTCAACTGGCCCAAGTCTTTGGCCCACTTTAATTTACTCATTTGATTTGAGAGCGC 2828  
Db 2701 GTATTTCAACTGGCCCAAGTCTTTGGCCCACTTTAATTTACTCATTTGATTTGAGAGCGC 2760  
Qy 2829 AACATGGGCGCTTTGGGATATCTGACATTTGATCTTTGATATCATATCTTATCTTTGCG 2888  
Db 2761 AACATGGGCGCTTTGGGATATCTGACATTTGATCTTTGATATCATATCTTATCTTTGCG 2820  
Qy 2889 GTATGGGAATGCAACTGTTGCGAAAGATTAATCATGATCAAGAGCCGCTTCCGAT 2948  
Db 2821 GTATGGGAATGCAACTTTCGAAAGATTAATTAATGACCAAGAGATCGCTTCAAGAGC 2880  
Qy 2949 GGGCACTGCGCGCTGGAACCTTCAACGACTTTATGACAGCTTCATGATCGTGTCCGG 3008  
Db 2881 CATGAATTAACGCGCTGGAATTTTCAACGACTTTATGACAGCTTCATGATGTGTCCGA 2940  
Qy 3009 GTGCTTCGCGAAGATGATGATGATCTGATGTCATGTCGATGTCATGTCGAGATGTCG 3068  
Db 2941 GTGCTTCGCGAAGATGATGATGATCTGATGTCATGTCGATGTCATGTCGAGATGTCG 3000  
Qy 3069 TGCAATCCCTCTTCTTTGGCAGCGTGTGATCGGCAATCTTTGATGTTAATCTTTTC 3128  
Db 3001 TGTAATCCCTCTTCTTTGGCAGCGTGTGATCGGCAATCTTTGATGTTAATCTTTTC 3060  
Qy 3129 TTAGCTTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGGCCGACGCGACAT 3188  
Db 3061 TTAGCTTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGGCCGACGCGACAT 3120  
Qy 3189 GATACGATTAATTAATGCGGAGGCTTCAATGATGTCGATTTAAAGTTGGGTTAG 3248  
Db 3121 GATACGATTAATTAATGCGGAGGCTTCAATGATGTCGATTTTAAAGTTGGGTTAG 3180  
Qy 3249 GGTATATATGCTGATGTTTCAAGTTAATAGTAAACAATTTGACAAATCAATTAAGTAT 3308  
Db 3181 GGTATATATGCTGATGTTTCAAGTTAATAGTAAACAATTTGACAAATCAATTAAGTAT 3240

Qy 3309 CAACCATCAGGTGAGAGGACCAACCAAGTATGATTTTGGAGGAGACATGTTGAC 3368  
Db 3241 CAACCATC-----AGAACATGCGAT 3261  
Qy 3369 AACGATCTGAGCTGGGCAACGAGATCTCTGCGACGCGCTCATCAAGAGGGATC 3428  
Db 3262 AATGACTGAGGTTGGGTCAATGACGAATATCATGAGCGATGCTTGATCAAAAAGGATG 3321  
Qy 3429 AAGAGCAAGACGCACTGAGAGTGGCATCGGGATGATGATGATTTCAAGATCAAGGC 3488  
Db 3322 AAGGCGAGACCCGAGCTGAGAGTGGCCATTTGGCATGAGGATTTCAACATCAAGGC 3381  
Qy 3489 GACATGAAGAACCAACGAGGAGAAATCCAAATATCTAAATTAAGCAAGATGATGGC 3548  
Db 3382 GATATGAAAAACAACGAGCCCAAGAAATCAAAATTTCAATTAACAACAACGATATGGA 3441  
Qy 3549 AACTCAATTAACCAACCAAGATGAGCTGGAACAGAGCTAAACATAGAGTTGTCC 3608  
Db 3442 AACTCAATTAACCAACCAAGATGAGCTGGAACAGAGCTAAACATAGAGTTGTCC 3501  
Qy 3609 TTACAGAGCAGACACTGCGACATTTACTCATATGATGATGATGATGATGATGATG 3668  
Db 3502 ATACAGAGCAGATGACACTGCGACATTTACTCATATGATGATGATGATGATGATGATG 3561  
Qy 3669 AAGGACGAGAGCCACAGAGGAGCGCGGACGATGAGAGGCGAGAGGAGAGGAGCGCC 3728  
Db 3562 AAGGACGAGAGCCACAGAGGAGCGCGGACGATGAGAGGCGAGAGGAGAGGAGCGCGC 3621  
Qy 3729 AGCAAGGAGATTAAGTCTTCAAGAGAACTGGAACGAGAGGCGGAAATGCGAGAGGCG 3788  
Db 3622 AGCAAGGAGATTAAGTCTTCAAGAGAACTGGAACGAGAGGCGGAAATGCGAGAGGCG 3681  
Qy 3789 CCGCTGACGCTGATATCATTTATGATG-----ACAGAGAGATATATCTGATGATAT 3845  
Db 3682 CAGCTGAGTGGTATCATATCATATGATGATGATGATGATGATGATGATGATGATGATG 3741  
Qy 3846 CCACTGATGCTGCGCGCGATGCTGATATTAAGAAATTTCCGATCTTACCGGATGATG 3905  
Db 3742 CCGGCGACGCTTTCCCGATGCTGATCAAGAAATTTCCGATCTTACCGGATGATGATG 3801  
Qy 3906 GACTGCGCTTCTGGCAAGATGAGGCAATTTAGCATGAAACCTTTCAATTAATGAA 3965  
Db 3802 GACTGCGCTTCTGGCAAGATGAGGCAATTTAGCATGAAACCTTTCAATTAATGAA 3861  
Qy 3966 AATTAATATTTTGAACAGCTGTTATCATATGATTTTATGATGATGATGATGATGATG 4025  
Db 3862 AATTAATATTTTGAACAGCTGTTATCATATGATTTTATGATGATGATGATGATGATG 3921  
Qy 4026 TTGAAGATGATCATCTGCAACAAAGCCATATCTGAGATATTTTATATATATGATGAC 4085  
Db 3922 TTGAAGATGATCATCTTACCCGATGACCTGTCTATGAGATATATATATATATATGAC 3981  
Qy 4086 AGATATTTTACGTTATATCTTCTGGAATGTTTATCAAGTGTGGCGCTGCGCTTC 4145  
Db 3982 AGATATTTTACGTTATATCTTCTGGAATGTTTATCAAGTGTGGCGCTGCGCTTC 4041  
Qy 4146 AAAGTACTTCAACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4205  
Db 4042 AAAGTACTTCAACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4101  
Qy 4206 ATCAACTTCTGCTTCACTTTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4265  
Db 4102 ATCAACTTCTGCTTCACTTTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4161  
Qy 4266 ACGTTAAGAGCAGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 4325  
Db 4162 ACGTTAAGAGCAGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 4221  
Qy 4326 GTTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4385  
Db 4222 GTTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4281

4386 TTTGGCTAATTTGGCATATGGGTGATGAGCTTTTGGTCGAGAAATATTAAGTGC 4445  
4282 TTTTGGCTAATTTTGGCATTAAGGAGTACAGCTTTTGGTGGAAATTTTAAGTGT 4441  
4446 GAGACATGAAATGGCAAGAGCTCAAGCAGAGATCATCAATATGCGAATGCTGAG 4505  
4342 AAGATGGGTAAATGACACTGTGTGAGCATGAATCATACGAATGTAATGCTGCAAA 4401  
4506 AGGAGAACTACACGTGGGTGAATTCAGCAATGAATTTGCAATCATAGTAAATGCGTAT 4565  
4402 AGTGAATACTACACCTGGGAAATTCGGCAATGAATCTGATCATGATGATATGCGTAT 4461  
4566 CTGTGCTTTTCAAGTGGCCACTTCAAGGCTGATATCAATATCATGAAAGATGCTATC 4625  
4462 CTGTGCTAATTTCAAGTGGCCACTTAAAGGCTGATCCAGTATTAAGCAATGCTATC 4521  
4626 GATTCACAGAGGTGACAAAGCAATTCGTAAACGAACATCTACATGATTTAATAT 4685  
4522 GATTCACAGAGGTGACAAAGCAGCTGAGAAACCAATATCTACATGATTTAATAT 4581  
4686 TTTGATTTCTTCAATATTTGATGCTTTTTCACACTCAATCTGTTCAATGCTGTTATC 4745  
4582 TTTGATTTCTTCAATATTTGATGCTTTTTCACACTCAATCTGTTCAATGCTGTTATC 4641  
4746 ATTGATTAATTTATGAGCAAAAGAAAAAGAGAGTGAATCATTAAGAAATGCTCATGCA 4805  
4642 ATTGATTAATTTATGAACAAAGAAAGAAAGAGAGTGAATCATTAAGAAATGCTCATGCA 4701  
4806 GAAGATCAGAAAAAGTACTTAATGCTATGAAAAAGATGGGCTCTAAAAAACATTAAAA 4865  
4702 GAAGATCAGAAAAAGTACTTAATGCTATGAAAAAGATGGGCTCTAAAAAACATTAAAA 4761  
4866 GCAATTCAGAACAGAGGTGGGACCAAGCAAGCAATGCTTTGAATATGAACCGTAAG 4925  
4762 GCAATTCAGAACAGAGGTGGGACCAAGCAAGCAATGCTTTGAATATGAACCGTAAG 4821  
4926 AATATGATTAATATCATTAATGATTAATCATTTGCTGACATGCTGCAATGCTGAT 4985  
4822 AATATGATTAATATCATTAATGATTAATCATTTGCTGACATGCTGCAATGCTGAT 4881  
4986 CGTTACGATGCGTGGACACGATTAACGCGGTCTTGAATCTATCAATGCGATATTCGTA 5045  
4882 CGGTACGATGCGTGGACACGATTAACGCGGTCTTGAATCTATCAATGCGATATTCGTA 4941  
5046 GTTATTTTTCAGTCCGAAATGCTTAATTAATTAATGCTTGAATCATCTATTTATTT 5105  
4942 GTTATTTTTCAGTCCGAAATGCTTAATTAATTAATGCTTGAATCATCTATTTATTT 5001  
5106 GAGCAGATGAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
5002 GAGCAGATGAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
5166 AGGAGATTAATGAGAAATCTTCTGTGTGCGGACCTGCTCGAGTGGTGGTGGG 5225  
5062 AGGAGATTAATGAGAAATCTTCTGTGTGCGGACCTGCTCGAGTGGTGGTGGG 5121  
5226 AAGTGGGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5285  
5122 AAGTGGGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5181  
5286 GCGTGGGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5345  
5182 GCGTGGGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5241  
5346 TTTGATCTTTGCGATTTTGGGATGCTTTTCAATGACGTAAGAGAAAGAGCGGAT 5405  
5242 TTTGATCTTTGCGATTTTGGGATGCTTTTCAATGACGTAAGAGAAAGAGCGGAT 5301  
5406 AAGAGATTAATGAGAAATCTTCTGTGTGCGGACCTGCTCGAGTGGTGGTGGG 5465  
5302 AAGAGATTAATGAGAAATCTTCTGTGTGCGGACCTGCTCGAGTGGTGGTGGG 5361  
5466 AAGAGATTAATGAGAAATCTTCTGTGTGCGGACCTGCTCGAGTGGTGGTGGG 5525

5362 ACCTGAGCGGCTTGGATGCTGTGTAGATGCTATTAATGAAGAGAAATGCTGATCA 5421  
5526 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5585  
5422 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5481  
5586 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5645  
5482 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5541  
5646 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5705  
5542 CCGGACGAGCAAGAGCTATCCGGGCAATTTGGTTCAGCCAGCTTGAATTAAGCTTT 5601  
5706 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5765  
5602 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5661  
5766 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5825  
5662 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5721  
5826 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
5722 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
5886 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5945  
5782 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
5946 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
5842 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
6006 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6065  
5902 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5961  
6066 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6125  
5962 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5976  
6126 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6185  
5972 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6036  
6186 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
6032 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6096  
6246 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6305  
6092 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6156  
6306 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6365  
6152 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6216  
6366 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6425  
6212 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6276  
6426 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6485  
6272 GATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6335

RESULT 13  
US-09-428-371-2  
; Sequence 2, Application US/09428371  
; Patent No. 6800435  
; GENERAL INFORMATION:

APPLICANT: Soderlund, David M.  
APPLICANT: Knipple, Douglas C.  
APPLICANT: Ingles, Patricia J.  
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND  
FILE OF INVENTION: INSECTICIDE-RESISTANT HOUSE FLIES  
FILE REFERENCE: 19603/606  
CURRENT APPLICATION NUMBER: US/09/428,371  
CURRENT FILING DATE: 1999-10-28  
EARLIER APPLICATION NUMBER: 08/608,618  
EARLIER FILING DATE: 1996-03-01  
EARLIER APPLICATION NUMBER: 08/772,512  
EARLIER FILING DATE: 1996-12-24  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 2  
LENGTH: 6315  
TYPE: DNA  
ORGANISM: Musca domestica  
US-09-428-371-2

Query Match 68.1%; Score 4434.2; DB 4; Length 6315;  
Best Local Similarity 81.8%; Pred. No. 0;  
Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;

Qy 24 ATGACAGAAAGATTCGATCGATATCTGAGGAAAGCAAGTTGTCGTCCTTAC 83  
Db 1 ATGACAGAAAGATTCGATCGATATCTGAGGAAAGCAAGTTGTCGTCCTTAC 60  
Qy 84 CGCGATCATTTGTCGCAATCGAACAGCATTTGCCGCTGAACATGAAGAGAG 143  
Db 61 CGCGATCATTTGTCGCAATCGAACAGCATTTGCCGCTGAACATGAAGAGAG 117  
Qy 144 CTGGAAGAAAGAGAGCCGAGGAGAGGTCCCGATATGCTGCAAGAAAAA 203  
Db 118 CTGGAAGAAAGAGAGCCGAGGAGAGGC----- 148  
Qy 204 GAATTCGATATGATGAGAGAGAGATGAAAGTCCAAACCGGATCTCACTTGA 263  
Db 149 -AGATCATATGATGAGAGAGAGATGAAAGTCCAAACCGGATCTCACTTGA 207  
Qy 264 CAGGATGTCGAATCTGTTGATTTGAGGAGCACTTCCGCGGAAATTTGCTCACT 323  
Db 208 CAGGATGTCGAATCTGTTGATTTGAGGAGCACTTCCGCGGAAATTTGCTCACT 267  
Qy 324 CTTCTGAGATATGATCGATCTCTAAGCAATGATGATGATGATGATGATG 383  
Db 268 CTTCTGAGATATGATCGATCTCTAAGCAATGATGATGATGATGATGATG 327  
Qy 384 GGAAGAAATATTTTGGCTTTTTCGATCAAAAGAAATGATGATGATGATGAT 443  
Db 328 GGAAGAAATATTTTGGCTTTTTCGATCAAAAGAAATGATGATGATGATGAT 387  
Qy 444 CCGATAGCTGTCGTCGCAATTTCACTTCTAGTGCATCTTATTTTCCCTATTCAT 503  
Db 388 CCGATAGCTGTCGTCGCAATTTCACTTCTAGTGCATCTTATTTTCCCTATTCAT 447  
Qy 504 ACCCAATTTCTGTCACATGATCTGTATGATATGCGCAACGCGCAAGTGAAGTCC 563  
Db 448 ACCCAATTTCTGTCACATGATCTGTATGATATGCGCAACGCGCAAGTGAAGTCC 507  
Qy 564 ACTGAGGATATTTCAACCGGAAATCTACATTTTGAATAGCTGTTAAAGTATGCGACGA 623  
Db 508 ACTGAGGATATTTCAACCGGAAATCTACATTTTGAATAGCTGTTAAAGTATGCGACGA 567  
Qy 624 GGTTCATTTTATGCGCTTACGATCTTGAAGATGATGATGATGATGATGATG 683  
Db 568 GGTTCATTTTATGCGCTTACGATCTTGAAGATGATGATGATGATGATGATG 627  
Qy 684 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
Db 628 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
Qy 744 ACGTTAGGATGTCGAGCGCTTAAACCGTATGATGATGATGATGATGATG 803

Db 688 ACATTTAGGATCTGCGAGCTCTGAACCGTATGATGATGATGATGATGATG 747  
Qy 804 GTGCGCGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 863  
Db 748 GTGCGCGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
Qy 864 TCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 923  
Db 808 TCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 867  
Qy 924 TGCAATCAAGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 983  
Db 868 TGCAATCAAGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 927  
Qy 984 TATCAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1043  
Db 928 TATCAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 987  
Qy 1044 TCGGCAATATATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1103  
Db 988 TCGGCAATATATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1047  
Qy 1104 GATCCGAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1163  
Db 1048 GATCCGAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1107  
Qy 1164 GCTTCGCGCTGATGACACAGACCTTGGAGAGATCTGACAGCTGATGTCGCGCC 1223  
Db 1108 GCTTCGCGCTGATGACACAGACCTTGGAGAGATCTGACAGCTGATGTCGCGCC 1167  
Qy 1224 GCGGACCATGTCACATGCTGTTCTTATGATCATCTTCTGATGATGATGATG 1283  
Db 1168 GCTGACCTCGGACACATGCTGTTCTTATGATCATCTTCTGATGATGATGATG 1227  
Qy 1284 GTGAATTTATTTTGGCATTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1343  
Db 1228 GTGAATTTATTTTGGCATTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1287  
Qy 1344 GAAAGAGAGCTGTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403  
Db 1288 GAAAGAGAGCTGTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347  
Qy 1404 GCGGCAAGCTGAG 1463  
Db 1348 GCGGCAAGCTGAG 1407  
Qy 1464 GCGGCAAGCTGAG 1523  
Db 1408 GCGGCAAGCTGAG 1467  
Qy 1524 TATGATGATTTTGTGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583  
Db 1468 TATGATGATTTTGTGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527  
Qy 1584 ATTGAGAGCTGAG 1643  
Db 1528 ATTGAGAGCTGAG 1587  
Qy 1644 ACCACAGACACCAAGCTACCAAGTTCTGTAATGAGAGAGAGAGAGAGAGAGAG 1703  
Db 1588 ACCACAGACACCC--GCTACTAAAGTCCGTAAATGAGAGAGAGAGAGAGAGAG 1644  
Qy 1704 GGTTCACCGTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763  
Db 1645 GGTTCACCGTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1704  
Qy 1764 GAGAGTGGCGCTTGTGATACCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823  
Db 1705 GAGAGTGGCGCTTGTGATACCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1764  
Qy 1824 CAGGATGCCAG 1883

Db 1765 CAGGATGCCAGACGATTTGCCCTATGCGGATGACTCGAATGCCGTAACCAATGTCC 1824  
QY 1884 GAAAGAAATGGGCGCATCATATAGTCCGCTGACTATGCGAATCTAGGCTCCGACACTCA 1943  
Db 1825 GAAGAAATGGTCCATTATAGTACGACCTACTATGTAATTTAGGTTTACAGCAATTC 1884  
QY 1944 TCGTATACCTCGGATGATCCCGAATAATGCTATACCTGACATGCGGATCTACTCGGCGC 2003  
Db 1885 TCAATATACCTCGGATGATCAATGAATCTGCTATACCTGACATGCGGATCTACTCGGCGC 1944  
QY 2004 ATGGCGGTCATGGGCGCTGACAGATGACCAAGAGAGCAAAATTTGGCGAACCGCAACA 2063  
Db 1945 ATGGCGGTCATGGGCGCTGACAGATGACCAAGAGAGCAAAATTTGGCGAACCGCAACA 2004  
QY 2064 CGCAATCATATGATGGGCGGCGACCAATGGCGGACCACTGTCTGACACCAATCACAG 2123  
Db 2005 CGCAATCATATGATGGGCGGCGACCAATGGCGGACCACTGTCTGACACCAATCACAG 2064  
QY 2124 CTGCAAT-----CATCGGCACTACGAAATTTGGCGGAGTGCAGGAGGAA 2168  
Db 2065 CCGGATGCCATGACAGGAAACAAAGGATTTAGAAATGGGTGAGATTTATAGAGAGAA 2124  
QY 2169 GCTGGCAAGATTAAGATCATGACAAATCTTTTATGAGGCGGTCCAGACAAACGGTG 2228  
Db 2125 GCTGGCAAGATTAAGATCATGACAAATCTTTTATGAGGCGGTCCAGACAAACGGTG 2184  
QY 2229 GTTGAATATGAAGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 2288  
Db 2185 GTTGAATATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2244  
QY 2289 AGTCGGGCAAGCATGCGGCTGTCTCGTTTACTATTTCCAAAGAGAGATGACGAG 2248  
Db 2245 AGTCGGGCAAGCATGCGGCTGTCTCGTTTACTATTTCCAAAGAGAGATGACGAG 2280  
QY 2349 GATGGCGCAAGCTTCAAG 2408  
Db 2281 GATGGCGCAAGCTTCAAG 2340  
QY 2409 TGTGTGTGGGATCTGT 2468  
Db 2341 TGTGTGTGGGATCTGT 2400  
QY 2469 TTGATGCCCTTGTGTCGAGCTCTTATCATGACGCTGTGATGTCGTCGTCGTCGTCGTC 2528  
Db 2401 TTGATGCCCTTGTGTCGAGCTCTTATCATGACGCTGTGATGTCGTCGTCGTCGTCGTC 2460  
QY 2529 GCAATGATCACAAGATGATGAAACAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAT 2588  
Db 2461 GCAATGATCACAAGATGATGAAACAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAT 2520  
QY 2589 TTGTCACCGGCACTTTGTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2648  
Db 2521 TTGTCACCGGCACTTTGTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
QY 2649 TACTATTTCCAGAGAGGCTGGAACATCTTGCATCTTATGTCGTCGTCGTCGTCGTC 2708  
Db 2581 TACTATTTCCAGAGAGGCTGGAACATCTTGCATCTTATGTCGTCGTCGTCGTCGTC 2640  
QY 2709 GAACTGGAGCTGAGGGGTGTCAGGGGTCTGTCCGATGTCGTCGTCGTCGTCGTCGTC 2768  
Db 2641 GAACTGGAGCTGAGGGGTGTCAGGGGTCTGTCCGATGTCGTCGTCGTCGTCGTCGTC 2700  
QY 2769 GATTTCAAACTGGGCAAGCTTGGGCGCACCTTAATTTACTCATTTGATGATGAGAGCG 2828  
Db 2701 GATTTCAAACTGGGCAAGCTTGGGCGCACCTTAATTTACTCATTTGATGATGAGAGCG 2760  
QY 2829 ACCATGGGCGCTTGGGTAATCTGACATTTGATCTTTCATTTATCTTTCATCTTTCG 2888  
Db 2761 ACCATGGGCGCTTGGGTAATCTGACATTTGATCTTTCATTTATCTTTCATCTTTCG 2820  
QY 2889 GTGATGGAGATGACATCTTTCGAGAGAGATTTATGATGATGATGATGATGATGATGAT 2948  
Db 2821 GTGATGGAGATGACATCTTTCGAGAGAGATTTATGATGATGATGATGATGATGATGAT 2880

QY 2949 GCGGACTTCGCGGCTGGAACCTTACCGACTTTATGACAGCTTCACTGATGCTGTTCGG 3008  
Db 2881 CATGAATTCGCGGCTGGAACCTTACCGACTTTATGACAGCTTCACTGATGCTGTTCGA 2940  
QY 3009 GTGCTTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3068  
Db 2941 GTGCTTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
QY 3069 TGCATTCCTTCTTCTTGGCGACGTTGTCATGCGCAATCTTGTGATTTAACTTTTC 3128  
Db 3001 TGCATTCCTTCTTCTTGGCGACGTTGTCATGCGCAATCTTGTGATTTAACTTTTC 3060  
QY 3129 TTAGCTTCCTTCTTCTTGGCGACGTTGTCATGCGCAATCTTGTGATTTAACTTTTC 3188  
Db 3061 TTAGCTTCCTTCTTCTTGGCGACGTTGTCATGCGCAATCTTGTGATTTAACTTTTC 3120  
QY 3189 GATACGATTAATATGACGAGGCTTCAATGCAATTTGGCGATTTAAAGTTGGTTAAG 3248  
Db 3121 GATACGATTAATATGACGAGGCTTCAATGCAATTTGGCGATTTAAAGTTGGTTAAG 3180  
QY 3249 CCGTATATTCCTGATTTGTTCAAGTTAATGCTTAATGCAATTAATTAATTAATTAAT 3308  
Db 3181 CCGTATATTCCTGATTTGTTCAAGTTAATGCTTAATGCAATTAATTAATTAATTAAT 3240  
QY 3309 CAACCATGAGGTGAGAGACCAACCATGATGATGATTTGGAGCGAAGAGATGCTGAC 3368  
Db 3241 CAACCATG-----AACAATGCGCAT 3261  
QY 3369 AACGATGAGCTGAGGCGACAGAGATCTGCGGACGCGCTCATCAAGAGAGGATC 3428  
Db 3261 AACGATGAGCTGAGGCGACAGAGATCTGCGGACGCGCTCATCAAGAGAGGATC 3321  
QY 3429 AAGAGCAAG 3488  
Db 3322 AAGAGCAAG 3381  
QY 3489 GACATGAAGACCAAGGCGAAGAAATCAATATCTAATTAAGCAAGATGATGTC 3548  
Db 3382 GACATGAAGACCAAGGCGAAGAAATCAATATCTAATTAAGCAAGATGATGTC 3441  
QY 3549 AACTCAATTAACCAAG 3608  
Db 3442 AACTCAATTAACCAAG 3501  
QY 3609 TTAAG 3668  
Db 3502 TTAAG 3561  
QY 3669 AAGAGCAAG 3728  
Db 3562 AAGAGCAAG 3621  
QY 3729 AGCAAGAGAGATTTAGTCTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAG 3788  
Db 3622 AGCAAGAGAGATTTAGTCTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAG 3681  
QY 3789 CCGCTGAGAGAGATTTAGTCTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAG 3845  
Db 3682 CCGCTGAGAGAGATTTAGTCTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAG 3741  
QY 3846 CCAGCTGATTTGCTGCGCGGATGCTATTAAGAAATTTCCGATCTTACCGGTCAGAT 3905  
Db 3742 CCAGCTGATTTGCTGCGCGGATGCTATTAAGAAATTTCCGATCTTACCGGTCAGAT 3801  
QY 3906 GACTGCGCGTTCGCGAGAGATGCGGCAATTTACGCTGAATACTTTCAATTAATTA 3965  
Db 3802 GACTGCGCGTTCGCGAGAGATGCGGCAATTTACGCTGAATACTTTCAATTAATTA 3861  
QY 3966 AATAATATTTTGAAG 4025  
Db 3862 AATAATATTTTGAAG 3921

4026 TTAGAGATGATACATCTGCGCAAAAGACCCAACTAGAGATATTTATACATATGAGAC 4085  
4086 AGAATATTTACGTTATATCTCTTTGGAAATGTATATCAAGTGGTGGCGCTCGCTTC 4145  
3982 AGAATATTTACGTTATATCTCTTTGGAAATGTATATCAAGTGGTGGCGCTTC 4041  
4146 AAATGTTATCTTACCAACGCGTGGTGGCTCGATTTGCGATTTGCGATGGTATCGCTT 4205  
4042 AAGGTCTACTTACCAATGCGTGGTGGCTCGATTTGCGATTTGCGATGGTATCGCTT 4101  
4206 ATCAACTCTGTTGCTTACCTTTGGAGCTGGTGGTATTTCAAGCTTTCAAGATATGGA 4265  
4102 ATTAATTTGGTGGCTTTGGTGGCTTTAAATGATATAGCCGTTTAAATCAATGCGC 4161  
4266 ACCTTAAAGAGACGATGAGACCACTACGTCGATCCGATGACAGGAGGATGCGTC 4325  
4162 ACACGTGGCGCGCTTAAGGCGATGGTGGCTGCTCTCTGATGAGGAGGATTAAGTGGT 4221  
4326 GTTATGCGCTGTTACAAAGCTATACCGTTCATCTTCAATGTTGTTGTTGTTAATA 4385  
4222 GTGATGCGCTGTTACAAAGCTATACCGTTCATCTTCAATGTTGTTGTTGTTAATA 4281  
4386 TTTTGGCTAATTTTGGCATATATGGGTGTACAGCTTTTGGTGGAAATATTTAAAGTC 4445  
4282 TTTTGGCTAATTTTGGCATATATGGGTGTACAGCTTTTGGTGGAAATATTTAAAGTC 4341  
4446 GAGGACATGATGAGACGAGACCACTACGTCGATCCGATGATATACCAATTCGATGCGAG 4505  
4342 AAAGATGTTATGACACTGTCGATGCGATGATATCAATGATGATGATGATGATGATG 4401  
4506 AGCGAGAACTACAGTGGGTGATTTACGATGATGATGATGATGATGATGATGATGAT 4565  
4402 AGTAAATCTACAGTGGGTGATTTACGATGATGATGATGATGATGATGATGATGAT 4461  
4566 CTGAGCTTTTCAAGTGGGTGATTTACGATGATGATGATGATGATGATGATGATGAT 4625  
4462 CTGAGCTTTTCAAGTGGGTGATTTACGATGATGATGATGATGATGATGATGATGAT 4521  
4626 GATTCAGAGAGTGGACCAAGCAATCTGTTGATGATGATGATGATGATGATGATGAT 4685  
4522 GATTCAGAGAGTGGACCAAGCAATCTGTTGATGATGATGATGATGATGATGATGAT 4581  
4686 TTGCTATTTCTCATATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4745  
4582 TTGCTATTTCTCATATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4641  
4746 ATTTGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4805  
4642 ATTTGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4701  
4806 GAAATGAG 4865  
4702 GAAATGAG 4761  
4866 GCGATTCAG 4925  
4762 GCGATTCAG 4821  
4926 AAATGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4985  
4822 AAATGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4881  
4986 GCGATTCAG 5045  
4882 GCGATTCAG 4941  
5046 GTTATTTTCTCATATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5105  
4942 GTTATTTTCTCATATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5001  
5106 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165

5002 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
5166 AGCGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5225  
5062 AGCGATATTTTATGAGCAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5121  
5226 AAATGAG 5285  
5122 AAATGAG 5181  
5286 GCGTGGAG 5345  
5182 GCGTGGAG 5241  
5346 TTATCTTTTGGCATATATGGGTGTACAGCTTTTGGTGGAAATATTTAAAGTC 5405  
5242 TTATCTTTTGGCATATATGGGTGTACAGCTTTTGGTGGAAATATTTAAAGTC 5301  
5406 AACGATCTTACAACTTACAAAGCTTTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 5465  
5302 AATGCTGTATATTTTAAAGCAATTTGGCCAAAGATGATGATGATGATGATGATGAT 5361  
5466 ACCTGAGCGGTGGAG 5525  
5362 ACCTGAGCGGTGGAG 5421  
5526 CCCGACAGCGCAAAAGGCTATCCGCGCAATTTGGTTCAGCGACGTTGAAATACGTTT 5585  
5422 CCCGACAGCGCAAAAGGCTATCCGCGCAATTTGGTTCAGCGACGTTGAAATACGTTT 5481  
5586 CTCTCTCATATCTTATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5645  
5482 CTCTCTCATATCTTATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5541  
5646 CTGAGAACTATATGATGAG 5705  
5542 CTGAGAACTATATGATGAG 5601  
5706 GACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5765  
5602 GATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5661  
5766 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5825  
5662 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5721  
5826 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
5722 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
5886 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5945  
5782 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
5946 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
5842 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
6006 TCAAGCTGTTGGCTGAG 6065  
5902 TCAAGCTGTTGGCTGAG 5961  
6066 AAGCACAAGGCGCGCGAG 6125  
5962 CGTTACAAAGATGCG----- 5976  
6126 GCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6185  
5977 CCAAGCAG 6036  
6186 GCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245



1314 TCGATGCGAATTGCGAAGGAGGCGGAGAGAGAGGCTGCGGAGAGAGGCGGATTA 1373  
1405 GCTTATGAGAA---CAGAACGAGGAACTGAGAGAGGAGAGAGGCGGAGGCGGAGGCGGATTA 1457  
1374 GGTGAGGCGGAGAGAGGCTGCGGCGGCGGAGAGGCGGAGAGGCGGAGGCGGAGGCGGATTA 1433  
1458 GCGATTCAGAGAGAGGCTGAGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1512  
1434 CAGGCTCAGGAGAGGCGGAGGCGGCGGCGGAGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1493  
1513 GCTGCAATGCGGAGGCGGAGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1569  
1494 GCGAAGGCTGCGGAGGCGGAGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1553  
1570 GAGAGGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1629  
1554 AACGATGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1613  
1630 GCGAAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1673  
1614 GTGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGATTA 1673  
1674 GCTGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1720  
1674 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1733  
1721 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1780  
1734 GGTGATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1793  
1781 GGAAGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 1840  
1794 GATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1853  
1841 GACATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1899  
1854 GACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1913  
1900 GGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1947  
1914 TACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 1973  
1948 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2007  
1974 TATACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2033  
2008 TACAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2067  
2034 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2093  
2068 AGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2127  
2094 GGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2153  
2128 GACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2187  
2154 GAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2213  
2188 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2247  
2214 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2273  
2248 GACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2297  
2274 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2333  
2298 GGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2344  
2334 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2393  
2345 -----AGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2386

2394 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2453  
2397 -----TCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2427  
2454 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2513  
2488 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2487  
2514 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2573  
2488 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2547  
2574 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2633  
2548 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2607  
2634 GCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2693  
2608 GCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2667  
2694 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2753  
2668 TCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2727  
2754 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2813  
2728 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2787  
2814 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2873  
2788 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2847  
2874 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2930  
2848 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2907  
2931 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 2990  
2908 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 2967  
2991 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3050  
2968 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3027  
3051 TACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3107  
3028 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3087  
3108 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3167  
3088 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3147  
3168 TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3227  
3148 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3179  
3228 GATTTAAAGTGGATTAAGGATTAAGTGGATTAAGTGGATTAAGTGGATTAAGTGGATTA 3287  
3180 -----CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3179  
3288 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3347  
3180 -----CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3198  
3348 TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3407  
3199 GCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3258  
3408 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3467  
3359 TTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATTA 3318  
3468 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 3527

Db 3319 AACTGATCGCCACCAACGAGGGGTGATATCCACCGCAACGGCCACTTCCAGAAAGAAC 3378  
Qy 3528 AATPAGCAACGATGATTGGCAACTAATTAACCAACCAAGACATAGACTGGAACAGAG 3587  
Db 3379 GGGAGACGAACCAACAGCGGCATCGGACGAGCGTGGAGAAATGATCATCATGACGAGAC 3438  
Qy 3588 CTAAACATAGAGGTTGTCTTAACAGACGAGACCTGCGACATTAATCTATATGT 3647  
Db 3439 CACG-----TGTCTTCAATTACAA-----CGAACTGACCGTCCGGGT 3479  
Qy 3648 AGCCATAGATCGACCATTCAGAGACGAGACCAAGGCAAGCGCCGAGACGATGAG 3707  
Db 3480 GCCCATGTGTGGGAGATC-----TGACTTGGAGAACTCAACAGAGATGTTAGC 3534  
Qy 3708 GGGAGAGAGAGCGACCGCAGCAGAGAGATTTAGGTCTCGACGAGAACTGAGACGAG 3767  
Db 3535 AGGAAATCAGACCTGAAAGGACAGCAAGATTA-----ACTGAGCGATACCACTCTCA 3588  
Qy 3768 GAGGGCGAATGCGAGAGGGCCGCTGACGATATCATTAATTCAGACGAGAG 3827  
Db 3589 GAGAGAAATGACATCGACATCAAGCTGAGGTGAGAGATTCCTGAGCAACCTGAG 3648  
Qy 3828 GATATATCGATGAATATCCAGCTGATGCTGCCCGCATTCGATTAAGAAATTTCCG 3887  
Db 3649 GAATPACTGG-----ATCCGAGCGCTGCTTTACAGAGGGTTGCTCCAGCGGTTCAAG 3702  
Qy 3888 ATCTTACCGGTGACGATGACTGCGCTTCTGGCAGAGATGGGCAATTTAGACTGAAA 3947  
Db 3703 TGTCTGCGAGGTCAACATCGAGAGAGACTAGGCAAGTGTGTGTGATCTTGGCCGAAAACC 3762  
Qy 3948 ACTTTCATTAATTAATTAATTAATTTGAAAACGCTGTATCTCATATGATTTTAATG 4007  
Db 3763 TGTCTTCTCATTTGTGAGCAAAATGTTGAGACCTTTCATCATCTTCAATGATTTGCTC 3822  
Qy 4008 AGTAGCTTACCTTGGCATTAGAGATGATCATCTGCGCAAAAGCCCATATGACAGAT 4067  
Db 3823 AGCAGTGGCGCCCTGGGCTTTGAGGACATCTACATTGACAGAGAAAGACATCCGCAAC 3882  
Qy 4068 ATTTTATACATNANGACAGAAATTTAGCGTTATATCTTCTTGAAGAAATGTTAAACAG 4127  
Db 3883 ATCTGAGATGCGGACAGAGGTCTTCACTCACTCAATCTTCACTGAGATGTTGCTCAAG 3942  
Qy 4128 TGTGTGCGCTCGGCTTCAAGATGTAATCTTACCAACCGCGTGTGTGCTGATTCGTG 4187  
Db 3943 TGGACAGCCCTACCGCTTCTGCAAGTTCTTCAACATGCCGTGTGTGTGAGACTTCTC 4002  
Qy 4188 ATTTGATGATGCTTATCACTTGTGCTTCACTTGTGAGCTGTGTATTTCAA 4247  
Db 4003 ATTTGAGCTGTCTTATGATCAGCTTAATGCTAATGCTGAGGCTAATCGGAATAGGT 4062  
Qy 4248 GCTTCAAGCTATGCGAAGCTTAAGAGCCTAGAGCACTAGTGCAGATGCCGTATG 4307  
Db 4063 GCCATTAAGTCCCTTAGAGACCTTAAGAGCTTGAAGCCCTTAAGAGCTTATACAGATTT 4122  
Qy 4308 CAGGCGATGAGGCTGCTGTTAATGCGTGTGTAAGCTATACCTGCTCAATGAGT 4367  
Db 4123 GAGGAGATGAGGTGTGTGTGATGCTTGTGGGCGCCATCCCTCTCATGATGAATGTG 4182  
Qy 4368 CTATGTGTGTCTAATATTTTGTGCTAATTTTTCATAATGAGGTGATACGCTTTTGTCT 4427  
Db 4183 CTCTGTGTGTCTCATCTTCTGCTGATTTTTCAGATCATGAGAGTTAACTGTTTGGC 4242  
Qy 4428 GGAATATTTTAATGTC---GAGGACATTAATGAGCAAGCTCAGCCACGAGATCA 4484  
Db 4243 GGGAAATATCACCTACTGCTTAAATGAGACTTGTAAATCGGTTCAAAATCGATATGTGTC 4302  
Qy 4485 CCAATTCGCAATGCTGCGAG-----AGCAGAACTACAGTGGGTG 4526  
Db 4303 AACAAATTAACGAGCTGTGTGAGAGCTCATGAGAGCAACGAGACGAGATCCAGTGAAG 4362  
Qy 4527 AATTTCAGCAATGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4586

Db 4363 AATGCAAGATCACTTTGACATGTCGAGAGAGGATACCTGACCCTTCTCAAGTGGCA 4422  
Qy 4587 ACCTTAAAGGCTGGATATCAATCATGAACGATGCTATGATTTACAGAGAGGTGACAG 4646  
Db 4423 ACCTTAAAGGCTGGATATCAATCATGATGTCGGCTGTGATTTCCGAAAGCCGACGAG 4482  
Qy 4647 CAACCAATTCGTGAACGAACATCTACATGATATTTATATTTGATTTCTTCAATATTT 4706  
Db 4483 CAGCTGACTCAGAGGCAACATCTACATGATATCTACTTGTGATCTTCAATCTTTC 4542  
Qy 4707 GATTCCTTTTCACTCAATCTGTTCAATGATGATGATGATGATGATGATGATGATGATG 4766  
Db 4543 GGCTCTTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4602  
Qy 4767 AAGAAAAAGCAGGAGATCATTTAAGAAATGTTCAAGACGAAGATGAGAAAGATCTAT 4826  
Db 4603 AAGAAAA---GTTGAGAGTCAAGACATTTCAAGACGAAGAAAGATGATGATGATGATG 4659  
Qy 4827 AATGCTATGAAAAAGATGGCTCTAATAAACCATTAAAGCCATTCAAGACCAAGTGG 4886  
Db 4660 AATGCTATGAAAAAGATGGCTCTCAAGAAAGCCAGAAAGCCATCCCGACCTTGAAC 4719  
Qy 4887 CGACCAAGCAATAGCTTTGAAATAGTAAACCGATTAAGAAATTCGATTAATATATG 4946  
Db 4720 AAATTCAGAGGATGTTGTTGATTTGTCATCAACAAGCTTGAATATGATGATGATG 4779  
Qy 4947 TTAATGATGTTGTTGAAATGTTCAACATGACCTCGATGATGATGATGATGATGATG 5006  
Db 4780 ATGCTCATGCTGCTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATG 4839  
Qy 5007 TATAACGCGGCTCTAGACTATCTCAATGCGATATTCGATGATTTTCACTTCCGATGT 5066  
Db 4840 ATGAGAAATATCTTATCTGATTAATCTGATCTTGTGATCTTCTTCACTGCAAGTGT 4899  
Qy 5067 CTATTAATAATATGCTTTTACGATATCAATATTTATGAGCCATGAAATTTATGAT 5126  
Db 4900 GTGCTCAAAATGTTGCTTGAAGACATCTATTTTCAACCATTTGGCTGGAACATCTTTGAC 4959  
Qy 5127 GTAGTATGTTGATTTATTCATCTTATGAGTCTTGAATTTAGAGATTTATGAGAGATGAC 5186  
Db 4960 TTTGTGTGTGATCTCTTCAATGTTGAGAAATGTTCTGCTGATATCATTAAGAAATGAC 5019  
Qy 5187 TTTGTGTGTGATCTCTTCAATGTTGAGAAATGTTCTGCTGATATCATTAAGAAATGAC 5246  
Db 5020 TTTGTGTGTGATCTCTTCAATGTTGAGAAATGTTCTGCTGATATCATTAAGAAATGAC 5079  
Qy 5247 CTGTGAAAGGAGCCAAAGGCAATTTGAGACATGCTTCTTGTGCTGATGCTGCTG 5306  
Db 5080 CTGATTCAGAGGCGCCAAAGGCAATTTGAGACATGCTTCTTGTGCTGATGCTGCTG 5139  
Qy 5307 GGCCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5366  
Db 5140 GGCCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5199  
Qy 5367 ATGCTGTTCTTATGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5426  
Db 5200 ATGCTCAATTTGCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5259  
Qy 5427 ACCTTGGCCAGAGATGATCTGCTCTTTCAGATGTGAGATGAGATGAGATGAGATGAG 5486  
Db 5260 ACATTTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5319  
Qy 5487 GTACTGAGAGCCATTAATCA-----TGAGAAAGATGAGATGATGATGATGATGATGATG 5537  
Db 5320 CTGCTGCTGCAATCTGTAACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5379  
Qy 5538 AAAAGCTATCCGAGCAATGTTGTTTCAAGCAAGCTTGAAGATTAAGCTTCTCTCTCATAC 5597  
Db 5380 AGTGTGTTCAAGAGGAGCTGTGGAACCTCTGAGGAGATCTTCTTCTTGTGAGTAC 5439  
Qy 5598 CTAGTTATAGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5657  
Db 5440 ATCATCATCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5499

QY 5658 AGTCAGGCGACCGAGAGAGAGGCTTAAACCAACAGACTAGCATGTACTAT 5717  
 DB 5500 AGCGTGCCACCGAGAGAGCGGACCCCTTGAGTGAAGTACTTGAGACTTTCTAT 5559  
 QY 5718 GAGATCTGGAGCAATTCGATCCGAGAGGACCAAGTACATACGCTATGACCTGTC 5777  
 DB 5560 GAGATCTGGAGAACTTGAACCCAGAGCCCAAGTTCACTGAGTACTGTAAGCTGCA 5619  
 QY 5778 GAATTCCTGAGAGTCTGAGAGCCCCCGCTGCAATCCAAACCGAACAAGTACAGATC 5837  
 DB 5620 GACTTGCAGCGCCCTGAGACACCCGCTCCAGATCCCAACCAACACCATGAGAGCTC 5679  
 QY 5838 ATATGATGAGCATACCATCTGTGCGGTGACCTCAATGTAAGTGTGATGATCCTGAC 5897  
 DB 5680 ATGCGCATGAGCTGCGCATGTGAGCGGAGATGCACTGCTGGAATCTTTTC 5739  
 QY 5898 GCCCTTACGAAAGACTTCTTGGCGGAGCAATCCGATGAGAGAGCGGTGAGATT 5957  
 DB 5740 GCCTTACCAAGCGAGTCTGGAGAGACGTGGAGATTGACATCTGCGGACAGAGATG 5799  
 QY 5958 GGTGAG-----ATAGCGGCGCGCCCGGATACGAGGCGTACGAGCCGCTCATCAAG 6011  
 DB 5800 GAGAGCGGCTTCTGTCGATCCATCTTCAAGGTCTTACGAGCTTATCAACCACT 5859  
 QY 6012 CTGTGCGCTACGCTGAGAGATCTGCGCCCGGCTAATCCAGCAGCTTGCGGAAAGAC 6071  
 DB 5860 CTGGGCGCAAGAGAGAGAGGTGTCTGAGTGTCTGACGCTTACAGGGGAGAC 5919  
 QY 6072 AAGCGCGCGGCG 6084  
 DB 5920 TTGGCTAGGCGG 5932

## RESULT 15

US-09-425-043-43

Sequence 43, Application US/09425043

Patent No. 6335172

## GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.

APPLICANT: FISH, LINDA M.

APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI

TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESS: JANET PAULINE CLARK

STREET: 3401 HILLVIEW AVENUE, MS A2-250

CITY: PALO ALTO

STATE: CA

COUNTRY: U.S.A.

ZIP: 94304-1397

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/425,043

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/024,020

FILING DATE: 16-FEB-1998

APPLICATION NUMBER: US 60/039,447

FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R0020B-REG

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-3097  
 TELEFAX: (650) 855-5322  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6586 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-425-043-43

Query Match 15.7%; Score 1021.4; DB 3; Length 6586;  
 Best Local Similarity 52.5%; Pred. No. 1.9e-272;  
 Matches 3125; Conservative 0; Mismatches 2486; Indels 342; Gaps 27;

QY 186 CGCAAGAAAAAAGAAATCCGATATGATACGAGAGCGAGATGAAGTCCACA 245  
 DB 268 CTCAAGAAACCAACCAAGGCGGATGAGAGCCAGGAGGAGATGAAGACAGAGCC 327  
 QY 246 CCGATCCTACACTTGAACAGGGGTGCAATACCTGTGATGACGGGAGCTCCG 305  
 DB 328 AAGCAAAAGTACCTGAGAGGCTGGAAGATTGCTTCACTACGAGGACATCCG 387  
 QY 306 CCGAATGCGCTTCACTCTCTGAGATATGATCCCTACTACAGCAATGTAAGTACA 365  
 DB 388 CAAGCGCTGTGGGTGCTCCCTGAGAGACTTGAACCTTATGATTTGAGCGAGAAAC 447  
 QY 366 TTGATGTTGTAAGCAAGAAAGATATTTTCTTTCTTTCGATCAAAAGCATGTGG 425  
 DB 448 TTGTGATATTAACAGAGGAAAACTCTTCAGATTGATGACACCTGCTTGTAC 507  
 QY 426 ATGCTGATCATTCATTCGATACGATGCTGAGGCAATTAATCTTATGATCATCA 485  
 DB 508 ATTTAAGCCCTTTTAACTGATTAAGAAATATCTTAAATTTGATCACTCACTT 567  
 QY 486 TTTTCCCTATTCATCATCACCAATTTCTGTCATGCAATCTGATGATATGCGACA 545  
 DB 568 TTCAAGATGATCATCATGATGACATCTGACCAAGTGTGTTGATGACCTTTAGTAC 627  
 QY 546 AAGCCACAGGTGAGTCACTGAGTG--ATATTCACCGAATCTACATTTGAATCA 602  
 DB 628 CCTCAGAAATGTCAGAAATGTGAGTACATTTCAAGGAGATTTACATTTGAATCA 687  
 QY 603 GCTTTAAGTATGATGAGAGAGTTTCAATTTATGCCGTTTATGATCTTAGAGATCA 662  
 DB 688 CTATGAAATCATGAGAGGTTTCTGATTAAGGCTTCACTTCTGCGAGACCG 747  
 QY 663 TGAATGCTGAGCTTCTGATATAGCTTTATGATGACATGAGTATGATTTA 722  
 DB 748 TGAATGCTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 807  
 QY 723 GGTATCTAGAGCCCTGCGAACCTTTAGGGTCTGAGGCGCTTAAACCGTACATT 782  
 DB 808 GGCATGTCTAGAGCTGAGAACCTTTAGGGTCTGAGGCGCTTAAACCGTACATT 867  
 QY 783 GTGCGAGCTTGAAGACATGAGGCGCTGATGATGAGGAGATCTGCGAGT 842  
 DB 868 ATTCAGGCTGAGAGACATGAGGCGCTTATGATGATGAGGAGATCTGCGAGT 927  
 QY 843 GTGATTAATCTGAGCATGCTTCTGAGTGTGCTGAGTGTGAGGCTTACATGATCTAT 902  
 DB 928 GTGATGATCTGAGAGATGCTGCTGAGTGTGCTGAGTGTGAGGCTTACATGATCTAT 987  
 QY 903 ATGGCGCTGCTACCGAAGTGCAT-----CAAGAGTTCCGCTGAGCGTTCC 953  
 DB 988 ATGGGGAACCTTCAAAAGAGTGTGCTGAGGCTTAACTTCAAGAGTACCTG 1047  
 QY 954 TGGGCAATCTGAGAGAGAGTGAAGTGAATGATGATGATGATGATGATGATGAT 1013  
 DB 1048 GAGAACGAGCACAAGGCTTGAAGTGAAGTGAATGATGATGATGATGATGATGAT 1107  
 QY 1014 TCCAGAGCAGAGGATCTCATTTCCGTTATGCGGCAATATATCCGCTGCGGCAATGC 1073

Db 1108 ATGGTCTGGGATGCTAGAAACCCCTTCTCTGGGGAGAACATTCATGCTGGGCAATGC 1167  
QY 1074 GACGACGATTACGTGTGCTGCGAGGGGTTTGTCCGAATCCGAATTATGCTACACAGC 1133  
Db 1168 CCAGAGGGATTCAGAGCAATGAAAG---CAGGAAGAACCCCACTACGCTTACACACAGC 1224  
QY 1134 TTGGATTGCTGGGATGCTTCTCTGCTGCGCTTCCGGCTGATGACACAGGACTTCTGG 1193  
Db 1225 TTGGAACCTTCACTGCTGGGCTTCTTGGCAATTATTCGCTTATGACCAAGACTATGG 1284  
QY 1194 GAGGATCTGACAGCTGTGTGTCGCGCGCCGACCAATGCGACATGCTGTTCCTTATA 1253  
Db 1285 GAGAACCTTATACGAGCTGACCTTACGAGCGCTGGGAAAAAGTACATGATCTTCTTGTTC 1344  
QY 1254 GTCATATCTCTCTAGCTTCACTTCTTGTGAAATTTGATTTTGGCCATGTTGGCAGT 1313  
Db 1345 TTGGTATCTTCTGGGTTCTTCTTCTGATCTGTGATCTGTGATCTGTGTGGGCGCATG 1404  
QY 1314 TCGTATGACGAATTGCAAAAGAGCCGAGAGAGAGAGGCTCCGAGAGAGAGCGCATTA 1373  
Db 1405 GCTTATGAGGAA---CAGAACGAGCAACACTGAGAGAGGAGAGAGAGAGAGG--- 1457  
QY 1374 CCGTAAACGAGAACCTGCGCGCCGCAAGCGCAAGCTGAGAGAGCGGCGCAATGCG 1433  
Db 1458 CGAGTTCAAGGCAATGCTGAGCACTCAAG---AAGCAGCAGGAGAGGAGCAGGCT 1512  
QY 1434 CAGGCTCAGGACAGCGATGCGGCTGCGCGCGAGAGAGGCTGCACTGATCCGAAATG 1493  
Db 1513 GCTGCAATGAGCCACTCAGCGGCGACTGTCTCGAAGA---CGCCATGAGAGAGAGAG 1569  
QY 1494 GCCAAGAGTCCGACGATCTTCTGATCAGCTATGATGATTTGTTGGCGGAGAGAGGCG 1553  
Db 1570 GAAAGTGGGGTAGGCTCTCCGAGAGACTCTTGTGAATGCTTAACTCACTTCCAAAGAC 1629  
QY 1554 AACGATGACAAACAAGAGAGAGATGTCATTGAGCGCTGAGGCTGAGTGCAGTGC 1613  
Db 1630 GCGAAGAGCGGCGGAA-----CCGACGAGAGAGAGAGAGAGAGAGAG 1673  
QY 1614 GTGAGGTTATCAAAAGACACAGCACTTACACAGCACCACCACTTACCAAAAGTTGCT 1673  
Db 1674 GCTCTGAAAGGAG 1720  
QY 1674 AAAGTAGACAGCATCTTATCTTACCTGATTCACCTGTTTAACTATACAGAGGAGATCA 1733  
Db 1721 CAGAGTCGAGAGAGCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780  
QY 1734 CCGTATCTTCAAGTACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793  
Db 1781 GGAAGTTTCCATCATGAATCAAGTCCGCTGCTCAGATTCAGAGCTGCGCTTCTCTCC 1840  
QY 1794 GATCGTAGCATTTGTTATTTGTCATATCATATCAGGATGCCAGAGCACTTGCCTATGCG 1853  
Db 1841 GACATACAGCAAAAGAGAGATTTCAAGCTTCCGGAGAGAGAGAGAGAGAGAGAGAG 1899  
QY 1854 GAGCACTCGAATGCGCTCAACCCGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913  
Db 1900 GGGCTGAGAGATG-----AGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1947  
QY 1914 TACTATGCGAATTAAGCTTCCGACACTATGCTATTAATCTCGCATAGTCCGAGATATG 1973  
Db 1948 AGGAGAGAGCGGAGTACTGCTCTTCAATCCGATCCGAGCGCGAGAGAGAGAGAGAG 2007  
QY 1974 TATACCTCAATGAGGATCTACTCGGCGGATGAGCGGCTGATGAGAGAGAGAGAGAG 2033  
Db 2008 TACAGTGGCTACAGCGGCTTACAGCCAGTGAAGCGGCTCGTCCGCTAATAATGATAGGC 2067  
QY 2034 AAGGAGAGCAAAATGCGCAACGCGCAACAGCAAGCAATCAATCAATGAGGCGCCCAATGCG 2093  
Db 2068 AGCTAGGAGAGAGGATCTTCCAGAGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 2127  
QY 2094 GGCACCACTGTCTGAGACCAATCAAAAGCTGATCATGCGACTACAGAAATTTGGCTTG 2153  
Db 2128 GACTGACAGCGGAGTAGTCACTCATCGGAGCGGCTCAGACATCGGAGCGGCTCGCTCT 2187

QY 2154 GAGTGCAGGAGAGAGAGAGAGAGAGAGAGAGATTAACATCATGACATCTTTTATCGAGCCGCTC 2213  
Db 2188 GAGGCAACCACTGAGGTGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2247  
QY 2214 CAGACCAAAAGCGGTGATTAATGAAAGATGATGATGCTGCTGAATGACATCATCAACAG 2273  
Db 2248 GACCAACTGCGCTCTACGAG 2297  
QY 2274 GCGGCTGTGCGACAGTGGGCAAGCATGCGGCTGTCTCGTTACTATTTCCCAACA 2333  
Db 2298 CCGTGTCACAAAACAGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2344  
QY 2334 GAG 2393  
Db 2345 -----AGTCCACCGTGTGCTGATTAAGATTGTTCCAAACATTTCTCTCA-- 2386  
QY 2394 GGCATCATGATGTTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2453  
Db 2387 -----TCTGGAGGTGTCAACCCCTACTGATTAATACTGAGAGAGAGATC 2427  
QY 2454 GTATGCTCATGTCTTGTGATCTTCTGTCAGCTCTTCATCAAGCTGTGATTTGGTTC 2513  
Db 2428 GTGAACCTTATGCTATGAG 2487  
QY 2514 AACAGAGTGTGATGAG 2573  
Db 2488 AATAGCTATTTATGAG 2547  
QY 2574 AAGAGTGCAGACTATTTCTTCCAGCCGACCTTGTGACATGAGAGAGAGAGAGAGAGAG 2633  
Db 2548 GCGGTAGAGAAATCTGTGTGTACCGGAGATCTTCAAGGAGAGAGAGAGAGAGAGAGAG 2607  
QY 2634 GCGATAG 2693  
Db 2608 GGCATGAG 2667  
QY 2694 GCGCTATGCTATTTGAG 2753  
Db 2668 TCCCTCATGTTATGAG 2727  
QY 2754 TTTGATTTGCTGCGGTATTTCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2813  
Db 2728 TTTCCAGCTGCTCGAGTCTTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2787  
QY 2814 TCGATTTAG 2873  
Db 2788 AAGATCATCGGAG 2847  
QY 2874 ATCTTCATCTTTCGCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2930  
Db 2848 GTCTTCATCTTTCGCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2907  
QY 2931 AAG 2990  
Db 2908 TGTAGATATCAACAG 2967  
QY 2991 TTTGATGATGCTTTCGCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3050  
Db 2968 TTTCTCATGCTTTCGAGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3027  
QY 3051 TACGTG---GGGAGATCTGCGATTCCTCTTCTTGGCCAGAGAGAGAGAGAGAGAGAG 3107  
Db 3028 GAGGTGCGCGGAG 3087  
QY 3108 CTGTGTGATCTTAACTTTCTTACCTTGTCTTGTGTCAAATTTTGGCTCATTAAGCTTA 3167  
Db 3088 CTGTGTGTGATCTTAACTTTCTTACCTTGTCTTGTGTCAAATTTTGGCTCATTAAGCTTA 3147  
QY 3168 TCAAGCGGAG 3227  
Db 3148 GCGGCGACAG 3179

QY 3228 CGATTAAAGTGGGTTAAGCGTAATATGCTGATGTTTCAAGTATATAGTAACAA 3287  
Db 3180 ----- 3179  
QY 3288 TTGACAAATCAAAATAGTATCAACCATCAAGTAGAGAGACCACCAATCATGTTGATT 3347  
Db 3180 ----- CTTGACATCTCAAGTATC 3198  
QY 3348 TGGAGCGAAGCATGTGTGACACGAACTGAGAGCTGGGCGACGACGAATCTCGCCGAC 3407  
Db 3199 CGGATTCAGAAAGGGCGTGGCTTGAGCAAAAGTGAAGGTGACAGCTTTCATGAGGCTCAC 3258  
QY 3408 GGCCTCATCAAGAGGGGATCAAGAGGAGAGCACTGAGGTGGCCATCGGGATCGG 3467  
Db 3259 TTCAAGCAGCGGGAGCGGATGAAGTGAACCCCTCGACGAGCTGTATGAGAAAGAGCC 3318  
QY 3468 ATGGAATTCAGATACACGGCGACATGAAAGACAAAGCCGAAAGAAATCCAAATATCTA 3527  
Db 3319 AACTGATCGCCAAACACAGGGCGTGGATATCCACGGGAAAGGCGATTCAGAAAGAAC 3378  
QY 3528 AATTAACGACAGATGATTTGGCACTCAATTAAACCAAGACATAGTGAACAGAG 3587  
Db 3379 GGGAAACGGAACACACGGGCGATCGGACAGCGTGAAGATCATCATCGACGAGAC 3438  
QY 3588 CTAACCATAGAGTTGTCTTACAGAGACGACGACCTGCGAGATTAACTCATATAGT 3647  
Db 3439 CACA-----TGTCTTCAATTAAAC-----CMAAAGTACGCTCGGCT 3479  
QY 3648 AGCCATTAAGATTCACATTCAGAGACGAGCCCAAGGCGAGCGGACGATGAG 3707  
Db 3480 GCCCATGTGTGGGCGAGTC-----TGACTTCGAAACCTCAACAGAGAGATTTAGC 3534  
QY 3708 GCGCGAAGAACCGGACCGCAGCAAGAGAGATTTAGTCTCGACGAGAACTGAGCAG 3767  
Db 3535 AGCCAAATCAGACCTCGAAGGAGCAAGATTA-----ACTGAGATTAACAGCTCTCA 3588  
QY 3768 GAGGCGCAATGCGAGAGGCGCGCTGACGCTGATCATTTATTCATGACACAGAGAG 3827  
Db 3589 GAAAGAAATACCATTCGACATCAAGCTGAGGTGAAGAGTTCCGTGAGACACTGAG 3648  
QY 3828 GATTAATCTGATGATATTCAGCTGATGCTGCCCCGATTCGATTAAGAAATTTCCG 3887  
Db 3649 GAATACTTGG-----ATCCGAGCGCTGCTTACAGAGGTTGGTCCAGGGTTCAAG 3702  
QY 3888 ATCTTAAGCCGCTGACATGATCCGCCGTTCTGCGAAGATGGGCAATTTACAGTGA 3947  
Db 3703 TGCTGCAAGTCAATCGAAGAAAGACTAGGCAAGTGTGTGATCTTCGGAAGAAC 3762  
QY 3948 ACTTTCAATTAATTAATAATAATTTTGAACAGCTGTTATCATATGATTTTAATG 4007  
Db 3763 TGCTTCTCATTTGAGACAAATTTGTTAGACTTCATCATCTTCATATGATTTCTGCTC 3822  
QY 4008 AGTAGCTTAAGCTTTGCAATTAAGAGATGATCATCTGCAACAAAGCCATCTGAGAGAT 4067  
Db 3823 AGCAGTGGCGCGCTTGAAGACATCTAACATGAGAGAGAAACATCCGACCC 3882  
QY 4068 ATTTTAATTAATTAAGACAAATTAATGAGTTATTTCTTTGGAATGTTATCAAG 4127  
Db 3883 ATCTGAGATGAGGAGCAAGAGTCTTCACTACATCTTCATCTGAGATGTTGCTCAAG 3942  
QY 4128 TGGTTGGCGCTCGGCTCAAGATGATCTTCAACAGCGGTGTGTGCTGATTTCTG 4187  
Db 3943 TGGAGAGCTAAGCGCTTCTCAAGATTTCTTCAACATGCTGTGTGTGAGACTTCTC 4002  
QY 4188 ATTTGATGATGATGCTTATCAATCTGTTCTTCACTTTGAGAGCTGTGTATTCAA 4247  
Db 4003 ATTTGGGTGTCTTTTATGATCAGCTTATAGTATAGTCCCTGGGCTATCTCGAACTAGT 4062  
QY 4248 GCGTTCAAGACTATGCGAACTTAAGAGACTGAGACCACTAAGTCCATGCTCCGTATG 4307  
Db 4063 GCGCTTAAGATCCCTTAAGAGCTTTGAAGACCTTAAGAGCTTTATCAAGATTT 4122  
QY 4308 CAGGCAATGAGGCTGTGTTAATGCGTGTGTAAGCTAATCCGTCACTTTCAATGTG 4367

Db 4123 GAAGGATGAGGCTGTGTGTAATGCTTGTGTGGGCGGCATCCCTCATCATGATGTG 4182  
QY 4368 CTATTTGTGTCTTAATATTTTGGCTAATTTTGGCATATAGGTGTAACAGCTTTTGTCT 4427  
Db 4183 CTGCTGTGTGTCTCATCTTCTGCTGATTTTCAAGCATCATGGAGTTAACTGTTTGG 4242  
QY 4428 GGAATAATTTTAAGTGC---GAGACATGAAATGGACGAAAGCTCAGCCAGCAATCTA 4484  
Db 4243 GGGAAATTCATCTGCTTTTAATGAGCTTCTAATAATCCGTTGAAATGATATGTGTC 4302  
QY 4485 CCAATGCAATGCTGCGAG-----AGCGAATCAACGCGGCTG 4526  
Db 4303 AAGCATTAAGAGCTGTGAGAAAGCTCATGAGAGGCAACAGAGAGATCCATGGAAG 4362  
QY 4527 AATTCAGATGAATTTGATCATGATGTAACGCTATCTGTGCTTTTCCAAGTGGCC 4586  
Db 4363 AATGCAAGATCACTTTGACATGTGCGACAGGGTACTGGCCCTTCTTCAAGTGGCA 4422  
QY 4587 ACCTTCAAGGCTGATTAATTAATCATGAGATGCTATCATTCACGAGAGTGAACAG 4646  
Db 4423 ACCTTCAAGGCTGATGATCATGATGATGCGCTGATATCCGAAACCAAGACAG 4482  
QY 4647 CAACCAATTCGTGAACGAAATCATCATGATTAATTAATTTGATTTTCTCATATATT 4706  
Db 4483 CAGCTGACTGAGAGGCAATCTACATGATCATCTTCTGATCTTATCATCTTC 4542  
QY 4707 GGAATCTTTTTCACATCTGATCTGTTGATGTTGATCATTTGATTAATTAAGCA 4766  
Db 4543 GGTCTCTTCTTCACTTCACTGATCTGTTGATGTTGATCATCTTCACTTCACTTCA 4602  
QY 4767 AAGAAAAAGAGGTGATCATTTGAATGTTCTATGACAGAAAGTCAAGAAAGTACTAT 4826  
Db 4603 AAGAAAA---GTTTGAAGGTCAAGACATCTTCAATGACAGAGAAAGAAAGTACTAC 4659  
QY 4827 AATGCTAAGAAAGATGAGGCTTAAGAAACCAATTAAGGCTTCCAAAGCAAGGTG 4886  
Db 4660 AATGCTAAGAAAGGCTGAGGCTCAAGAGGCAAGAAAGGCTTCCGAGCTTGAAC 4719  
QY 4887 GACCAACAGATAGTCTTGAATAGTAACGATTAAGAAATTCATTAATCATATATG 4946  
Db 4720 AAATTCAGAGGATGTTGATGATTTGATGTTGATGATCAAGGCTTGAATGATGAT 4779  
QY 4947 TTATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5006  
Db 4780 ATGCTCATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4839  
QY 5007 TATAACGCGCTAGACATCTCAATGAGATAATGATGATTTTCAAGTTCGAAATGT 5066  
Db 4840 ATGAGAAACATTTCTTACTGATTAATCTGATCTTTGATCTTCTTCACTGAGATGT 4899  
QY 5067 CTATTAATAATTTGCTTTAAGATATCAATTTTAATGAGCAAGAAATTTAATTTGAT 5126  
Db 4900 GTGCTCAAAATGTTGCTTGAAGACATGATTTTCAATGCTGGAACATCTTTGAC 4959  
QY 5127 GTAGTAGTGTGATTTATCATCTTATGATCTTATGATCTTATGATCTTATGATCTT 5186  
Db 4960 TTGTGTGTGTGATCTTCTCATTTGTGGAATGTTCTGCTGATGATCATTTGAAGATAC 5019  
QY 5187 TTGTGTGTGTGATCTTCTCATTTGTGGAATGTTCTGCTGATGATCATTTGAAGATAC 5246  
Db 5020 TTGTGTGTGTGATCTTCTCATTTGTGGAATGTTCTGCTGATGATCATTTGAAGATAC 5079  
QY 5247 CTGTGTAAGGAGGCAAGGAGATTCGACATGCTCTTGTGCTTGTGAGCAATGTGCTG 5306  
Db 5080 CTGATCAAGGAGGCAAGGAGATTCGACATGCTCTTGTGCTTGTGAGCAATGTGCTG 5139  
QY 5307 GCGCTTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5366  
Db 5140 GCGCTTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5199  
QY 5367 ATGCTGCTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5426

Db 5200 ATGTCCAACTTGGCATACGTGAAGCAGAGCGCGCATTTGACGACATGTTCAACTTGGAG 5259  
QY 5427 ACCTTTGGCCAGAGCATGATCTGCTCTTTCAATGTCAGCTGAGCCGGTTGGAGTGGT 5486  
Db 5260 ACATTTGGCAACAGCATGATCTGTTGTTCCAGATCAACAGCTGCTGGGATGGC 5319  
QY 5487 GTACTGAGCGCATTTATCA-----TGAGGAAGCANTGCATCCACCGACAGCGAC 5537  
Db 5320 CTGCTGTGCAATCTGAAACCGCCCCCTGACTGCACTTGACAAAGACACCAAGG 5379  
QY 5538 AAAGGCTATCCGGGCAATTGTTGTTAGCAGCCGTTGATTAACGTTTCTCTCATAC 5597  
Db 5380 AGTGGCTTCAAGGGGAGTGGGAACCCCTCGTGGGATCTTCTTTGTAAGTAC 5439  
QY 5598 CTAGTTATAAGCTTTTGAATGTTAATATGTAATGCTGTCAATTCGGAACAT 5657  
Db 5440 ATCATCATCTCTTCTGATTTGGTGAACATGTACATGCCATCATCTCGGAACCTTC 5499  
QY 5658 AGTCAGGCGCACGAGGACGTGCAAGAGGGTCTAACCGACGAGCTAACGACATGTACTAT 5717  
Db 5500 AGCGTGCCACCGAGAGAGCGCCGACCTCTGATGAGATGATCTTCAGACTTTCTAT 5559  
QY 5718 GAGATCTGGAGCAATTGATCCGAGGGGACCCAGTACATACGTATGATCAGCTGCC 5777  
Db 5560 GAGATCTGGGAGAAGTTGACCCAGACGCCACCCAGTTATCGAGTACTGTAGCTGGCA 5619  
QY 5778 GAATTCCTGAGCTGTACTGGAGCCCCCGCTGCAATCCAAACCGAACAAGTCAAGATC 5837  
Db 5620 GACTTTGCCGACGCCCTGGAGCACCCGCTCCAGTACCCAAAGCCAAACATCGAGCTC 5679  
QY 5838 ATATCGATGAGCATACCATCTGTCGGGTGACCTCATGTACTGCGTCGACATCTCGAC 5897  
Db 5680 ATGGCATGSACTTGCCATGTAAGCGAGATCGCATCCACTGCTTGGACATCTTTTC 5739  
QY 5898 GCCCTTAAGAACTTCTTTGCCGGAAGGCAATCCGATAGAGAGACGGGTGAGATT 5957  
Db 5740 GCCTTACCAAGAGAGTCTCGGAGACAGTGGGAGTGGACATCTGCGGACAGATG 5799  
QY 5958 GGTAG-----ATAGCGGCCGCCCGGATACGAGAGGCTTACGAGCCGCTCATCAG 6011  
Db 5800 GAGGAGCGGTTCTGAGATCAATCTTCCAAAGTGTCTTACGAGCCTATCACACCACT 5859  
QY 6012 CTGTGCGTCAAGCGTGAAGTACTGCGCCGGCTAATCCAGCAGCCTGGCGAAGACAC 6071  
Db 5860 CTGCGGCGCAAGCAGAGAGTGTCTGCAGTGTCTCTGAGGCTGCTTACAGGGGACAC 5919  
QY 6072 AAGCGCGCGCGG 6084  
Db 5920 TTGGCTAGGCGGG 5932

Search completed: May 9, 2005, 17:49:26  
Job time : 1041 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 04:13:21 ; Search time 3369 Seconds  
(without alignments)  
11820.771 Million cell updates/sec

Title: US-08-554-424-7

Perfect score: 6513

Sequence: 1 TCTAGACGTTGGCCGATAG.....ACGGAGATTAGCTTAGA 6513

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4447.8	68.3	6318	10	US-09-428-371-1
2	4434.2	68.1	10	US-09-428-371-2	
3	1019.4	15.7	6586	17	US-10-152-319A-1723
4	1019.4	15.7	6586	18	US-10-377-139-14
5	974	15.0	6503	18	US-10-377-139-16
6	944.8	14.5	7052	16	US-10-202-824-5
7	941	14.4	6027	17	US-10-297-022-40
8	940.6	14.4	8491	17	US-10-333-191-3
9	940.2	14.4	6048	18	US-09-896-994-1
10	940.2	14.4	6048	18	US-10-685-237-1
11	940.2	14.4	6048	18	US-10-852-840-1

12	939.4	14.4	6048	9	US-09-840-125-3	Sequence 3, Appli
13	939.4	14.4	6048	18	US-10-914-133-3	Sequence 3, Appli
14	939.4	14.4	8490	15	US-10-101-610-617	Sequence 617, App
15	938.4	14.4	8491	17	US-10-333-191-1	Sequence 1, Appli
16	937.8	14.4	6172	18	US-10-632-342-1	Sequence 1, Appli
17	937.8	14.4	6172	18	US-10-632-342-3	Sequence 3, Appli
18	936.6	14.4	6091	16	US-10-077-054-1	Sequence 1, Appli
19	936.6	14.4	6169	18	US-10-632-342-5	Sequence 5, Appli
20	936.6	14.4	6169	18	US-10-632-342-7	Sequence 7, Appli
21	936.4	14.4	8380	19	US-10-482-834-1	Sequence 1, Appli
22	935.4	14.4	5922	9	US-09-930-871-13	Sequence 13, Appli
23	935.4	14.4	5922	19	US-10-925-369-13	Sequence 11, Appli
24	935.4	14.4	6030	9	US-09-930-871-11	Sequence 11, Appli
25	935.4	14.4	6030	19	US-10-925-369-11	Sequence 11, Appli
26	934.6	14.3	8381	18	US-10-451-126A-8	Sequence 8, Appli
27	934.6	14.3	8381	18	US-10-451-126A-9	Sequence 9, Appli
28	933	14.3	8379	18	US-10-806-899-53	Sequence 53, Appli
29	933	14.3	8380	18	US-10-806-899-15	Sequence 15, Appli
30	933	14.3	8381	18	US-10-451-126A-5	Sequence 5, Appli
31	933	14.3	8381	18	US-10-451-126A-11	Sequence 11, Appli
32	933	14.3	8381	18	US-10-451-126A-11	Sequence 11, Appli
33	933	14.3	8381	18	US-10-482-834A-8	Sequence 8, Appli
34	933	14.3	8381	19	US-10-482-834A-9	Sequence 9, Appli
35	933	14.3	8381	19	US-10-482-834A-20	Sequence 20, Appli
36	932.6	14.3	8380	18	US-10-806-899-18	Sequence 18, Appli
37	931.4	14.3	8381	18	US-10-451-126A-1	Sequence 1, Appli
38	931.4	14.3	8381	18	US-10-451-126A-3	Sequence 3, Appli
39	931.4	14.3	8381	18	US-10-451-126A-7	Sequence 7, Appli
40	931.4	14.3	8381	18	US-10-806-899-1	Sequence 1, Appli
41	931.4	14.3	8381	18	US-10-806-899-2	Sequence 2, Appli
42	931.4	14.3	8381	18	US-10-806-899-3	Sequence 3, Appli
43	931.4	14.3	8381	18	US-10-806-899-4	Sequence 4, Appli
44	931.4	14.3	8381	18	US-10-806-899-5	Sequence 5, Appli
45	931.4	14.3	8381	18	US-10-806-899-6	Sequence 6, Appli

#### ALIGNMENTS

RESULT 1

US-09-428-371-1

Sequence 1, Application US/09428371

Publication No. US20030096336A1

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Knipple, Douglas C.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND TITLE OF INVENTION: INSECTICIDE-RESISTANT HOUSE FLIES

FILE REFERENCE: 19603/606

CURRENT APPLICATION NUMBER: US/09/428, 371

CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 08/608, 618

EARLIER FILING DATE: 1996-03-01

EARLIER APPLICATION NUMBER: 08/772, 512

EARLIER FILING DATE: 1996-12-24

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 6318

TYPR: DNA

ORGANISM: Musca domestica

US-09-428-371-1

Query Match

Best Local Similarity 68.3%; Score 4447.8; DB 10; Length 6318;

Matches 5998; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

QY 24 ATGACAGAGATTTCGACTGATATCTGAGAGAGACGACTTTGTTCCGCTTTACG 83

DB 1 ATGACAGAGAGATTTCGACTGATATCTGAGAGAGACGACTTTGTTCCGCTTTACG 60

QY 84 CGGATATCTTGGTGGCAATGAGACAGCACTTCGCGTGAACATGAAAAGCAGAGAG 143

Db 61 CGGATTCATGTTTACAAATCGAACAACGAT---CGCTGACATGAAAAACAAAGAG 117  
 Qy 144 CTGAAAGAAAGAGAGCCGAGGAGAGTCCCGCATATGTCGCAAGAAAAACAAAA 203  
 Db 118 CTGAAAGAAAGAGAGAGCCGAGGAGAGAGC----- 148  
 Qy 204 GAATTCGATATATATGACGAGAGCGAGGATGAAGGTTCACACCGGATCTCACTTGA 263  
 Db 149 -AGATTACATATATATGACGAGAGCGAGGATGAAGGTTCACACCGGATCTCACTTGA 207  
 Qy 264 CAGGATGTCGCAATACCTGTTTCATGTCAGAGGAGCTTCCCGCGAATTGGCTCCACT 323  
 Db 208 CAGGATGTCGCAATACCTGTTTCATGTCAGAGGAGCTTCCCGCGAATTGGCTCCACT 267  
 Qy 324 CTTCTGAGGATATCGATCCCTTACTACGACATATGACTGACATTCGTAGTTGTAAGCAA 383  
 Db 268 CTTCTGAGGATATCGATCCCTTACTACGACATATGACTGACATTCGTAGTTGTAAGCAA 327  
 Qy 384 GGAAGATATTTTGTGCTTCTGATCAAAAGCAATGAGATGCTCGATTCATTCAT 443  
 Db 328 GGAAGATATTTTGTGCTTCTGATCAAAAGCAATGAGATGCTCGATTCATTCAT 387  
 Qy 444 CCGATACGTGTCGTCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 503  
 Db 388 CCGATACGTGTCGTCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 447  
 Qy 504 ACCAATATTCGTCAATCGATCCTGATGATATATGCGCAACGCCCGATGAGTCC 563  
 Db 448 ACCAATATTCGTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 507  
 Qy 564 ACTGAGGATATTCACCGGATCTACATTCATTCATTCATTCATTCATTCATTCATTC 623  
 Db 508 ACTGAGGATATTCACCGGATCTACATTCATTCATTCATTCATTCATTCATTCATTC 567  
 Qy 624 GATTTCATTTATGCCCCGTTTACGATCTTACGATGATGATGATGATGATGATGATG 683  
 Db 568 GATTTCATTTATGCCCCGTTTACGATCTTACGATGATGATGATGATGATGATGATG 627  
 Qy 684 GTATATGCTTACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
 Db 628 GTATATGCTTACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
 Qy 744 ACCTTATGAGGTGTCGAGAGCGCTTAAACCGTAGCCATGTCGAGGCTTGAAGCATC 803  
 Db 688 ACCTTATGAGGTGTCGAGAGCGCTTAAACCGTAGCCATGTCGAGGCTTGAAGCATC 747  
 Qy 804 GTGAGGCGCGTCATCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 863  
 Db 748 GTGAGGCGCGTCATCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
 Qy 864 TCCCTGCGGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 923  
 Db 808 TCCCTGCGGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867  
 Qy 924 TGCATCAAGAAGTTCGCGTGAAGCGTTCGAGGCGAATCTGACCGACGAGCTGGAC 983  
 Db 868 TGCATCAAGAAGTTCGCGTGAAGCGTTCGAGGCGAATCTGACCGACGAGCTGGAC 927  
 Qy 984 TATCAATCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1043  
 Db 928 CTACACATATGCAACAGTTTCAATGTTTACGAGAGAGATGAGGAGTATTCGGGTG 987  
 Qy 1044 TGGGCGATATATCCGTCGCGGCGCAATGCGACGACGATTAAGTGTGCTGCGAGGGTTT 1103  
 Db 988 TGGGCGATATATCCGTCGCGGCGCAATGCGGAGAGATTAAGTGTGCTGCGAGGGTTT 1047  
 Qy 1104 GGTCCGAATTCGCAATTAAGCTACACAGCTTGCATTCGTTGAGAGGGCTTCCTGCTC 1163  
 Db 1048 GGTCCGAATTCGCAATTAAGCTACACAGCTTGCATTCGTTGAGAGGGCTTCCTGCTC 1107  
 Qy 1164 GGTCCGAATTCGCAATTAAGCTACACAGCTTGCATTCGTTGAGAGGGCTTCCTGCTC 1223

Db 1108 GCGTTTGTCTCATGACCCAGATTTCTGAGAGATCTGTATACGACGCTGTGACAGA 1167  
 Qy 1224 GCGGACATATGCAATGCTGCTTATATGATCATCTTCCTAGTTCATTCATTCATTC 1283  
 Db 1168 GCTGAGCCCTGAGACATGTTGTTTATATGATCATCTTCCTAGTTCATTCATTCATTC 1227  
 Qy 1284 GTCAATTTGATTTTGGCATATGTTGTCATGTCATGTCATGTCATGTCATGTCATGTC 1343  
 Db 1228 GTCAATTTGATTTTGGCATATGTTGTCATGTCATGTCATGTCATGTCATGTCATGTC 1287  
 Qy 1344 GAAAGAGGCTGCGAGAGAGAGGCGATATGCTGAAGCGGAAGAGTCCCGCCGAA 1403  
 Db 1288 GAAAGAGGCTGCGAGAGAGAGGCGATATGCTGAAGCGGAAGAGTCCCGCCGAA 1347  
 Qy 1404 GCGGCGCAATGAGAGAGGCGGCAATGCGAGGCTCAAGGCGAGCGGATGCGCTGCC 1463  
 Db 1348 GCGGCGCAATGAGAGAGGCGGCAATGAGAGGCTCAAGGCGAGCGGATGCGCTGCC 1407  
 Qy 1464 GCGGAGAGGCTGCACTGATCCGGAATGCGCAAGTCCGACGTAATCTTGCATCAGC 1523  
 Db 1408 GCGGAGAGGCTGCACTGATCCGGAATGCGCAAGTCCGACGTAATCTTGCATCAGC 1467  
 Qy 1524 TATGACTTATTTTGTGCGCGGAGAAAGGCAACGATGACCAACAAAGAGATGTC 1583  
 Db 1468 TATGAACTGTTTGTGCGCGGAGAAAGGCAACGATGACCAACAAAGAGATGTC 1527  
 Qy 1584 ATTGAGAGGTCGAGGTGAGATGCGATGCGGTGATGATGATGATGATGATGATGATG 1643  
 Db 1528 ATTGAGAGGTCGAGGTGAGATGCGATGCGGTGATGATGATGATGATGATGATGATG 1587  
 Qy 1644 ACCACAGCACACCAAGCTACCAAGGTCGTAAGTGAAGACAGACATCTTATCTTACCT 1703  
 Db 1588 ACCACAGCACCC---CGTACTAAAGTCGTAAGTGAAGACAGACATCTTATCTTACCT 1644  
 Qy 1704 GATTACCGTTTATACATACGAGGAGATCACTAGTCTCAACAGTACGATACGAAAC 1763  
 Db 1645 GATTACCGTTTATACATACGAGGAGATCACTAGTCTCAACAGTACGATACGAAAC 1704  
 Qy 1764 GAGCGTGGCGGCTTGTATACCGGATGACGATTCGTAACGATGATGATGATGATGATG 1823  
 Db 1705 GAGCGTGGCGGCTTGTATACCGGATGACGATTCGTAACGATGATGATGATGATGATG 1764  
 Qy 1824 CAGATGCCACAGACGATTCGCTATGCGGACGATCGATGATGATGATGATGATGATG 1883  
 Db 1765 CAGATGCCACAGACGATTCGCTATGCGGACGATCGATGATGATGATGATGATGATG 1824  
 Qy 1884 GAAAGATGAGGCGCATCATATGTCGCTGATATGCAATCTGATGATGATGATGATGATG 1943  
 Db 1825 GAAAGATGAGGCGCATCATATGTCGCTGATATGCAATCTGATGATGATGATGATGATG 1884  
 Qy 1944 TCGTATACCTGCGATCAGTCCGGAATATGCTATACCTGATGATGATGATGATGATGATG 2003  
 Db 1885 TCGTATACCTGCGATCAGTCCGGAATATGCTATACCTGATGATGATGATGATGATGATG 1944  
 Qy 2004 ATGGCCGTCATGGGCGCTCAGCAATATGACCAAGAGAGCAATTTGCGAACCGCAACA 2063  
 Db 1945 ATGGCCGTCATGGGCGCTCAGCAATATGACCAAGAGAGCAATTTGCGAGCGCAACA 2004  
 Qy 2064 CCGCAATCAATCAATGAGGCGCACCAATGAGGCGCACCACTGTCTGACCAATACAAAG 2123  
 Db 2005 CCGCAATCAATCAATGAGGCGCACCAATGAGGCGCACCACTGTCTGACCAATACAAAG 2064  
 Qy 2124 CTGCAAT-----CATGCGCATACGAAATTTGCGTGAAGTGCACGAGCA 2168  
 Db 2065 CCGCAATCAATCAATGAGGCGCACCAATGAGGCGCACCACTGTCTGACCAATACAAAG 2124  
 Qy 2169 GCTGGCAATTAATCAATCATGATCATCTTTTATGAGCCCGTCCAGACCAACAGGTTG 2228  
 Db 2125 GCTGGCAATTAATCAATCATGATCATCTTTTATGAGCCCGTCCAGACCAACAGGTTG 2184  
 Qy 2229 GTTGAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2288  
 Db 2185 GTTGAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244

QY 2289 AGTCGGGAGAGATCGGGTGTCTCCGTTTACTATTTCCCAAGAGAGATGACAG 2348  
DB 2245 AGTCGTCTAGTGAACGAGGT-----GAGAGCATATACGAA 2280  
QY 2349 GATGGGCCGACGTTCAAGACACAGGACACTCGAAGTATCTCAAGAGCATGATGTTT 2408  
DB 2281 GATGGTCCCACTTCAAGGACATCGCCCTCGAATACCTTAAAGGACATGAAATCTTT 2340  
QY 2409 TGTGTGGGAGACTGTTGCTGGGTTTGGTGAATTTCAAGAGTGGTATCGTCAATGTC 2468  
DB 2341 TGTGTATGGGACTGTTGTTGGGTGTGTTAAATTTCAAGAGTGGGTCTCTTATTTG 2400  
QY 2469 TTGCATCCCTTGCTGAGCTCTTCATCAAGCTGTCATTTGGTGAACAGATGTTTCAG 2528  
DB 2401 TTGCATCCATTCGTGGAGCTCTTCATCACTGTGTATGTGGTCAATACGATGTTTATG 2460  
QY 2529 GCAATGATCAACACGATATGAAACAGAGATGAAACGCGTGTCAAGAGTGGCACTAT 2588  
DB 2461 GCAATGATCAATCAAGACATGATCCGGAATTAGAGAGTGTCTGAAAGTGTAACTAT 2520  
QY 2589 TTCTTACCGCACCTTTTGCATCGAGGCGACATGAAGCTAATGSCATAGCCCCAAG 2648  
DB 2521 TTCTTACGCGCACCTTTTGCATTTGAAAGCCAGCATGAATGATGATGAGCCGAG 2580  
QY 2649 TACTATTTCCAGAGAGGCTGGAACAATCTTCACTTATATGCTGAGCCCTATGCTATG 2708  
DB 2581 TACTATCTTCAAGAGAGGCTGGAACAATCTTCACTTATATGCTGAGCCCTATGCTATG 2640  
QY 2709 GAACGAGACTCGAGGCTGTCCAGAGGCTGTCCGATTTAGCGTTCTTTCATTTGCTG 2768  
DB 2641 GAATTTGGGCTGTGGAGGCTGTCCAGGCGCTGTCCGATTTAGAGAGTTTCTGTTGCT 2700  
QY 2769 GTATTCAAACTGGCCAAATCTTGGCCCACTTAAATTTACTCATTTCAATATGAGGCG 2828  
DB 2701 GTATTCAAAATTTGGCCAAATCTTGGCCCACTTAAATTTACTCATTTCAATATGAGGCG 2760  
QY 2829 ACCATGGGCGCTTTGGGTAATCTGACATTTGTAATTTGATTTATATCTTCAATCTTGG 2888  
DB 2761 ACCATGGGCGCTTTGGGTAATCTGACATTTGTAATTTGATTTATATCTTCAATCTTGG 2820  
QY 2889 GTATGAGGATGCACTGTTCGAAAGAAATTAATCATGATCAACAGACCGCTTCCGAT 2948  
DB 2821 GTATGAGGATGCACTTTTGGAAAGAACTAATTAATGACACAGATCGCTTCAAGAG 2880  
QY 2949 GGGCACTGCGCGCTGGAATTTCAACGATTTATGCAACAGCTTCAATGATGCTTCCG 3008  
DB 2881 CATGAATTAACGCGCTGGAATTTCAACGATTTATGCAACAGCTTCAATGATGCTTCCG 2940  
QY 3009 GTGCTCGCGGAGAAATGATGAGATGATGATGATGATGATGATGATGATGATGATG 3068  
DB 2941 GTGCTCGCGGAGAAATGATGAGATGATGATGATGATGATGATGATGATGATGATG 3000  
QY 3069 TGCATTCCTCTCTTGGGACACGCTTGTCAATGCGCATTTGTTGTTACTTAACCTTTC 3128  
DB 3001 TGTATACCTCTCTTGGGACACGCTTGTCAATGCGCATTTGTTGTTACTTAATCTTTC 3060  
QY 3129 TTAACCTTGTCTTGTCCAAATTTTGGCTCATCTAGCTTATCAAGCGCCGATCAAC 3188  
DB 3061 TTAACCTTGTCTTGTCCAAATTTTGGCTCATCTAGCTTATCAAGCGCCGATCAAC 3120  
QY 3189 GATACGAAATTAATGCGGAGGCTTCAATGAAATGCGGATTTAAAGTTGGTTAAG 3248  
DB 3121 GATACGAAATTAATGCGGAGGCTTCAATGAAATGCGGATTTAAAGTTGGTTAAG 3180  
QY 3249 CGTATATTTGCTGATTTGTTCAAGTATATGTAACAAATTTGACAAATCAATATAGTAT 3308  
DB 3181 CGTATATTTGCTGATTTGTTCAAGTATATGTAACAAATTTGACAAATCAATATAGTAT 3240  
QY 3309 CAACCATCAGGTGAGAGCAACCAAGTCAATGATTTGAGCGAAGAGCATGATGAC 3368  
DB 3241 CAACCATC-----AGAACATGSCGAT 3261

QY 3369 AACGAATGAGCTGGGCGACAGACGATCCGCGAGCGCTCATCAAGAGGGGATC 3428  
DB 3282 AATGAATGAGGTTGGTCAATGACGAATTCATGGCGATGGCTTGAATAAAAGGATATG 3321  
QY 3429 AAGGACGAGACGCACTGAGGTGGCCATCGGGATCGATGATGAAATTCACATACCGC 3488  
DB 3322 AAGGCGAGACCGAGCTGAGGTGGCCATTTGGCGATGAGGATTCACATATCATGTC 3381  
QY 3489 GACATGAAGAAACAAACAGCCGAGAAATTCAAATTTCTAAATTAACGACATGATGGC 3548  
DB 3382 GATATGAAACAAACAGCCGAGAAATTCAAATTTCTAAATTAACGACATGATGGA 3441  
QY 3549 AACTCAATTAACCAAGACATGATGATGATGATGATGATGATGATGATGATGATG 3608  
DB 3442 AACTCAATTAACCAAGACATGATGATGATGATGATGATGATGATGATGATGATG 3501  
QY 3609 TTAACGAGACGACACTGCGAGATTAATCATATGATGATGATGATGATGATGATG 3668  
DB 3502 ATACGAGACGATGACACTGCGAGATTAATCATATGATGATGATGATGATGATGATG 3561  
QY 3669 AAGGACGAGACCAACAGGCGAGCGGACGATGAGAGGCGAGAGAGCGGCGC 3728  
DB 3562 AAGGACGAGACCAACAGGCGAGCGGACGATGAGAGGCGAGAGAGCGGCGC 3621  
QY 3729 AGCAAGAGGATTTAAGTCTGACAGAGGAACTGACAGAGAGGCGGAAATGGAGAGGCG 3788  
DB 3622 AGCAAGAGGACCTGCGCTGACAGAGGAACTGACAGAGAGGCGGAAATGGAGAGGCG 3681  
QY 3789 CCGCTCGAGGATGATATCATTAATCATATGCT--ACACGACGAGATATCTCATGATAT 3845  
DB 3682 CAGCTGATGATGATATCATTAATCATATGCGGAAACGACGAGATATGACGACAT 3741  
QY 3846 CCAAGTATGCTGCGCGGATGCTGATTAAGAAATTTCCGATCTTACCGGTCGAT 3905  
DB 3742 CCGGCGGATGCTTCCCGGATGCTGATTAAGAAATTTCCGATCTTACCGGTCGAT 3801  
QY 3906 GACTCGCGCTTCCGAGAGATGAGGCGAATTTAGAGCGAAGCTTTCAATTAATGAA 3965  
DB 3802 GACTCGCGCTTCCGAGAGATGAGGCGAATTTAGAGCGAAGCTTTCAATTAATGAA 3861  
QY 3966 AATTAATTTTGAAGAGCTGTTATCATATGATTTTAAATGATGATGATGATG 4025  
DB 3862 AATTAATTTTGAAGAGCTGTTATCATATGATTTTAAATGATGATGATGATG 3921  
QY 4026 TTAAGAGTGAATCTGCGCAACAAAGCCATCTGACGATATTTATATATGAGAC 4085  
DB 3922 TTAAGAGTGAATCTTTTACCGATGACCTGTCAATGAGATATATCTATATGAGAC 3981  
QY 4086 AGATATTTTACGTTATATCTTCTTGAAGATTTTAAATGATGATGATGATG 4145  
DB 3982 AGATATTTTACGTTATATCTTCTTGAAGATTTTAAATGATGATGATGATG 4041  
QY 4146 AAGGTATCTTCAACCAACGCGTGTGTTGCTGATTTGATGATGATGATGATG 4205  
DB 4042 AAGGTATCTTCAACCAATGCTGTGTGTTGCTGATTTGATGATGATGATGATG 4101  
QY 4206 ATCAACTTGTGCTTCACTTGTGAGCTGTGTATTTCAAGCTTCAAGCATATGGA 4265  
DB 4102 ATCAACTTGTGCTTGTGAGCTGTGTATTTTAAATGATGATGATGATGATG 4161  
QY 4266 ACGTTAAGAGACATGACCACTACGTCGATGTCCTGTATGACGAGGATGAGGTGTC 4325  
DB 4162 ACGTTAAGAGACATGACCACTACGTCGATGTCCTGTATGAGGAGGATGAGGTGTC 4221  
QY 4326 GTTATGCGCTGATCAAGCTATACGTCATCTTCAATGATGATGATGATGATG 4385  
DB 4222 GTTATGCGCTGATCAAGCTATACGTCATCTTCAATGATGATGATGATGATG 4281  
QY 4386 TTTTGGCTAATTTTGTGCATATGAGGTGATACGCTTTTCTGAGAAATTTTAAAGTGC 4445  
DB 4282 TTTTGGCTAATTTTGTGCATATGAGGTGATACGCTTTTCTGAGAAATTTTAAAGTGC 4341  
QY 4446 GAGGACATGATGACAGAGGCTGACGACGAGATCATATCAATATGCAATGCTGAG 4505

Db 4342 AAAGATGTRATACACTGCTGAGCCATGAATATACCGAATGCTAATGCTGCATA 4401  
 Qy 4506 AGGAGAACTACACGCTGGTGAATTCAGCAATGAATTCGATCATGTAAGTAAACGCGTAT 4565  
 Db 4402 AGTGAATACTACACCTGGGAAATTCGGGCATGAATTCGATCATGTAAGTAAACGCGTAT 4461  
 Qy 4566 CTGTGCTTTTCCAAATGGCCACTTCAAGAGCTGATCAATTCATGAAACGATGCTATC 4625  
 Db 4462 CTGTGCTTTTCAAGTGGCCACTTCAAGAGCTGATCAATTCATGAAACGATGCTATC 4521  
 Qy 4626 GATTCAAGAGGTGACAAAGCAACAAATTCGTGAACGAACTCAATGATTTATAT 4685  
 Db 4522 GATTCAAGAGGTGACAAAGCAACGATCCGAAACCAATTCATGATTTATAT 4581  
 Qy 4686 TTGCTATTTCTTCAATTTGATGCTTTTCACTCATCTGTTGATGCTATC 4745  
 Db 4582 TTGCTATTTCTTCAATTTGATGCTTTTCACTCATCTGTTGATGCTATC 4641  
 Qy 4746 ATTGATATTTTATGACAAAGAAAGAGAGGTGATCATTAAGAAATGTTCAAGCA 4805  
 Db 4642 ATTGATATTTTATGACAAAGAAAGAGAGGTGATCATTAAGAAATGTTCAAGCA 4701  
 Qy 4806 GAAGATCAGAAAAAGTACTAATATGCTATGAAAAAGTGGCTCTAATAAACCATTTAAA 4865  
 Db 4702 GAAGATCAGAAAAAGTACTAATATGCTATGAAAAAGTGGCTCTAATAAACCATTTAAA 4761  
 Qy 4866 GCCATTCAGAACCAAGGTGGGACCAAGCAAGTATGCTTTGAAATAGTAAACGATTAAG 4925  
 Db 4762 GCCATTCAGAACCAAGGTGGGACCAAGCAAGTATGCTTTGAAATAGTAAACGATTAAG 4821  
 Qy 4926 AAATGATATTAATCATTTATGATTTATCATTTGATGCTGAACATGTTCAACATCCCGAT 4985  
 Db 4822 AAATGATATTAATCATTTATGATTTATCATTTGATGCTGAACATGTTCAACATCCCGAT 4881  
 Qy 4986 CGTTAAGATGCTGACGACATGATTAACGCGGCTCTAGACTATCATAGCGATTTGTA 5045  
 Db 4882 CGTTAAGATGCTGACGACATGATTAACGCGGCTCTAGACTATCATAGCGATTTGTA 4941  
 Qy 5046 GTTATTTTCACTTCCGATGCTCTAATTAATAATTTGCTTTAGATATCATATTTTAT 5105  
 Db 4942 GTTATTTTCACTTCCGATGCTCTAATTAATAATTTGCTTTAGATATCATATTTTCAA 5001  
 Qy 5106 GAGCCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
 Db 5002 GAGCCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
 Qy 5166 AGGATATTAATCGAAGATCTTCTGTCGCGACCTGCTCGAGTGTGCGTGTGCGG 5225  
 Db 5062 AGGATATTAATCGAAGATCTTCTGTCGCGACCTGCTCGAGTGTGCGTGTGCGG 5121  
 Qy 5226 AAAGTGGGCGGCTCTTCCGATGCTGTAAGAGGACCAAGGCTTTGGGACACCTGCTTC 5285  
 Db 5122 AAAGTGGGCTGCTCTTCCGATGCTGTAAGAGGACCAAGGCTTTGGGAGTGTGCTTC 5181  
 Qy 5286 GCGTGTGGCCATGCTGCTGCGGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTG 5345  
 Db 5182 GCGTGTGGCCATGCTGCTGCGGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTG 5241  
 Qy 5346 TTGATTTTCCGATTTTCCGATGCTGCTGCTTCAATGACGTAAGAGAGAGAGCGCAT 5405  
 Db 5242 TTGATTTTCCGATTTTCCGATGCTGCTGCTTCAATGACGTAAGAGAGAGAGCGCAT 5301  
 Qy 5406 AAGAGGCTGACAACTTCAAGACCTTTGGCGAAGATGATCTGCTTTCAAGATGCTG 5465  
 Db 5302 AAGGCTGCTGATATTTTAAAGATTTGGCAAGATGATGATGCTGCTTTCAAGATGCTG 5361  
 Qy 5466 AAGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5525  
 Db 5362 AAGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5421  
 Qy 5526 CCGGACGACAAAGGCTATCCGCGCAATGCTGCTGACGACGCTGGAATTAAGCTTT 5585

Db 5422 CCGGACGACAAAGGCTATCCGCGCAATGCTGCTGACGACTGTTGAATTAAGCTTT 5481  
 Qy 5586 CTCTCTCTACTACTGATTAATAGCTTTTGAATGATTAATTAATGATTAATGATTAATG 5645  
 Db 5482 CTCTCTCTACTACTGATTAATAGCTTTTGAATGATTAATTAATGATTAATGATTAATG 5541  
 Qy 5646 CTCTGAGAACTATAGTACGAGGACCGGAGGACGTAAGAGGCTTAAACGACGACGACTAC 5705  
 Db 5542 CTCTGAGAACTATAGTACGAGGACCGGAGGATGATGACGAGGCTTCAACGACGATTAAC 5601  
 Qy 5706 GACATGATCTATGATGCTGAGCAATTCGATCCGAGAGGACCCGATGATTAATGATG 5765  
 Db 5602 GATATGATCTATGATGCTGAGCAATTCGATCCGAGAGGACCCGATGATTAATGATG 5661  
 Qy 5766 GATGATGCTCTGAGATTTCTGAGCAATTCGATCCGAGAGGACCCGATGATTAATGATG 5825  
 Db 5662 GATGATGCTCTGAGATTTCTGAGCAATTCGATCCGAGAGGACCCGATGATTAATGATG 5721  
 Qy 5826 AAGTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5885  
 Db 5722 AAGTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5781  
 Qy 5886 GACATCTCTGAGCGCTTAAAGAACTTTCTTGGCGGAGAGGCAATCCGATTAAGAGAG 5945  
 Db 5782 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5841  
 Qy 5946 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6005  
 Db 5842 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5901  
 Qy 6006 TCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6065  
 Db 5902 TCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5961  
 Qy 6066 AAGCAAGAGCGCGCGGCGAGAGGCTGCTTGAACGCGATGATGATGATGATGATGATG 6125  
 Db 5962 CGTTACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5994  
 Qy 6126 GCGGATGATGCGGATGCGGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6185  
 Db 5995 GCGGATGATGCGGATGCGGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6054  
 Qy 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6245  
 Db 6055 GCGGATGATGCGGATGCGGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6114  
 Qy 6246 AATGATTAATGCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6305  
 Db 6115 AATGATTAATGCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6159  
 Qy 6306 GCGGATGATGCGGATGCGGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6365  
 Db 6160 GCGGATGATGCGGATGCGGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6219  
 Qy 6366 GTTCTGCTGAGAGGACCGGATGCTGTAAGAAAGGCGCACAGGCTGCTGCTGCTGCTGCTG 6425  
 Db 6220 GTTCTGCTGAGAGGACCGGATGCTGTAAGAAAGGCGCATTAAGGCTGCTGCTGCTGCTG 6279  
 Qy 6426 CGATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6464  
 Db 6280 AGATGCGCGAGATTAACATCCAGAGCGGATGCTGTA 6318

RESULT 2  
 US-09-428-371-2  
 ; Sequence 2: Application US/09428371  
 ; Publication No. US20030096336A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soderlund, David M.  
 ; APPLICANT: Knipfle, Douglas C.  
 ; APPLICANT: Ingles, Patricia J.  
 ; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND  
 ; TITLE OF INVENTION: INSECTICIDE-RESISTANT HOUSE FLIES

```

; FILE REFERENCE: 19603/606
; CURRENT APPLICATION NUMBER: US/09/428,371
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 08/608,618
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/772,512
; EARLIER FILING DATE: 1996-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6315
; TYPE: DNA
; ORGANISM: Musca domestica
; US-09-428-371-2

```

Query Match	68.1%	Score 4434.2	DB 10	Length 6315
Best Local Similarity	81.8%	Pred. No. 0		
Matches 5284	Conservative 0	Mismatches 1013	Indels 162	Gaps 8
QY	24	ATGACAGAAATTCGGACCTCGATCTGATCTGAGGAAAGAACGAGTTGTCGCTCCCTTAC	83	
Db	1	ATGACAGAAATTCGGACCTCGATCTGATCTGAGGAAAGAACGAGTTGTCGCTCCCTTAC	60	
QY	84	CGCGAATCATTTGGTCCAAATCGAACAGCATTTGCGCTGAAACATGAAAAGCAGAAAGAG	143	
Db	61	CGCGAATCATTTGGTTCAAATCGAACAGCATTTGCGCTGAAACATGAAAAGCAGAAAGAG	117	
QY	144	CTGGAAGAAAGAGAGCCGAGGAGAGAGTCCCGCATATGCTCGCAAGAAAAACAATAA	203	
Db	118	CTGGAAGAAAGAGAGCCGCGCAAGAGAGC-----	148	
QY	204	GAAATCCGATPNTGATGAGAGGACGAGATGAAAGGTCCACAAACGGATCTTACATTGAA	263	
Db	149	-AGATACATATGATGACGAGGACGAGATGAAAGGTCCACAGCCGATCTCCACATTGAA	207	
QY	264	CAGGCTGTGCCAATCCCTGTCGATTGCAAGGCACTTCCGCGCGAAATTTGGCTTCACT	323	
Db	208	CAGGCTGTGCCAATCCCTGTCGATTGCAAGGCACTTCCGCGCGAAATTTGGCTTCACT	267	
QY	324	CCTCTCGAGATATGATTCCTCTACTACAGCAATGTATGACATTTGTGTGTTGTAAGCAA	383	
Db	268	CCTCTCGAGATATGATTCCTCTACTACAGTAATGTATGACATTTGTGTGTTGTAAGTAA	327	
QY	384	GAAAAGATATTTTTCGCTTTCTGCATCAAAAAGCAATGTGATGCTGCATTCATTAAT	443	
Db	328	GAAAAGATATTTTTCGCTTTCTGCCTCCTCAAAAGCAATGTGATGCTGCATTCATTAAT	387	
QY	444	CGATACGCTGTGCGCATTTTACATTTAGTGATTCATTAATTTTCCCTATTCATATC	503	
Db	388	CGATACGCTGTGCGCATTTTATATTTTATGATTCATTCCTGTTTTCGTTATCATATC	447	
QY	504	ACCAATATTCCTGCACTGCACTCTGATGATATATGCGGACAAAGCCCAAGGTTGATGCC	563	
Db	448	ACCAATATTCCTAATTTGTAATTTATGATTAAGTAAAGCCCAAGGTTGATGCCAATCC	507	
QY	564	ACTGAGTGATATTAACCGGAAATCTACCATTTGAAATCAGCTGTAAAGTGATGCGACGA	623	
Db	508	ACAGAGTGATATTAACCGGAAATCTACCATTTGAAATCAGCTGTAAAGTGATGCGACGA	567	
QY	624	GGTTTCATTTATGCGCGTTTACGATCTTATGAGATGATGGAATTTGCTGGACTTCGTA	683	
Db	568	GGTTTCATTTATGCGCGTTTACGATCTTATGAGATGATGGAATTTGCTGGACTTCGTA	627	
QY	664	GTAATAGCTTATAGCTATATGACCAATGGGATATAGTTTATAGTAATCTTACGACCTCGGA	743	
Db	628	GTAATAGCTTATAGCTATATGACCAATGGGATATAGTTTATAGTAATCTTACGACTTGA	687	
QY	744	ACGTTTAAAGGTCCTCGAGCGCTTAAACCGTAAAGCATTTGTCGAGGCTTGAAGCATTC	803	
Db	668	ACATTTAAAGGTCCTCGAGCGCTTGAAGAACCGTAAAGCATTTGTCGAGGCTTGAAGCATTC	747	
QY	804	GTCGCGCGCTGATCGAATCGGTGAAGATCTGCGGATGATGATTTATCTGACCATGTTTC	863	

D	b		748	GTCGGTGTCTGATCGAATCTGTAAATAATCTACGCCAGTGTGAATATTTTGCATATGTT	807
O	y		864	TCCCTGTGGTGTTGCGCGTTAGTGGGCTCAAGATCTATATGGCGTGTACCAGANG	923
D	b		808	TCCCTGTGGTGTTGCGCGTATGGGCTTAACAATCTATATGGGTTCTAACAAAAG	867
O	y		924	TGCATCAAGAAGTTTCCGCTGGAAGGTTCTTGGGGCAATCTGACCGACGAAGACTGGGAC	983
D	b		868	TGCATTTAAACGATTTCCCCTGGAAGGCGCATTTGGGGCAATCTGACCGAATGAATACTGGTTTT	927
O	y		984	TATCACAATCGCAATAGCTCCAAATTGGATTTCCGAGACGAGGGGATCTCAATTCCTTA	1043
D	b		928	CTACACAATAGCACAGTTTCCAATTGGTTTACGAGAAACAATGGCGATCATATCCGATG	987
O	y		1044	TGCGGCATATATTCGCGTGCAGGGCAATCGACAGCATTAAGTGTGCTGCAAGGGTTT	1103
D	b		988	TGCGGGAATGATTCGCGTGGGGCAATGCGGGCAAGATTACGTGCTGCAAGGGCTTC	1047
O	y		1104	GCTCCGAATCCGAATTATGCTTACACAGCTTCGATTGTTGCGATGGGCTTTCTGTCC	1163
D	b		1048	GGCCCCAATCCCACTACAGCTACACCAAGTTTCGATTCATTTCGTTGGGCTTTCTGTGCG	1107
O	y		1164	GCTTTCGGCGTAGAGACACAGACTCTGGGAGATCTGTACCGAGCTGTGTGGGGCGCC	1222
D	b		1108	GCGTTTGTCTCATGACCCAAAGATTTCTGGAGAGATCTGTACAGCACTGTCTGAAACA	1167
O	y		1224	GCCGACCATAGGACATGCTGTTCTTTATGATCATCTTCTCTAGTTCAATTCATCTT	1283
D	b		1168	GCTGGACCTTGCAATGTGTTCTTTATGATCATCTTCTCTAGTTCAATTCATCTT	1227
O	y		1284	GTAATTTGATTTTGGCCATTGTTGCCATGTGTAAGCAATTGCAAAAGAAAGGCCGAA	1343
D	b		1228	GTGAATTTGATTTTGGCCATTGTTGCCATGTGTAAGCAATTGCAAAAGAAAGGCCGAA	1287
O	y		1344	GAAGAAGAGCTGCCGGAAGAGAGAGGCCATATGTAAGCGGAAGAGCTGCCGCCGCAA	1400
D	b		1288	GAAGAAGAGCTGCCGGAAGAGAGGCCATATGTAAGCGGAAGAGCTGCCGCCGCAA	1347
O	y		1404	GCGGCAAGCTGAGAGAGAGCGGGCCAAATGCGAGGCTCAGCGAGACGCGATGCGGCTCC	1463
D	b		1348	GCGGCAAGCTGAGAGAGAGCGGGCCAAATGCGAGGCTCAGCGAGACGCGATGCGGCTCC	1407
O	y		1464	GCCGAAGAGCTGCATCTGCATCCGGAATGGCCAAAGTCCGACGATTTCTTGATCAGC	1523
D	b		1408	GCCGCTGGGAGCTCTGCATCCGGAATGGCCAAAGTCCGACGATTTCTTGATCAGC	1467
O	y		1524	TATGAGCTATTTGTTGGCGCGGAAGAGGGCAAGATGACACACAAAGAAAGATGTCC	1583
D	b		1468	TATGAGCTATTTGTTGGCGCGGAAGAGGGCAAGATGACACACAAAGAAAGATGTCC	1527
O	y		1584	AATTGGAGCGTGCAGAGTGCAGATGCGGATGCGGTATATACAAAGAACACAGCACTT	1643
D	b		1528	ATTGGAGCGTGCAGAGTGCAGATGCGGATGCGGTATATACAAAGAACACAGCACTT	1587
O	y		1644	ACCAAGACACCAAGCTACCAAAAGTTCGTAAGTAGACGAGACTCTTATCTTAACTT	1703
D	b		1588	ACCAAGACACCAAGCTACCAAAAGTTCGTAAGTAGACGAGACTCTTATCTTAACTT	1647
O	y		1704	GCTTCACTGTTTAACTATGCGAGGGGATCACTATGTTCTCAACAATGACATACGAAAC	1763
D	b		1645	GCTTCACTGTTTAACTATGCGAGGGGATCACTATGTTCTCAACAATGACATACGAAAC	1707
O	y		1764	GGAGGTGGCGCTTTGGTATACCGGGATGCGATGCTAAGCAATTTGGTATTTGTCAACATAT	1823
D	b		1705	GGAGGTGGCGCTTTGGTATACCGGGATGCGATGCTAAGCAATTTGGTATTTGTCAACATAT	1767
O	y		1824	CAGATGCGCAGACACTTGCCTTATGCGACGACTGAAATGCGGTCACTCCCGATGTCC	1883
D	b		1765	CAGATGCGCAGACACTTGCCTTATGCGACGACTGAAATGCGGTCACTCCCGATGTCC	1827
O	y		1884	GAAGAAGATGGGGCAATCATATGTGCGCGGTATCTATGGCAATCTAAGCTCCGACACTCA	1943
D	b		1825	GAAGAAGATGGGGCAATCATATATGATACAGCCCTACTATTTGATTTTATGTTCTAGACATCT	1887

1944 TGGTATACCTCCGATAGTCCGAAATGTGATACCTCAGATGGCGATCTACTCGCGGC 2003  
Db 1885 TATATACCTCCGATACATCAAGAAATCTGTATATACATCATGTGATATTATGGGTGCG 1944  
Qy 2004 ATGGCGGTATGGGGCGTCCAGACATGACCAAGAGAGCAAAATTTGGCAACGCAACAA 2063  
Db 1945 ATGGCGGTATGGGGCGTCCAGACATGACCAAGAGAGCAAAATTTGGCGATGGCAACAA 2004  
Qy 2064 CGCAATCAATCAGTGGGGCGCCAAATGGCGGACCACTGTCTGACCAATCAACAAG 2123  
Db 2005 CGCAATCAATCAGTGGGGCGCCAAATGGCGGAGTACGCGCGGTGGTGGCTAT 2064  
Qy 2124 CTGGAT-----CATGGCGCTAGGAATTTGGCGGTGGAGTGGAGCGAA 2168  
Db 2065 CCGGATGCCAATCAAGAAACAAAGGATTTAAGAAATGGGTGAGATTAATACAGAGAA 2124  
Qy 2169 GCTGGCAAGATTAACATCATGACAAATCTTTATCGAGCCGCTCCAGACAAACGATG 2228  
Db 2125 GCTGGCAAAATTAACCAACAGCAATCTTTATCGAGCCGCTCCAACTCAACAGT 2184  
Qy 2229 GTTGATATGAAGATGTGATGTCTGATGACATCATGACAGGCGCGTGGTGGCAC 2288  
Db 2185 GTGACATGAAGATGTGATGTCTTAAATGATATCATGACAGCGCGTGGTGGCACAT 2244  
Qy 2289 AGTGGCGCAAGCATGGCGGTGTCTCGTTACTATTTCCCAACAGAGACGATGACAG 2348  
Db 2245 AGTGGCTATAGTACAGAGT-----GAGGACGATGACGAA 2280  
Qy 2349 GATGGGCGGAGCTTCAAGACAGAGCACTGAGATGATCTCAAGAGCATCATGATGTTT 2408  
Db 2281 GATGGTCCCATTTCAAGACATCGCCCTTGAAATATCTTAAAGGACATCGAAATCTTT 2340  
Qy 2409 TGTGTGGGAGCTGTGTGGGTGGTTGGTGAATTTCAAGAGTGGGTATCGCTCATGCTC 2468  
Db 2341 TGTGTGGGAGCTGTGTGGGTGGTTGGTGAATTTCAAGAGTGGGTATCGCTCATGCTC 2400  
Qy 2469 TTTGATCCCTTGTCCAGCTCTTCACTACAGCTGTGCAATGTGGTCAACAGATGTTCATG 2528  
Db 2401 TTTGATCCATTTGTGGAGCTCTTCACTACAGCTGTGCAATGTGGTCAACAGATGTTCATG 2460  
Qy 2529 GCATGATCACCACGATATGAACAGAGATGAAACGCTGTCTCAAGATGGCAACTAT 2588  
Db 2461 GCATGATCATTACAGCATGAATTCGGGAATTTGGAAGAGTGTCTGAAGATGGTAACTAT 2520  
Qy 2589 TTTCTTACCGCCACTTTTGCATTCAGGCGCACTGAGAGCTAATGGCGATGAGCCCAAG 2648  
Db 2521 TTTCTTACCGCCACTTTTGCATTCAGGCGCACTGAGAGCTAATGGCGATGAGCCCAAG 2580  
Qy 2649 TACTATTTTCAGAGGGGTGGAACTTTGCACTTATTCGTTGCGCTATGCTATTTG 2708  
Db 2581 TACTATTTTCAGAGGGGTGGAACTTTGCACTTATTCGTTGCGCTATGCTATTTG 2640  
Qy 2709 GAACTGGGACTCGAGGGGTGTCTGAGGATGTGCTGCTTTCGATTTGCTGCGT 2768  
Db 2641 GAATTTGGGCTCGAGGGGTGTCTGAGGATGTGCTGCTTTCGATTTGCTGCGT 2700  
Qy 2769 GTATTTCAACTGGCCAAATCTTTGGCCCACTTATTTACTCATTTTGGATTTAGGAGCGC 2828  
Db 2701 GTATTTCAAAATTTGGCAAAATCATGCCCCACATGAATTTACTCATTTTGGATTTAGGAGCGCG 2760  
Qy 2829 ACCATGGGCGCTTTGGGTATTCGACATTTGTACTTTGCACTTATCATCTTCATCTTTGGC 2888  
Db 2761 ACATGGGTGTATGGGTATTCGACATTTGTACTTTGCACTTATCATCTTCATCTTTGGC 2820  
Qy 2889 GTATGGGAATGCAACTGTTCGAGAAAGATTAATCATGATCAAGAGCGCTTTCCGAT 2948  
Db 2821 GTATGGGAATGCAACTTTTCGAGAAAGATTAATTAATCAAGAGATGCTTTCAAGAGAC 2880  
Qy 2949 GGGGAGCTGGCGGCTGGAACTTTCAGCACTTTATGACAGCTTTCATGATCGTGTTCGG 3008  
Db 2881 CATGAATTAACCGGCTGGAAATTTCCAGCACTTCATGACAGCTTTCATGATGTGTTCGA 2940

Qy 3009 GTGCTCTGGGAGAGTNGATGAGTGCATGAGTGGGACTGCACTGATGCGGCGATGCTCG 3068  
Db 2941 GTGCTGTGGGAGAGTNGATGAGTGCATGAGTGGGACTGCACTGATGCGGCGATGCTCG 3000  
Qy 3069 TGCATTTCCCTTTCTTTGGGCAACGTTGTATCGGCAATCTTTGGTACTTAACTTTTC 3128  
Db 3001 TGTATACCTTTCTTTGGGCAACGTTGTATCGGCAATCTTTGGTACTTAACTTTTC 3060  
Qy 3129 TTAGCTTGTCTTTTGCATTTTGGCTCATCTTATGAGGCGCGATGCGGATAC 3188  
Db 3061 TTAGCTTGTCTTTTGCATTTTGGCTCATCTTATGAGGCGCGATGCGGATAC 3120  
Qy 3189 GATACGAATTAATTAAGCGGAGCTTTCATCGAATTTGGCGGATTTAAAGTTGGTAA 3248  
Db 3121 GATACGAATTAATTAAGCGGAGCTTTCATCGAATTTGGCTCATCTTATGAGGATGAAA 3180  
Qy 3249 CGTAAATTTGTGATTTGTTTCAAGTTAATCGTAACTTAACTTAACTTAACTTAACT 3308  
Db 3181 CGTAAATTTGTGATTTGTTTCAAGTTAATCGTAACTTAACTTAACTTAACTTAACT 3240  
Qy 3309 CAACCTCAGTGGAGAGCAACCAAGTCACTTGGATTGGAGGAGAGCATGATGATC 3368  
Db 3241 CAACCATC-----AGACATGCGAT 3261  
Qy 3369 AACGAATGAGCTGGGCGACAGAGATCTCGCGCAAGCGCTCATCAAGAGGAGATC 3428  
Db 3262 AATGAATGAGATTTGGGTCTATGACGAATCATGGGAGATGGCTTATCAAAAGGATATG 3321  
Qy 3429 AAGGACAGAGCAACTGAGGTTGGCATGGGAGATCGGATGGAATTTCACTATACAGCGC 3488  
Db 3322 AAGGCGCAAGCAGCTGAGGTTGGCATGGGAGATCGGATGGAATTTCACTATACAGCGC 3381  
Qy 3489 GACATGAAGAACAACAGCGGAGAAATCCAAATATCTAATTAACGACATGATTTGCG 3548  
Db 3382 GATATGAAGAACAACAGCGGAGAAATCCAAATATCTAATTAACGACATGATTTGGA 3441  
Qy 3549 AACTCAATTAACCAACCAAGACATGATGAGCAACAGCTAATAGAGTTGTTC 3608  
Db 3442 AACTCAATTAACCAACCAAGACATGATGAGCAACAGCTAATAGAGTTGTTC 3501  
Qy 3609 TTAACAGAGAGAGCACTGCGCATTTAATCTATGTTAGGCTTAAGATGACATTC 3668  
Db 3502 ATACAGAGAGAGCACTGCGCATTTAATCTATGTTAGGCTTAAGATGACATTC 3561  
Qy 3669 AAGGACAGAGCAACAGGCGAGCGCGAGAGATGAGGCGAGAGCGCGC 3728  
Db 3562 AAGGACAGAGCAACAGGCGAGCGCGAGAGATGAGGCGAGAGAGCGCGC 3621  
Qy 3729 AGCAAGAGAGATTTAGTCTGACAGAGATGAGAGAGGCGAGATGCGAGAGCGC 3788  
Db 3622 AGCAAGAGAGATTTAGTCTGACAGAGATGAGAGAGGCGAGAGGCGAGATGAGAGCGC 3681  
Qy 3789 CCGCTGAGCGGTATATCTTATTCATGCG--ACACGAGAGAGATTAATCTGATGAAT 3845  
Db 3682 CAGCTGAGAGAGATTAATCTTATTCATGCG--ACACGAGAGAGATTAATCTGATGAAT 3741  
Qy 3846 CAGCTGATTTGCTGCGCGATTTCTGATTAAGAAATTTCCGATTTTACCGGTGAGAT 3905  
Db 3742 CCGGCGGAGCTGTTTCCCGCATCTGATCAAGAAATTTCCGATTTTACCGGTGAGAT 3801  
Qy 3906 GACTCGCGTTCTGGAGAGATGGGCAATTTACGACTGAAATCTTTCAATTAATGAA 3965  
Db 3802 GACTCGCGTTCTGGAGAGATGGGCAATTTACGACTGAAATCTTTCAATTAATGAA 3861  
Qy 3966 AATTAATTTTGAACAGCTGTATCTATGATTTTATAGTACGTTAGCTTGGGCA 4025  
Db 3862 AATTAATTTTGAACAGCTGTATCTATGATTTTATAGTACGTTAGCTTGGGCA 3921  
Qy 4026 TTAGAGATGATCATGCGCAACAAAGACCATTAAGATTTTATATATATGAC 4085  
Db 3922 TTAGAGATGATCATTTACCGATGACCTGTATGACAGATTAATCTGATGATGAC 3981  
Qy 4086 AGAATATTAACGTTAATTTCTTGGAAATGTTAATCAAGTGTGGCGCTGCGCTTC 4145

Db 3982 AGGATATTTACGGGATATTTCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTT 4041  
 Qy 4146 AAAGTGTACTTACCAACGCGTGTGTGGCTCGATTTTCGTGATTTGATGATGATTCGCTT 4205  
 Db 4042 AAGGCTATCTTACCAATAGCCGTGGTGTGGCTGATTTGTTGATGATGATGATTCGCTT 4101  
 Qy 4206 ATCAATTCGTTGCTTACCTTGTGGAGCTGTGTGATTTCAAGCTTCAAGACTATGCGA 4265  
 Db 4102 ATAAATTTGGTTGGCGTTGGTGGCTTAAATGATTAAGCCGTGTTTAAATCAATGCGC 4161  
 Qy 4266 ACCTTAAGAGCAGTGAACCACTACGTGCGATGTCCTGATGACAGGAGGATGGGTCGTC 4325  
 Db 4162 ACATGCGCGCCCTTAAGGCCATTTGGTGTCTGTCTCTAGATGAGGAGGATTAAGAAATTTTC 4221  
 Qy 4326 GTTAATGCGTGTGACAAAGCTATACCGTCAATCTTCAATGCTATTTGCTGTCTAATA 4385  
 Db 4222 GTGAATGCGTGTGATCAAGCTATACCGTCAATCTTCAATGCTATTTGCTGTCTAATA 4281  
 Qy 4386 TTTTGGCTAATTTTGGCTATATGGGTGTACAGCTTTTGTGGAATAATTTTAAAGTC 4445  
 Db 4282 TTTTGGCTAATTTTGGCTATATGGGTGTACAGCTTTTGTGGAATAATTTTAAAGTC 4341  
 Qy 4446 GAGACATGATGCGACAAAGCTCAGCCAGAGATCATACCAAAATCGCAATGCGTCGAG 4505  
 Db 4342 AAAGATGATATGACATGTGTCTGAGCCATGATATCAACGAATCGTATGCTGCAAA 4401  
 Qy 4506 AGCAGAACTACACGTGGTGAATTCAGCAATGAATTTGCATCATGATGATGATGCGGTAT 4565  
 Db 4402 AGTGAATCTACACCTGGGAATTCGCGCATGAACTTCGATCATGATGATGATGCGGTAT 4461  
 Qy 4566 CTGTGCTTTTCCAAAGTGGCCACTTCAAGGCTGTGATACAAATCATTAAGATGCTATC 4625  
 Db 4462 CTGTGCTTTTCCAAAGTGGCCACTTCAAGGCTGTGATACAAATCATTAAGATGCTATC 4521  
 Qy 4626 GATTCAAGAGAGTGAACAAGCAACCAATTCGTGAAGCAACATCTACATGATTTATAT 4685  
 Db 4522 GATTCAAGAGAGTGAACAAGCAACCAATTCGTGAAGCAACATCTACATGATTTATAT 4581  
 Qy 4686 TTGCTATTTCTCATATTTGATTCCTTTTCACTCACTCAATCTGTGATTTGATGCTATC 4745  
 Db 4582 TTGCTATTTCTCATATTTGATTTGATTCATTTTCACTCACTCAATCTGTGATTTGATGCTATC 4641  
 Qy 4746 ATTGATATTTTATGAGCAAAAGAAAGAGAGTGTGATCTTATGAATGTTCAATGCA 4805  
 Db 4642 ATTGATATTTTATGAGCAAAAGAAAGAGAGTGTGATCTTATGAATGTTCAATGCA 4701  
 Qy 4806 GAAGATCGAAGAAAGTACTATATGCTATGAAAAAGATGGGCTTAAGAAACCAATTAATA 4865  
 Db 4702 GAAGATCGAAGAAAGTACTATATGCTATGAAAAAGATGGGCTTAAGAAACCAATTAATA 4761  
 Qy 4866 GCCATTCGAGACCAAGGTGGCGACCAACAGCAATAGTCTTTGAATGATGAACGATGAG 4925  
 Db 4762 GCCATTCGAGACCAAGGTGGCGACCAACAGCAATAGTCTTTGAATGATGAACGATGAG 4821  
 Qy 4926 AAATTCGATATATATATGTTATGCTATGCTGTGAAGATGTTCAACCATGACCTCGAT 4985  
 Db 4822 AAATTCGATATATATATGTTATGCTATGCTGTGAAGATGTTCAACCATGACCTCGAT 4881  
 Qy 4986 CGTTACGATGCGTGGACACGATATACGCGTCTAGACTATCTCAATGCGATATTCGTA 5045  
 Db 4882 CGGTACGATGCGTGGACGCTACACGATATCTCTCGACAAATCAATGAGATTTGCTA 4941  
 Qy 5046 GTTAATTTGAGTTCGAAATGCTATTAATAAATATTCGTTTACGATATCACTATTTAT 5105  
 Db 4942 GTTAATTTGAGTTCGAAATGCTATTAATAAATATTCGTTTACGATATCACTATTTAT 5001  
 Qy 5106 GAGCAGTGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5165  
 Db 5002 GAGCAGTGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5061  
 Qy 5166 AGCAGATTTATCGAAGATATCTGCTGCGCGACCTGCTCCGAGTGGTGGTGGCG 5225

Db 5062 AGCAGATCAATGAGAGATTTTGTATTCGCGACCACTGCTCGGTGTGTGAGATGGCC 5121  
 Qy 5226 AAAGTGGCGCTGTCTTCCACTGTGAGAGGAGCCAAAGGCAATTCGACACTGCTTTC 5285  
 Db 5122 AAAGTGGCGCTGTCTTCCACTGTGAGAGGAGCCAAAGGCAATTCGACACTGCTTTC 5181  
 Qy 5286 GCGTTGGCGATGAGTGGCGCGCGCTGTGAAACATGCGCTGCTGCTGCTGCTGCTGCTG 5345  
 Db 5182 GCGTTGGCGATGAGTGGCGCGCGCTGTGAAACATGCGCTGCTGCTGCTGCTGCTGCTG 5241  
 Qy 5346 TTCAATCTTGGCATTTTTCGCGATGCTGCTTCAATGCACTGAGAGAGAAAGCGGCAAT 5405  
 Db 5242 TTCAATCTTGGCATTTTTCGCGATGCTGCTTCAATGCACTGAGAGAGAAAGCGGCAAT 5301  
 Qy 5406 AACGAGCTTACAACTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTCAATGCTG 5465  
 Db 5302 AATGCTGTATTAATTTTAAACATTTGGCCAAAGTATGATTTGCTGTTTCAATGCTG 5361  
 Qy 5466 ACCTGAGCGGTTGGGATGCTGTACTGAGCGCCATTTCAATGAGAGAAAGATGGCATCA 5525  
 Db 5362 ACCTGAGCGGTTGGGATGCTGTACTGAGCGCCATTTCAATGAGAGAAAGATGGCATCA 5421  
 Qy 5526 CCCGACAGCGACAAAGGCTATCCGCGCAATTTGCTTCAAGCACTGTTGATTAACGTTT 5585  
 Db 5422 CCCGACAGCGACAAAGGCTATCCGCGCAATTTGCTTCAAGCACTGTTGATTAACGTTT 5481  
 Qy 5586 CTCTCTCTATACCTGATTAATGATTTTGTATGATTAATGATTAATGATTAATGATTAAT 5645  
 Db 5482 CTCTCTCTATACCTGATTAATGATTTTGTATGATTAATGATTAATGATTAATGATTAAT 5541  
 Qy 5646 CTGAGAACTATATCTAGCGCCAGCGAGAGCTGCAAGAGGCTCAACCGAGAGAGACTAC 5705  
 Db 5542 CTGAGAACTATATCTAGCGCCAGCGAGAGCTGCAAGAGGCTCAACCGAGAGAGACTAC 5601  
 Qy 5706 GACATGATATGATGATCTGCGACCAATTCGATCCGAGAGGCAACCCAGTATACATGCTAT 5765  
 Db 5602 GATATGATATGATGATCTGCGACCAATTCGATCCGAGAGGCAACCCAGTATACATGCTAT 5661  
 Qy 5766 GATGATGATGATGATCTGCGACCAATTCGATCCGAGAGGCAACCCAGTATACATGCTAT 5825  
 Db 5662 GATGATGATGATGATCTGCGACCAATTCGATCCGAGAGGCAACCCAGTATACATGCTAT 5721  
 Qy 5826 AAGTAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5885  
 Db 5722 AAGTAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5781  
 Qy 5886 GACATCTGCAAGCGCTTACGAAAGACTTCTTTCGCGGAAAGGCAATCCGATAGAGAG 5945  
 Db 5782 GATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5841  
 Qy 5946 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6005  
 Db 5842 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5901  
 Qy 6006 TCAAGCTGTGGCGCTGACGCGTGAAGATGATGATGATGATGATGATGATGATGATGATG 6065  
 Db 5902 TCAAGCTGTGGCGCTGACGCGTGAAGATGATGATGATGATGATGATGATGATGATGATG 5961  
 Qy 6066 AAGCACAAGGCGCGCGCGAGAGGATGCTTGTGAGCGGATGACGATCATGCGAT 6125  
 Db 5962 CGTTACAAAGATGCG----- 5976  
 Qy 6126 GCGGATATCCGATGCGCGGAGACCGCGCGCGCGATGAGCAACGAGCGGATGCGCC 6185  
 Db 5977 CCAACCGAGAGGATGATGAGAGGCGAGAGCGCGCGCGATGAGCAACGAGCGGATGCGCC 6036  
 Qy 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6245  
 Db 6037 GAGGATGAGAGCGGAGAGGCGGCGGCGGATGATGATGATGATGATGATGATGATGATGATG 6096  
 Qy 6246 AATGTAATATGCTCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 6305  
 Db 6097 GAGGATGAGAGCGGAGAGGCGGCGGCGGATGATGATGATGATGATGATGATGATGATGATG 6156

QY 6306 GCGGCGGCGACGACGCGGGAAGTCCCGGAGCGGCTAGCCCGCGGCGACGACCGCC 6365  
DB 6157 GGTGGGCGGCGCCCTTGTATGCTGGGCTGTGTATGAGGCGGCGATGATGCGCCCGCCAAACGGCC 6216  
QY 6366 GTTCTGTGGAGAGCAGCGGCTGTGTAGAGAGAGAGCGGCGACAGGTTGTCATCCACTCG 6425  
DB 6217 GTACTGTGTGAAGGCGATGTTTGTATCAAAAACGGTGTATAGGTTGTATACACTCG 6276  
QY 6426 CGATCGCGGACGATCAGTCGCGCAGCGGCGGATGTCTGA 6464  
DB 6277 AGATCGCGGACGATACATCAGAGCGGCGGATGTCTGA 6315

RESULT 3  
US-10-152-319A-1723  
; Sequence 1723, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Blashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1723  
; LENGTH: 6586  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_019266  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(6586)  
; OTHER INFORMATION: n = a or c or g or t  
US-10-152-319A-1723

Query Match 15.7%; Score 1019.4; DB 17; Length 6586;  
Best Local Similarity 52.8%; Pred. No. 1.5e-272;  
Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;

QY 186 CGAAGAAAAAAGAAAAATCCGATATGATGAGAGAGAGAGATGATGATCCAGAA 245  
DB 268 CTCGAAAGAACCAAGAGGCGATGCGACCGCGAGAGCGATGAAGAGAGAGAGCC 327  
QY 246 CCGGATCTTACACTTGAACAGGCGTGTGCCAATCTGTTGATTTGACAGGCGAGCTTCCG 305

DB 328 AAGCCAAACAGTACCTGAGGCTGGGAAAGATTGCTTTCATCTACGGGACATCCCG 387  
QY 306 CCGAATTTGGCCCTCCACTCTCTCGAGATATCGATCCCTTACAGCAATGATGACA 365  
DB 388 CAAGGCTGTGTTCCGGTTCCTCTGGAGGACTTGAACCTTATCTATTTGACGAGAAAAC 447  
QY 366 TTCTGATTTGTAAGCAAGAAAGATATTTTGGCTTTCTGCAATCAAAAGCAATGTGG 425  
DB 448 TTTGATGATTTAAACAGAGGAAACTCTTCAGATTTAGCCACACTGCTCTTGAC 507  
QY 426 ATGCTGATCCATTCATCCGATCGTGTGGCCATTTACATTCATGATGATCATTAT 485  
DB 508 ATTTTAAGCCCTTTTAACTGATTAAGAAATAGCATTAATTTGATTAACATCAGTT 567  
QY 486 TTTTCCATTCATCATCCACCAATCTCTGCACTGATCATCTGATGATTAATGCCACA 545  
DB 568 TTCAGCATGATCATCATGATGACCACTCCGACCAACTGTGTGATGACCTTTAGTAAC 627  
QY 546 ACGCCACGCTGATGATCCACTGAGTG---AATTCACCGGAACTTCACATTTGAATCA 602  
DB 628 CTTCCAGAAATGTCAGAGATGTGAGTACATTCACAGGATTTACATTTGATATCA 687  
QY 603 GCTGTTAAAGTATGAGCAGAGGTTTCAATTTATGCCGTTTACGATCTTGAAGATGA 662  
DB 688 CTAGTCAAAATATCATGCAAGAGGTTTCTGCAATGACGCTTCACTTCTTGGAGACCG 747  
QY 663 TGGAAATGCTGACTCTGTGATTAATGCTTATGCTTATGACCAATGGGATTAATTA 722  
DB 748 TGGAACTGTTAGACTTCACTGATCATGATGAGGATATGATGACAGAGTTTGTGACCTG 807  
QY 723 GGTAAATCAGACCCCTGGAAGTTTGGGCTGCGAGGCTTAAACCGTAGCAAT 782  
DB 808 GGCATGTCAGCGGTGAGACATTCAGGCTTCTCGAGCTTTGAAACATATCTCTGTA 867  
QY 783 GTCCAGGCTTGAAGACATCTGCGCGCCCTCATGATCGGTGAGAGATCTGCGCAT 842  
DB 868 ATTCAGGCTGTAAGACATCTGCGCGCCCTTAATCAGATCGGTGAAGAGTGTGCGAG 927  
QY 843 GTGATTAATCTGACCATGTTCTTCCCTGTGCTGTGCTGCTGATGAGGCTTACAGATCTAT 902  
DB 928 GTGATGATCTGACAGTGTCTGCTGAGTGTCTGCTGCTGAGGCTTGTGAGGCTTCTTC 987  
QY 903 ATGGGCTGTCTACCGAGAGTGCAT-----CAAGAAATTCGCGCTGACCGGTTCC 953  
DB 988 ATGGGAACTTCGAAACAGTGTGTCTGTGCGCCATTAATCTTACAGAGGATCACTG 1047  
QY 954 TCGGGAATCTGACCGACGAGAACTGGGACTATCAATCGCAATGATCTCCATTTGAT 1013  
DB 1048 GAGAACGCGACAGAGGCTTTGACTGGGAGGAAATATATCAACATTAAGAACTTTTAC 1107  
QY 1014 TCCGAGAGACAGAGGATCTCATTTCCGTTATGCGGCAATATATCCGGTCCGGGCAATGC 1073  
DB 1108 ATGTTCTCTGGCATCTGAACCTTCTCTCGGGAACAGTTCTGATGCTGGGCAATGC 1167  
QY 1074 GACGACGATTAAGTGTGCTGCGAGGAGTTTGTCCGAATCCGAATTAATGCTTACACAGC 1133  
DB 1168 CAGAGGATTTCAATGATGAAG---CAGGAAGAAACCCCACTACGTTTACACAGC 1224  
QY 1134 TTGATTCGTTGAGATGAGGCTTCTGTCGCGCTTCCGCTGATGACACAGACTTCTGG 1193  
DB 1225 TTGACACTTCACTGAGGCTTCTTGGCATTAATCCGCTTATGACCAAGACTTATGG 1284  
QY 1194 GAGGATCTGATCAGCTGTGTGCGCGCGCGGACCAATGACATGCTGTTCTTATTA 1253  
DB 1285 GAGAACTTATACACTGACCTTACGAGCGCTGGGAAACCAATATGATATCTTTTGTG 1344  
QY 1254 GTCATCATCTTCCPAGTTTCAATCTTATCTGATGATTTGATTTGACCTTTGTCAGT 1313  
DB 1345 TTGCTCATTTCTGTGGTCTTTCTTATCTGTAACCTTATTTGCTGTGTGATG 1404  
QY 1314 TCGTATGACGAATTCGAAAGAGGCGGAAAGAGAGGCTTCCGAAAGAGAGCGATTA 1373

Db 1405 GCTTATGAGAA---CAGAACGAGCAACCTGAGAGAGAGCAAGCAAAAGAGC----- 1457  
Qy 1374 CGTGAAGGGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCG 1433  
Db 1458 CGAGTTCAAGGCAATGCTGAGAGCACTCAG---AAGCAGAGAGAGAGGACACAGGCT 1512  
Qy 1434 CAGGCTCAGGAGAGAGCGGATGCGGCTGCGCGCAAGAGAGCTGCACTGCTCGGAAATG 1493  
Db 1513 GCTGGAATGGCCACTTCAGCGGGGCACTGCTCGAGAG---CGCATGGAAGAGAGAGG 1569  
Qy 1494 GCCAAGACTCCGACCTATTCTTGCACTGAGCTATGAGCTATTTGTTGGCGGAGAGGCG 1553  
Db 1570 GAAGATGGGTAGGCTCTCCAGAGAGCTCTTCTGAATGCTTAACCTCAGTTCCAGAGC 1629  
Qy 1554 AACCATGCAACAAAGAGAGATGTCATTCGAGAGCTGAGAGTGAAGTCCGAGTCG 1613  
Db 1630 GCGAAGGAGCGGCGAA-----CCGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1673  
Qy 1614 GTGAGCGTTATCAAAAGCAACAGACCTTACACAGAGACCAAGCTAACCAAGTTGCT 1673  
Db 1674 GCTCTGAGAGCGAG 1720  
Qy 1674 AAGAGAGACGACATCTTATCTTACCTGCTGACCGTTTAACTAGCGAGGAGATCA 1733  
Db 1721 CAGAGTCGAGAGAGGCTATGAGAGAGAGGCTTCCGCTCCAGACCAAGAGATAGGGA 1780  
Qy 1734 CGTAGTTCTCAAGTACAGATACAGATACGAGAGAGAGCTGCGCTTGTGATACCGGATAGC 1793  
Db 1781 GGAAGTTTTCATCATGATGATGATGCTGCTGACAGATTCAGAGCTCGGCTTCTCTCC 1840  
Qy 1794 GATGCTAAGCCATGTTGTTATGTCACATATGAGATGCGGAGAGACTTGCCTTATGCC 1853  
Db 1841 GACATTAACAGAAAG 1899  
Qy 1854 GAGCACTGGAATGCCCTGACCCGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913  
Db 1900 GGGCTGCGAGATG-----AGTTCCAGAGAGATGAACAGAGAGAGAGAGAGAG 1947  
Qy 1914 TACTATGAGCATTAAGCTTCCGACACTCATCTGATTAAGCTGATCAGTCCGAAATAGC 1973  
Db 1948 AGCAGAGGCGGCGTGAATGCTCTTCTTATCCGATCCGCGCGGAGAGCGGAGAGAGC 2007  
Qy 1974 TATACCTCAACATGAGCTTACTCGGCGGAGATGCGGCTGATGAGAGAGAGAGAGAGC 2033  
Db 2008 TACAGTGGCTACAGCGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
Qy 2034 AAGAGAGCAAAATGGCGCAACCGCAACACAGCAATCAATGATGGGCGGAGAGAGAG 2093  
Db 2068 CGGCGAGCGTGAAGCGCAAGCA-----CGGTGAGCTGCAAGCGC 2109  
Qy 2094 GGCACCACTGTCTGAGACCAATCAAGCTCGATCATGCGGAGCTACGAAATGGCGCTG 2153  
Db 2110 G-----TAGTCTCACTATCGGCGCGGCTGACATCGG 2144  
Qy 2154 GAGTGAACGAGCAAGAGCTGCAAGATTAACATCATGAGCAATCCTTTATGAGAGCGGCTC 2213  
Db 2145 GCGGCTCTGCTGAGTGAAGTGA---GATTAAGGAGCTTACGAGAGAGAGAGAGAG 2193  
Qy 2214 CAGACCAAAACGATGATGATGATGAAG---ATGATGATGCTCTGAATGAGATCATGAGAA 2270  
Db 2194 ACGACTAGAGGTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2253  
Qy 2271 CAGGCGCGTGTGCGGACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2330  
Db 2254 CTCGCCCTCTACGAGAGAGAGAGAGAGAGATCAACAGCATTAAGAGAGAGAGAGAGAG 2313  
Qy 2331 ACAGAGAGAGATGAG 2390  
Db 2314 CTATGAG 2363  
Qy 2391 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2449  
Db 2364 TAAAGTTGCGCAACCTTCTCATCTGAGAGAGTCAACCCCTAATGATTAAGAGAGAGAG 2423

Qy 2450 GTGGATTCGCTCATTCGCTTTCGATCCCTTGTGAGAGCTTTCATCACGCTGATTTGT 2509  
Db 2424 GATGTAATCTTAATCGTATGAGAGCTTTTGTGAGCTTACCATTCATCATCTGATTCGT 2483  
Qy 2510 GGTCAACAGATGTTTCAATGAGAGATGATCAACAGATATGAACAAGAGATGAAGAGCGGT 2569  
Db 2484 TGTGAATAGCTATTTATGAG 2543  
Qy 2570 GCTCAAG 2629  
Db 2544 CTGGCGGTAGAGATCTGAGTGTCAACGGAGATCTTCAACGCGGAGAAATGTTTCAAGCT 2603  
Qy 2630 AATGGCAATGAG 2689  
Db 2604 CATAGCCATGAG 2663  
Qy 2690 CGTGGCGCTATCGCTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2749  
Db 2664 TGTCTCCCTCATGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2723  
Qy 2750 TTCTTGTGATGCTGCTGATTTCAAACTGGCCAGTCTTGGCCACATTAATTTACT 2809  
Db 2724 GTCTTCCGAGCTCTCGAGAGCTTCAAGCTGGCCAGAGCTTGGCCACCTGAGAGAGCT 2783  
Qy 2810 CATTTGATTAATGAG 2869  
Db 2784 GATCAAGATCAATCGAG 2843  
Qy 2870 TATCATCTTCACTTTGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2926  
Db 2844 CATGCTTATCATCTTCCCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2903  
Qy 2927 TCACAG 2986  
Db 2904 CGTCTGAAGATCAACAG 2963  
Qy 2987 CAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3046  
Db 2964 CTCTTCTCATGCTCTTCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3023  
Qy 3047 CATGTAAGT---GGCAGATCTGTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3103  
Db 3024 CATGAGAGTGGCGGAG 3083  
Qy 3104 CAATCTTGTGATCTTAACCTTTTCTTACCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 3163  
Db 3084 CAACCTGT 3143  
Qy 3164 CTATACAGCGCGAGCTGCGATACAGATACAGATTAAGATTAAGATTAAGATTAAGATTA 3223  
Db 3144 CTGTGGCGGAG 3179  
Qy 3224 TGGCGATTTAAAGTTGGGTTAAGCTTAATGCTGATTTTCAAGTTAATACGTAA 3283  
Db 3180 ----- 3179  
Qy 3284 CAATGTAACAAATCAATTAAGATGATCAACATCAGGTGAGAGAGAGAGAGAGAGAGAG 3343  
Db 3180 -----CTGAGAGATCAGT 3194  
Qy 3344 GATTGAGAGAGAGAGAGAGATGATGATCAACAGATGAGAGAGAGAGAGAGAGAGAGAGAG 3403  
Db 3195 GATTCGATCAAG 3254  
Qy 3404 CAGAGCGCTCATCAAG 3463  
Db 3255 TCATTTAAG 3314  
Qy 3464 TCGAGTGAATTCAGATACAG 3523  
Db 3315 GGCCAATGATGAG 3374

QY 3524 TCTAATTAACGACGATGTTGGCACTCACTTAACCAACGAACATTAAGATGGAACA 3583  
DB 3375 GAAACGGAAACGGAACCAACGACGCGCATCGCAGACACGTGAGAAATATCATTCACGA 3434  
QY 3584 CGAGCTAAACCAATAGAGGTTTGTCTTACGAGCAAGACATCGCAGCATTAATCATTA 3643  
DB 3435 GGAACCA-----TGTCTTCACTTAACAC-----CCAAACCTGACCGTCC 3475  
QY 3644 TGTAGCCATTAAGATTCGACCATTCAGAGCAAGACCAACAGGAGCGCCGAGACAT 3703  
DB 3476 GGGTGGCCATTCGTGTGGGGAATC-----TGACTTCAGAAACCTCAACAGAGATGT 3530  
QY 3704 GGAAGGCGAGAGAAAGCGCAGCCGACGAAAGAGATTAGTCTCGAAGAGAACTGGA 3763  
DB 3531 TAGACGATTCAGACCCCTGAAAGGCAAGATTA-----ACTGACGATTAACAGCTC 3584  
QY 3764 CGAGGAGGCGAATGCGAGGAGGCGCCCTCGACGGGATATCATTAATTCATGACACGA 3823  
DB 3585 CTGAGAAAGAAATGACATCGACATCAAGCTTGAGGTGAGAAAGTTCCCGTGAAGCAC 3644  
QY 3824 CGAGATATATCTGATGATATTCAGCTGATGCTGCCCGCATTCGATTAAGAAAT 3883  
DB 3645 TGAAGATATCTG-----ATCCGAGCGCTGCTTTACAGAGGTTGCGTCAGCGGT 3698  
QY 3884 TCCGATCTTAGCCGATGACATGACGCGCTTCGCAAGAGATGGGCGCAATTAAGACT 3943  
DB 3699 CAAGTGTCCAGGTCAACATCGAGAGAGACTAGGCAAGTCGTGTGGATCTTGCGAA 3758  
QY 3944 GAAACCTTTCAATTAATTAATAAATATTTTGAACAGCTGTTATCATTAATTAAT 4003  
DB 3759 AACCTGCTTCTCATTCGTGAGACAAATGTTTGAAGACTTCATCATATCTTAATTC 3818  
QY 4004 AATGAGTACTTACGCTTTGGCATTTAGAAATGATACATTCGCCAAGAACCCATCTGCA 4063  
DB 3819 GCTCAGAGATGGCGCCCTGCGCTTTGAGCAATCATCATGAGCAGAGAAACCATCCG 3878  
QY 4064 GGAATTTTATCATTAATGAGCAAGATTTAGGTTATGCTTATCTCTTGAAATGTTAT 4123  
DB 3879 CACCATCTGAGATATGCGACAGAGTCTTCACTTACATCTTCACTTGAGATGTTCT 3938  
QY 4124 CAAGTGTGGCGCTGCGCTTCAAAAGTATCTTCAACCAACGCGTGTGTGCTCGATTT 4183  
DB 3939 CAAGTGAACAGCTTACCGCTTCTGCAAGTCTTCAACCAAGCGCGTGTGTGAGCTT 3998  
QY 4184 CGTATGTCATGATGATCGCTTATCAACTTCGCTTCACTGTTGAGAGCTGTGTAT 4243  
DB 3999 CCTCATTTGGCTGTCTCTTATGACAGCTTATAGCTAATGCCCTGGCTACTCGAATC 4058  
QY 4244 TCAAGCTTCAAGCATATGGAAGCTTAAGAGCACTGAGACCATAGTGCATGTCGCG 4303  
DB 4059 AGGTGCATTAAGTCCCTTAGAGCCCTAAGAGCTTGAAGCCCTTAAGAGCTTATACG 4118  
QY 4304 TATGACAGGCAATGAGGTCGTCTGTTAATGCGCTGTGACAAAGCTATACCTCATCTTCA 4363  
DB 4119 ATTGGAAGGATGAGGGTGTGTGAGATGCTGTGTGTGGGCGCATCCCTCATCATGAA 4178  
QY 4364 TGTGCTATGCTGTCTTATATTTTGGCTAATTTTGGCTAATTTGGGTGTACAGCTTT 4423  
DB 4179 TGTGCTCTGTGTGTCTCATCTTCTGCTGATTTTAGCATCATGGAAGTTAACTGTT 4238  
QY 4424 TGTGCGAAATATTTTAAGTGC---GAGGACATGAATGGGCGAAGCTGACCGCAGAT 4480  
DB 4239 TGGCGGGAATACCACTATGCTTTAATGACATTTCTGAATTCGGGTTCCGAATCGATAT 4298  
QY 4481 CATACCAATTCGCAATCGCTGCGAG-----AGCGAGAACTACACGTG 4522  
DB 4299 TGTCAACAATTAACGAGCTGTGAGAGCTCATGAGGCGCAACGACGAGATCCGATG 4358  
QY 4523 GGTGAATTCAGCAATGAAATTTTCATGATGATGATGATGATGATGATGATGATGATG 4582  
DB 4359 GAAAGATGTCAAGATCAACTTTCAGATGTCGAGAGGAGTACCTGCGCTTCTTCAAGT 4418  
QY 4583 GGCACACTTCAAGGCTGATATGAATCATGAAGATGCTATCATGATTCAGAGAGTGA 4642

DB 4419 GGCACACTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4478  
QY 4643 CAAGCAACCAATTCGTGAACGACATCTCATGATTTATTTATTTTATTTATTTATTTAT 4702  
DB 4479 CGAGGAGCTGATCGAGGCGCAACATCTACATGATGATGATGATGATGATGATGATGAT 4538  
QY 4703 ATTGATTCCTTTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4762  
DB 4539 CTTCGCTCTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4598  
QY 4763 GCAAAAGAAAAAGCAGGTGATCTTGAATGTTCAATGACAGAAATCAGAAAAAGTA 4822  
DB 4599 GAGAAAGAAAA---GTTTGAAGTCAGAGACATCTTCAATGACAGAGAAACAGAAAGTA 4655  
QY 4823 CTATATGCTATGAAGAAAGATGGCTCTTAAACCACTTAATAAGCATTTCCAGGCGAAG 4882  
DB 4656 CTACATGCTATGAAGAAAGCTGGCTCCAAAGAGCAGAAAGCCCATCCCGACCTT 4715  
QY 4883 GTGGGACCAACAGCAATGCTTTGAATAAGTAACCGTAAGAAATCGATATATCAT 4942  
DB 4716 GAACAAAATCGAAGGATGCTTTGATTTGCTCACTCAACAGCTTTGACATTTGAT 4775  
QY 4943 TATGTTATTCATGCTGAGACATGTTCACTGACCTGATCGTTAGATGCTGCGA 5002  
DB 4776 CATGATGCTCATCTGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 4835  
QY 5003 CACGATTAACGGGCTCTTACATCTCAATGCAATTCGATGATTTTCAAGTTCGA 5062  
DB 4836 CGAGATGAGAAACATTTCTTACGATTAATCTGCTTGTGATCTTCTTCACTGCGA 4895  
QY 5063 ATGCTATTAATAAATATGCTTTACGATATCACTATTTATTTAGCCATGAAATTTAT 5122  
DB 4896 GTGTGCTCAAAATGTTTGTCTTGAACACATCAATTTACCATTTGGTGAATCTT 4955  
QY 5123 TGAATGATGATGCTTATTTATTCATCTTACGCTTTGATCTTACGATATTTAGAA 5182  
DB 4956 TGACTTTGTGTGATCATCTCTCATGATGAGAAATGTTCTGCGATATCATGAGAA 5015  
QY 5183 GTACTTGTGTGCGCCACCTGCTCGGATGATGATGATGATGATGATGATGATGATGAT 5242  
DB 5016 GTACTTGTGTGCTCCCAACCTTATCCGATTAATCCGATGAGCCGATTTGGGCGCATCT 5075  
QY 5243 TGAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5302  
DB 5076 GCTGTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5135  
QY 5303 GCCGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362  
DB 5136 GCCGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195  
QY 5363 CGGATGATGCTTTTATGACATGTAAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 5422  
DB 5196 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5255  
QY 5423 CAAGACCTTTGGCAGAGCATGATCTGCTCTTCAATGATGATGATGATGATGATGATGAT 5482  
DB 5256 CGAGAAATTTGGAACAGCATGATCTGTTTTCAGATCAACAGCTGCTGCTGCTGCTGCT 5315  
QY 5483 TGTGTATGAGAGGCAATATCA-----TGAGAAAGCATGCGATTCACCCGACAG 5533  
DB 5316 TGGCTGCTGCTGCTCAATCTGAAACGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCT 5375  
QY 5534 CGACAAAGGATATCCGGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 5593  
DB 5376 AGGAGATGCTTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5435  
QY 5594 ATACCTAGTTATTAAGCTTTTATGATTTATTAATGATGATGATGATGATGATGATGATG 5653  
DB 5436 CTATATCATATCTCTCTTCTGATTTGTGGAACATGATGATGATGATGATGATGATGATG 5495  
QY 5654 CTATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5713

```

Db 5496 CTTGACGCTGGCCACCGAGAGAGCGCCACCTCTGAGTAGAGATGATCGACCTTT 5555
Qy 5714 CTTAGAGATCTGGAGAGATTCGATCCGAGAGGAGCCAGATACATACGCTATGATCACT 5773
Db 5556 CTTAGAGATCTGGAGAGAGATTTGACCCAGACGCCACCAAGTTCACTGAGTACTGAACT 5615
Qy 5774 GTCCGAATTTCTGGAGACTGAGAGCCCGCTGAGATCCACAAACGAAACAAAGTACAA 5833
Db 5616 GGCAGACTTTGGCCAGCGCCCTGGAGACACCGCTCCGAGATACCCAAAGCCCAACATGGA 5675
Qy 5834 GATCATATGATGAGACATACCATCTGTGCGGAGTACCTCATGTACTGCGATCCCT 5893
Db 5676 GCTCATGCGCATGAGCTGCGCATGATGAGAGATGCAATCCACTGCTTGAATCATCT 5735
Qy 5894 CGAGCCCTTACGAAAGACTTTTGGCGCGAGAGGCAATCCGATAGAGAGAGGCTGA 5953
Db 5736 TTTGGCTTCAACAAAGCAGATCTGGAGAGACATGAGGAGTTCGATCTGCGGCACCA 5795
Qy 5954 GATTGCTGAG-----ATAGCGGCGCGCCCGGATACGAGAGGCTACGAGCCGCTCATC 6007
Db 5796 GATGAGAGAGCGGCTTCGTCGATCCATCTTCCAAAGTGTCTTACGAGCTTATACAC 5855
Qy 6008 AACGCTGTGCGTCAAGCTGAGAGTACTGCGCCGCGCTAAATCCAGCAGCGCTGCGAAA 6067
Db 5856 CACTCTGGCGGCAAGAGAGAGGTGTCTGCAAGTGTCTCGACAGCGTGCCTACAGGGG 5915
Qy 6068 GCACAGGCGCGCGCGG 6084
Db 5916 ACACCTTGCTAGGCGGG 5932

```

## RESULT 4

```

US-10-377-139-14
; Sequence 14, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jjiang, Youxiong
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seg. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6586
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6535)..(6579)
; OTHER INFORMATION: n is any nucleotide: a, c, g, t (u)
US-10-377-139-14

```

```

Query Match 15.7%; Score 1019.4; DB 18; Length 6586;
Best Local Similarity 52.8%; Pred. No. 1.5e-272;
Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;

```

```

Qy 186 CGCAAGAAAAAACAAGAAATCCGATATGATGACGAGAGAGATGAAGTTCACAA 245
Db 268 CTCAAGAAACCAACAAAGGCGATGCGACCCGCGAGACGATGAGACAGAGAGCC 327
Qy 246 CCGGATCTTACCTTGAACAGGATGTGCAATACCTGTTGATTCAGAGGAGAGCTTCCG 305
Db 328 AAGCAAAACAGTACCTGAGAGGCTGGAAAGTTTGCCTTTCATCTACGGGGAATCCG 387
Qy 306 CCGGAATTGCGCTTCATCTCTTCGAGAGATTCATCTTACTACAGAGATGTAAGCA 365
Db 388 CAAGGCTGTTGGGTTCCCTCGAGGACTTGAACCTTACTATTGACGCAAGAAAAC 447

```

```

Qy 366 TTCCAGTTGTAGCAAGAAAGAAATATTTTCGCTTTTCGATCAAGAAAGATGTGG 425
Db 448 TTTGTAGTATTAACAGAGAAAACCTCTTCAGATTTATGTCACACTGCTGTGAC 507
Qy 426 ATGCTGATTCATTCATTCGATACGTGCTGCGCATTTTACATTCATGATCATTATTA 485
Db 508 ATTTAAGCCCTTTTAACTGATTAAGAAATAGCTATTAATTAATTTGATACACTGAGT 567
Qy 486 TTTTCCATTCATTCATTCACCAATTTGCTCACTGATCCGATGATTAATGCGGCA 545
Db 568 TTACAGATGATCATATGTGACATCTGACCACTGTGTGTCATCACTTTAGTATAC 627
Qy 546 AGCCCAAGGTTGAGTCACTGAGGTG---ATATTACCGGAATCTACATTTGAATCA 602
Db 628 CTTGAGATGATGTCAGAAATGTGAATGACATTCACAGGAAATTTACATTTGAATCA 687
Qy 603 GCTGTTAAAGTATGAGCAGAGGTTTCATTTTATGCCCCGTTTAAAGTATCTTAAAGATGCA 662
Db 688 CTTAGTAAATCATGCAAGAGGTTTTCGATTAAGAGGCTTCACTTCTTGAGAGACCG 747
Qy 663 TGAATTGCTGACTTGTGATGTAATGCTTTAGCTTATGTAACCATGAGTATGATTTA 722
Db 748 TGAATCTGTGATGATTCAGTATGATGATGATGATGATGATGATGATGATGATGATG 807
Qy 723 GGTATCTAGAGGCTGCGCAACGTTTAAAGGTTGCTGAGAGGCTTAAACGTTAGCAT 782
Db 808 GGCATGCTCTAGGCTGAGAACTTCAAGGTTTCTGAGCTTTGAAATCATCTGTGA 867
Qy 783 GTGCGAGCTTGAAGACATGCTGCGGCGCTCATTCGATGATGATGATGATGATGATG 842
Db 868 ATTCAGGCTTGAAGACATGCTGCGGCGCTTATTCAGTCTGATGATGATGATGATGATG 927
Qy 843 GTGATTTATCTGACATGTTTCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
Db 928 GTGATGATCTGAGAGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
Qy 903 ATGGGCGGCTCACCGAAGTGCAT-----CAAGAGTTCCCGCTGAGAGGTTCC 953
Db 988 ATGGGAACTTTCGAAACAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
Qy 954 TGCGGCAATCTGACCGACGAGAACTGAGACTATCAATCCAAATAGCTCCAAATGCTAT 1013
Db 1048 GAGAAACGACACAGAGGCTTTGACTGGGAGGAAATATCAAAATTAACAAACCTTTTAC 1107
Qy 1014 TCCAGAGACAGAGGCACTCTATTTCCGTTATGCGCAATATATCCGCTGCGGCAATGC 1073
Db 1108 ATGCTTCTGCGATGTAAGACCTTGTCTGCGGAAACAGTTCTGATGCTGGGCAATGC 1167
Qy 1074 GAGACGATTAACGTGCTGCGAGAGGTTGTGCTGCAATCCGAATTCGTAACACGAC 1133
Db 1168 CCAAGGAAATTCAGTCAATGAAG---CAGAAAGAAACCCCACTACGTTACACGAC 1224
Qy 1134 TTGATTCGTTGAGAGGCTTTCTGCTGCGCTTTCGCGCTGATGACACAGACTTCTG 1193
Db 1225 TTTGACACCTTCAAGCTGCGCTTCTTGCAATATTCGCGCTTATGACCCAGACTATGG 1264
Qy 1194 GAGATCTGACAGCTGTGTGCGCGCGCGCGAGACATGCAATGCTTTTATTA 1253
Db 1285 GAGAACTTAATACAGTACCTTACGAGCGCTGGAAACGTAATGATCTTCTTGTGC 1344
Qy 1254 GTCATCATCTTCCAGGTTCAATCTATCTGTGTAATTTGATTTGGCATTTGTCATG 1313
Db 1345 TTGTCATCTTCTGAGGTTCTTCTTATCTGTGTAATTTGATCTTGGCTGTGTGCGCATG 1404
Qy 1314 TCGATGACGAATTTGCAAGAAAGCCGAAAGAAAGAGGCTGCGCAAGAGAGCCGATA 1373
Db 1405 GCTTATAGGAA---CAGAACAGGCAACCTGAGAGAGGAGAGCAAAAAGAGG--- 1457
Qy 1374 CGTGAGCGAAGAGAGTGTGCGCGCGCAAGCGCCAGAGCTGAGAGAGCGGCAATGCG 1433
Db 1458 CGAGTTCAAGGCAATGTGAGGCAATCAAG---AAGCAGCAGAGAGGAGGCAAGGCT 1512
Qy 1434 CAGGCTCAGGAGCAGAGGATGCGGCTGCGCGCAAGAGGCTGACATCCGAATG 1493

```

DB 1513 GCTGCATGCGCCCTCAGCGGCACTGCTCGAAGA---GCGCATTTGAAGAAGAGG 1569  
QY 1494 GCCAAGATCCGACGTAATCTTGCATCAGCTATAGCTATTTGTGGCGGAGAAAGGC 1553  
DB 1570 GAAGATGGGGTAGGCTCTCCGAGAGCTCTTGAACGTCTAACTCAGATTCAGAGC 1629  
QY 1554 AACGATGACAAACAAGAGAGATGTCTATTCGAGCGTGCAGGTGAGTCCGAGTGG 1613  
DB 1630 GCCAAGGAGCGGAGAA-----CCGACGGAAGAAGAGAGAGAGGA 1673  
QY 1614 GTGAGGCTTATACAAAGACACAGCACCACACAGACACCAAGCTAACAAAGTTCCG 1673  
DB 1674 GCTCTCGAAGGAGAGAGAAAGGAGACCCGAGAAAGTCTTAA-----GT 1720  
QY 1674 AAGTAGACACGACATCTTATCTTACCTGTTCACCGTTTAACTAGCAGGAGATCA 1733  
DB 1721 CAGAGTCGGAAGCGGATATGAAGAGAGGCTTCGCGGTGCAGACAACAGGATAGGA 1780  
QY 1734 CTTAGTTCTCAAGTACAGATACGGAACGAGCGTGGCGCTTTGGTATACCCGGTAGC 1793  
DB 1781 GGAAGTTTTCATCATGAATCAGTCCGTCTCAGCATTTCCAGGCTGCCCCCTCTCTCC 1840  
QY 1794 GATCGTAAGCATTGGATTTGTCAACATATCAGATGCGCCAGACGACTTGCCTATGCC 1853  
DB 1841 GACATTAACGCAAAAGACGATCTTACGCTCCGCGGAGCCCG-GTGCGTTCCGGAGCCC 1899  
QY 1854 GACGACTCGAATCCGTCACCCCGATGTCGGAAGAAATGGGCGCATCATAGTGCCTGTG 1913  
DB 1900 GGGCTCGAGATG-----AGTTGCGAGACGATGAACAGACACGTCGAGAGAG 1947  
QY 1914 TACTATGGCATTTAGGCTTCCGACACTATCGTATACCTCGATCAGTCCCGAATATCG 1973  
DB 1948 AGGAGAGCGCGGATGATCTGCTCTTATCCGATCCGCGCGCAGCGCCGACAGC 2007  
QY 1974 TATACCTCAATGAGCATCTACTCGCGGCGATGCGCGTCATVGGCGCTCAGACATAGACC 2033  
DB 2008 TACAGTGGCTACAGCGGCTACAGCCAGTGAAGCGCGCTCGCGCATCTTCCCAAGCTG 2067  
QY 2034 AAGGAGACAAATTTGGCGAACCGCAACACAGCAATCATCAGTGGGCGCAACAAATGCG 2093  
DB 2068 CGCGCAGCGCTGAAGCGCAACAGCA-----CGGTGAGCTCTCAACGCGC 2109  
QY 2094 GGCACCACTGTGTGACACCATCAACAGCTGATCATGCGACATCAAGAAATTTGCGCTG 2153  
DB 2110 G-----TAGTGTACTCATGAGCGCGGCTCAACATCGG 2144  
QY 2154 GAGTGCACGACGACGAGCTGCGAAGATTTAAACATCATGACCAATCCTTTTATCGACCGCTC 2213  
DB 2145 GCGGCTCTGCTCGAGGCTGAATA-----GATTAAGCAGCTACGACAGCGCA 2193  
QY 2214 CAGACACAAACGCTGTTGATATGAAG--ANGTATGCTCTGTAATGACATCATCGAA 2270  
DB 2194 ACACATGAGGTGAAATTAGAGAAAGGCGCTGATCTCTTTAGTTTCTATGACCAA 2253  
QY 2271 CAGGCGCTGTGGGACACATCGGCGCAAGGATCGCGGTCTCCGTTTACTATTTCCCA 2330  
DB 2254 CTGCGCTCTACGAGCGAAGAGCAAGATCAACAGATTAATGACGCTGTCACAAACAG 2313  
QY 2331 ACAGAGCAGATACGAGATGAGCGGACGTTCAAAACAAGGCACTCGAATGATCTTC 2390  
DB 2314 CTAGTGGAGAGCTGGAAGA-----GTCTCAGAGAAAGTCCCAACCGTGTGTA 2363  
QY 2391 AAGGACATCATGTGTTTTGT-GTGTGGACCTGTGTGGGTTTGTGTAATTTCAAGA 2449  
DB 2364 TAAGTTTGCACAACTTTCTCATCTGGAGGTGACCCCTACTGGATTAACCTGAAGA 2423  
QY 2450 GTGGGATCGCTCATGCTTTGATCCCTTCGTGAGCTCTTATCAGCGTGTGCAATGT 2509  
DB 2424 GATCGTGAATCTTATCTCATGAGCCCTTTTGAATTAAGCATCAACATCTGCAATCGT 2483  
QY 2510 GGTCAACAGATGTCATGCGCATGATCACCAAGATATGAACAGAGATGGAAGCGCT 2569

DB 2484 TCTGAATACGTAATTTATGGAATGAGGACCATCCATGACACCAAGTTGGAACGCT 2543  
QY 2570 GCTCAAGATGGCACTATTTCTTACCGCCACCTTTGCATCGAGGCCACCATAGAGCT 2629  
DB 2544 CTTGGCCGTAGGAATCTGGGTGTCAACGGAATCTTCAAGCGGGAATGTTTCTGAAGCT 2603  
QY 2630 AATGGCATGAGCCCAAGTACTATTTCCAGAGGAGTGAACATCTTCACTTCAATAT 2689  
DB 2604 CATAGCATGAGACCCCTACTATTTTCCAGAAAGCTGGAACTTTTGAAGGATTTAT 2663  
QY 2690 CGTGGCTTATCGCTATTGGAACCTGGGACTCGAGGCTGCAAGGTCTGTCCGTATTTGG 2749  
DB 2664 TGTCTCCCTCAGTTTATATGAGCTGAGTCCAGATGTGAGGCGGCTCTCAGTCTGCG 2723  
QY 2750 TTCTTTGATTTGCTGGCTGTATTCAAATGGCCAAAGCTTGGCCCACTTAATTTACT 2809  
DB 2724 GTCTTTCGACGCTCCGAGCTTCAAGTGCACAGTCTGGCCACCTGAACATGCT 2783  
QY 2810 CATTTGATTTAGGACGACCATGAGCGCTTTGGTAACTGACATTTGTACTTTGCA 2869  
DB 2784 GATCAAGATCATCGGAACCTCGTGGGTGCCCTGGCAACCTGACCTGTGTGCGCAT 2843  
QY 2870 TATCATCTTCACTTTGCGGTATGGAATGCACTGTTGGAAGATTTATCATGA--- 2926  
DB 2844 CATGCTTTCATCTTCCGCTGTGGGATGACGCTGTTGGAAGAGTTTACAAGAGATG 2903  
QY 2927 TCACAAAGACCGCTTCCGGAATGGGACCTGCGCGCTGGAATTTCAACGACCTTATGA 2986  
DB 2904 CGTCTGTAAATCAACAGAGATGCAAGCTCCCGCTGACATGAAGACTTCTTCA 2963  
QY 2987 CAGCTTCATGATCGATTCGCGGTGCTGCGGAGATGATGAGTCCATGCTGAGCTG 3046  
DB 2964 CTCTTCTCAGCTCTTCCAGTGTCTGTGGGAGTGAATGAGACCATGTGGAGCTG 3023  
QY 3047 CATGTAAGT---GGGATGTCTGTGATTCCTCTTCTTGGCCACCGTTGTATCGG 3103  
DB 3024 CATGAGATGGCGCGGCAAGGCATGTGCTCATTTGCTCATGATGTTATGATCATTTGG 3083  
QY 3104 CATCTTTGTGATCTTAACTTTCTTACCTTGTGCTTTGTGCAATTTTGGCTCATCTAG 3163  
DB 3084 CAACCTGTGTGTGAATCTATCTGCGCTTGTCTGAGCTCCTTCAAGCGAGACAA 3143  
QY 3164 CTTATCAGCGCGACCTGCGGATTAACGATCAAGTAAATATAGCGGCGCTTCAATCGAT 3223  
DB 3144 CTTGGCGGCGACAGACGAGACGAGCGGGAATGAACA----- 3179  
QY 3224 TGGCGATTTAAAGTTGGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATACGTA 3283  
DB 3180 ----- 3179  
QY 3284 CAAATTGACAAATCAAAATAGATCAACATCAGGTGAGAGGACCAACGATCAGTTG 3343  
DB 3180 -----CTGCAAGTCTCAGT 3194  
QY 3344 GATTTGAGCGAAGCATGTGTGACAAACGACTGAGCTGGCGACAGAGATCTCTCG 3403  
DB 3195 GATCGGATCAAGAGGCGGTGCTGTGACAAAGTGAAGTGAACGCTTATCAGAGG 3254  
QY 3404 CGAGCGCTCATCAAGAGGAGATCAAGACGACGCAACTGAGGTGGCCATCGGGGA 3463  
DB 3255 TCACTTCAAGACGCGGAGCGGATGAAGTGAACCCCTCGACGAGCTGTATGAGAAAGA 3314  
QY 3464 TCGGATGGAATTCAGATTCACGCGCACTGAAAGAACAAAGCCGAGAAATTCGAATA 3523  
DB 3315 GGGCAACTGATCGCCAAACACAGCGGCGTGAATTCACCGGAACGCGACTTCAGAA 3374  
QY 3524 TCTAAATACGCAACGATGATTGGCACTCAATTAACCAAGAACATATGACTGAGACA 3583  
DB 3375 GAAACGGAACGGAACCAAGCGGCAATCGGACGAGCGTGGAGAGTACATCAAGCA 3434  
QY 3584 CGAGCTTAAACATATGAGGTTTGTCTTACAGAGCAAGCACTGCGACGATTAATCTCAT 3643  
DB 3435 GAGACACA-----TGTCTTCAATTAACAC-----CCAAACGTGACGCTCC 3475

3644	UGTGTGGCCATTAAGAAATGCACCATTTCAAGAGACGCAACAAAGGACAGCCGCCAGACGAT	3703	
OY			
3476	GGGTGCCATTGTCTGTGTGGCCGAGTC-----TGACTTGCAGAACTCTAAACAGAGGATGT	3530	
Db			
OY	3704	GAAGGGCCGAGGAGAAAGCCGACGCCGACGACAGAGAGATTTAGTCTCGACGAGAACTTGA	3763
Db	3531	TAGCAAGCAATTCAGACCTCTGAAGGACGAAAGATTA-----ACTGGACGATTACAGTCC	3584
OY	3764	CGAAGAGGGCCAAATTCGAGAGAGGGCCGCTGACGGTGATATCAATTATTCATGACACGA	3823
OY	3585	CTCAGAAAGAAAGTACATCGACATTAAGCCTGAGGTGGAAGAGTCTCCGTGGAGCAAC	3644
Db	3824	CGAGGATTAATCTCGATGAATATTCAGCTGATTTGCTGCCCATTCGTAATTAAGAAAT	3883
OY	3645	TGAGGAATTAATCTGG-----ATCCGAGACGCTGGCTTTACAAAGGTTGGCTGCCAGCGGTT	3698
Db	3884	TCCGATCTTAAGCCGGTGACGATGACTCGCCGTTCTGGCAGAGATGGGGCAATTTACACT	3943
OY	3699	CAAGTGCCTGCAGGTCACATCGAGGAAGACTAGGCAAGTCCGTGGTGAGATCTTGGCGAA	3758
Db	3944	GAATACTTTCAATTAATTGAATAATTAATTTTGAACAGCTGTATCACTATGATTTT	4003
OY	3759	AACCTGCTCTCTCATTTGTGAGACAAATTTGGTTGAGCCTTCACTCATCTTCATGATTTCT	3818
Db	4004	AATGAGTAGCTTAAGCTTTGGCATTAAGAGATGATCATCTGCCAATAAGCCCATCTGCA	4063
OY	3819	GCTCAGCAGTAGGCGGCTGGGCTTTGAGGACATCTACATTGAGACGAGAAAGACATCCG	3878
Db	4064	GGATATTTTATACATATATGAGACAGAAATTTTACGGTATATTTCTTTTGGAAATGTTAAT	4123
OY	3879	CAACCATCTGAGATATGCGGACAAGAGCTTCACTCACTTCAATCTTGAGAGATGTTGCT	3938
Db	4124	CAAGTGTGTGGCGCTCGGCTTCAAAAGTGTACTTACCAACGCGGTGGTGGCTGCATTT	4183
OY	3939	CAAGTGGACAACCTCAGCCTTCCTGTCAGATTTTACCAATAGCCTGGTGTGGAGCTT	3998
Db	4184	CGTGAATGTCAATGATATCGCTTATTCAACTTCGTTGCTTCACTTGTGGAGCTGGTGAT	4243
OY	3999	CCTCATTTGTGCTGTCTCTTTAGTCAGGCTTATAGCTAATGCGCTCGGGCTTACTGGAACT	4058
Db	4244	TCAGGCTCTTAAGACTATGCGAAGGTTAAGACCTAGACCACTAAGTGCATGTCGCC	4303
OY	4059	AGTGGCCATAAAGTCCCTTAGAGACCTTAAGGCTTTGAGACCTTAAAGGCTTATACG	4118
Db	4304	TATCAGGGGCTAGAGGTCGTCTGTTAATGCGCTGTGCAAGCTTACCGTCCATCTTCAA	4363
OY	4119	ATTGGAAGGATGAGGGGTGGTGGTGAATGCTTGTGGGGGCCATCCCTCCATCATGA	4178
Db	4364	TGTGCTATTTGGTGTGTCTAATATTTTGGCTAATTTTGCATTAATGGGTGACAGCTTTT	4423
OY	4179	TGTCTGTGTGGTGTGTCTCATCTTCTGGCTGATTTTACAGATCATATGGAGATTAACCTGTT	4238
Db	4424	TGCTGGAAAAATATTTTAAATGTC---GAGGACATGAATGGGACGAAGCTCAGCCACGAGAT	4480
OY	4239	TGCGGGGGAATAACACACTACTGCTTTAATGAGACTTGGAAATCCGGTTCCAAATTCATAT	4298
Db	4481	CATACCAAATTCGCAATGCTTGCAG-----AGCAGAACTACACGTTG	4522
OY	4299	TGTCAACAATTAATAACGACTGTGGAAGGCTCATGAGGGCAACGACGAGATCCGATG	4358
Db	4523	GGTGAATTCAGCAATGAAATTTCCATCATATGTAAGTAAGCGGTAATCTGTCTTTCCAAAT	4582
OY	4359	GAAAGATGTCAAGATCAACTTTTGACAAATGTGGAGCAGGGGTAACCTGGCCCTTCTTCAAGT	4418
Db	4583	GGCCACCTTCAAAAGGCTGATATCAAAATCATGAAAGATGCTATCGATTCAGAGAGGTGA	4642
OY	4419	GGCAACCTTCAAAAGGCTGATGACATCATATATAGCGGCTGTAGATTTCCGAAAGCCAGA	4478
Db	4643	CAAGCAACCAATTTGTGTAAAGCAACATCTACATGTAATTTATTTGTAATTTTCATCAT	4702
OY	4479	CGACACGCTGTACTACAGAGGCAACATCTACATGTAATCTTCACTTCTGTACTTTCATCAT	4538

OY	4703	ATTGAGATCCCTTTTCAACATCACTGTCATTTGGTGTATTCATGTAAATTTAAAGA	4765
Db	4539	CTTGCGGCTCCTTCTTCAACCCTCAACCTGTTCAATCGGTGTCATCGACAACTTAAACA	4591
OY	4763	GCAAAAGAAAAAGCAGGTGATCATTTGAAATGTTCAATGACAGAAATCAGAAAAAGTA	4823
Db	4599	GCAGAAAGAAAAA - - - GTTTGGAGGTCAAGACATCTTTCATGACAGAGAAACAGAAAGTA	4655
OY	4823	CTATTATGCTATGAAAAAGATGGGCTCTAAAAAACATTAAAGCATTTCCAAAGCCAAAG	4883
Db	4656	CTACATGCCATGAAAAAGCTGGGGCTCCAAAGAGCCACAGAAAGCCATCCCCGACCTT	4715
OY	4883	GTGGGCAACCAAGCAATAGTCTTTGAAATAGTAAACGATAGAAATTCGATATATACAT	4944
Db	4716	GAACAAATCCAAAGGATTTGTTTGAATTTTGTCATCTCAACAGCCTTTGACATTTGAT	4772
OY	4943	TATGTTATTCAATGGTCTGAAACATGTCACCATGACCTCGATCGTAAAGATCGCTCGGA	5002
Db	4776	CATGATGCTCATTCGCTTAAACATGTTGACATGATGTTGGAGACAGACATCGACAGCA	4833
OY	5003	CACGTATTAACCGGCTCTTACACTATCTCAATGCGATATTGCTGATTTTTCAGTTCCGA	5066
Db	4836	GCAGATGAGAGAACTTTCTTACTGGATTAACCTGGCTTGTGTCATCTTTCACCTCGGA	4895
OY	5063	ATGTCATATAAANAATTCGGCTTAAACGATACATTAATTTATGAGCAATGGAATTAAT	5122
Db	4896	GTGTGTGCTCAAAATGTTTGCCTTGAACACTACTATTTTCAACATTGCTGGAAACATCT	4955
OY	5123	TGATGTAGTATGTTGTCATTTTATCCATCTTATAGCTTGTACTTATGACGATATTAATGAGAA	5187
Db	4956	TGACTTTGTGTGGTGCATCCTCTCCATTTGTGGAAATGTTCTGTGGTATATCATTTGAGAA	5011
OY	5183	GTACTTGTGTGCGCGACCTGTCTCCGAGTGTGTGGATGCGAAAGTGCGGCGGTGCT	5244
Db	5016	GTACTTGTGTCCTCCCAACCTATTCCAGATTACGATTTGGCCGGTATTTGGGCGCATCT	5075
OY	5243	TCGACTGTGTAAGGAGACGAAGGGCATTCGACACTGCTCTTGGCTTGGCGCATATCGCT	5302
Db	5076	GCGTCGTATCAAGGGGCGCAAAAGGAATCCGACCCCTGCTCTTGTGCTTAATGATATCGCT	5135
OY	5303	GCGGCGCCCTGTTCAACATCTGCGCTGCTGTTCTGTGTCATGTTCACTTTGGCATTTT	5366
Db	5136	GCGGCGCTGTCAACATCGGCGCTCTGCTCTTCTGTCATGTTCACTTTCCATTTT	5195
OY	5363	CGGCAATGCTGTTCTTCAATGACAGTGAAGAGAAAGCGGCACTTAAACGATCTAACATTT	5422
Db	5196	TGGCATGTCCAACTTCGATACGTGAAGCAAGAGGCGGCAATTGACGACATGTTCAACTT	5255
OY	5423	CAAGACCTTTTGGCAAGACATGATCTGCTCTTTCAAGTTCGACGTGACGCGGTTGGGA	5488
Db	5256	CGAACAATTTGGCAACAGCATGATCTGTTTGTTCAGATTCACAAAGTCTGCTGGCTGGGA	5315
OY	5483	TGAGTATCTGGAAGCCATTTATCAA - - - - - TGAGGAACATGCGCATCCACCGACAG	5533
Db	5316	TGGCGCTGTGCTGCCAATCTGAAACGCGCCCTGACTGACGTTGGCAAAAGACACCC	5375
OY	5534	CGACAAAGGCTATCCGCGCAATTGTGTTCAAGCAGCGTTGGAATTAAGTTTCTCTCTC	5593
Db	5376	AGGAGATGCGCTCAAAAGGAGCTGTGGGAACCCCTCGGTGGGCACTTCTTCTTTGTGAG	5433
OY	5594	ATACCTTAGTTAAGACTTTTGTATGATTAATTAATATGATCAATTGCTGTCAATCTTCGAGA	5653
Db	5436	CTTACATCATCATCTCTTCTCTGATTTGTGTGAACATGTACATCCCATCATCTTCGAGAA	5495
OY	5654	CTTAATGTCAGGCCACGAGACGTGTGAAGAGGGCTTAAACGACGACGATCTACGACATGTA	5713
Db	5496	CTTCAGGTGGCCACGAGAGAGAGCGCGCACTCTTAATGTAGGATGATCATTTTCGAGACTTT	5555
OY	5714	CTATGAGATCTGGGAGCAATTCATCTCGAGAGGCAACCGAGTACATTAAGCTATGATCAAGCT	5773
Db	5556	CTAATGATCTGGAGAAAGTTTGAACCAAGACGCCAACCAATTCATCGAGTACTGTAAAGCT	5615
OY	5774	GTCCGAATTCCTGGACGTACTGAGACCCCGCTGCAAGATCCACAAACCGAACATGTAACA	5833

```

Db      5616 GGCAGACTTTGCGGAGCCCTTGAGACACCGCTCCAGATCCCAAGCCCAACCACTCA 5675
Qy      5834 GATCATATCGATGAGACATACCACTCTGTGCGGTGAACCTCAGTACTGTGCGACATCCT 5893
Db      5676 GCTCATGCGCATGACCTGCTCCCATGTGTGAGCGGAGATCCGATCCACTGCTTGAACATCC 5735
Qy      5894 CAGCGCCCTTACGAAGAATCTTTTGGCGGAGGCAATCCGATAGAGAGACGGGTGA 5953
Db      5736 TTTGCGCTTACACAGCAAGTCTCTGGAGACAGTGGGAGGTTGACATCTCTGCGACGA 5795
Qy      5954 GATTGTGAG-----ATAGCGGCCGCCCGAGTACGAGAGGGCTACGAGCCCTCTCATC 6007
Db      5796 GATGAGAGAGCGGTGTGTGTGCAATCCATCTTCCAAAGTCTTTAGAGCTTATCAAC 5855
Qy      6008 AACGCTGTGCGTACAGGTGAGATGATGCGCCCGGCTTATCAGACGCGCTGGGAAA 6067
Db      5856 CACTTGGCGCGCAGAGAGAGAGGTGTCTGCAGTGTCTTCAAGTGTCTTACAGGGG 5915
Qy      6068 GCACAGAGCGCGCGGCG 6084
Db      5916 ACACTTGGCTTAGCGGG 5932

```

## RESULT 5

```

US-10-377-139-16
; Sequence 16, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxiong
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Bos Taurus
US-10-377-139-16

```

```

Query Match      15.0%; Score 974; DB 18; Length 6503;
Best Local Similarity 55.7%; Pred. No. 7e-260;
Matches 2068; Conservative 0; Mismatches 1570; Indels 72; Gaps 8;

```

```

Qy      2413 TGTGGAGCTGTGCTGGGTTTGTGTAATTTCAAGAGTGGGTATGCTCATGCTCTTG 2472
Db      2175 TCTGGAGTGTCTGCTCCCTGTGATGTCCATTAGCAGAAATGAGATTCATGTG 2234
Qy      2473 ATCCCTTGTGAGCTCTTTCATCAAGCTGTGATTTGTATCAACAGATTTTATGCAA 2532
Db      2235 ACCATTGTGCTGACTCACCATCAACATGTGATCGTGTAAACAGCTCTTATGCGAC 2294
Qy      2533 TGGATCAACGATATGAACAGAGATGGAACCGCTGCTCAAGAGTGGCACTATTTCT 2592
Db      2295 TGAAGCACTTCAACATGACACGAAATTTAGAGAGATGAGTGTGAGAAACCTGTCT 2354
Qy      2593 TCACCGCACTTTCGATGAGGCGCACATGAAGCTAATGGCCATGAGCCCAAGTACT 2652
Db      2355 TCACGAAATTTTCAACGAGATGACCTTCAAGATCAATTCCTTGAACCTTACTACT 2414
Qy      2653 ATTTCCAGAGGGGTGAGACATTTTCACTTATCTGTGCTTATTCCTATTGGAAC 2712
Db      2415 ACTTCCAGAGGGGTGAGACATTTTGAACAGATCACTGTCTCAGCTCATGAGC 2474
Qy      2713 TGGGACTCGAGGGGTTCAGGGTGTCTCGTATTTGCGTTCTTTTCATGTTCTGCTGTAT 2772
Db      2475 TGGGCTGTCTCCGATGGCAATCTGTGGTGTCTTCTGCTCTTCTGCTCTTCTGAGGTCT 2534

```

```

Qy      2773 TCAAACTGGCCAAAGTCTTGGCCCAACAATTATTTACTCATTTTGCATTTATGGAGCCACCA 2832
Db      2535 TCAAGTGGCAAGTCTTGGCCCAACCTGACACACTTATCAAGATCATTTGGAACTCAG 2594
Qy      2833 TGGGCGCTTTGGGTAATCGAATTTGATCTTTGCAATTATCATCTTCACTTTTGGGTGA 2892
Db      2595 TGGGCGCGCTTAGCAACCTGACGTTGTGTCTGGCCATCATTTGTTCATCTTCTGCTGTG 2654
Qy      2893 TGGGAATGCACTGTTCGGAAGAATATATCATGATCAAGAACCGCTTTCCGGAT---G 2949
Db      2655 TGGGCAATGAGCTCTTTTGGCAAGMACTACTCAGAGAGAGGACCGTATCAGTGAATCGG 2714
Qy      2950 GCGACCTGGCCGCGTGGAACTTCAACGATTTATGACAGCTTATGATGTTGTTCCGGG 3009
Db      2715 GCTCTGTGCGCGCTGCGTGGACATGATGGAATTTCTTCACATGCTTCTCCTCATCTTCCGA 2774
Qy      3010 TGTCTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3066
Db      2775 TCTCTGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2834
Qy      3067 CGTGCATTTCCCTTTCTTTTGGCCACCGTGTGATGCGGCAATCTTGTGATTAACCTT 3126
Db      2835 TATGCTGTGTGCTTCTTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 2894
Qy      3127 TCTTACCTTGTCTTGTGCTCAATTTTGTGCTCAATCTTATGAGCGCGCACTGCGGATA 3186
Db      2895 TCTGTGCTTTATCTGCTGACCTCTTCAAGGACAGACACTCAGCTCCGACAGAGATG 2954
Qy      3187 ACGATAAGATAAATAATAGCGAGGCTTCAATGAAATTTGCGCGATTTAAAGTGGTTA 3246
Db      2955 GGGAGATGAACAACCTCCAGTGTGCTGCGCGCATCCAGAGAGGCTGCGCTTCATCA 3014
Qy      3247 AGGTATATTTGTGATTTTCAATTTATGATTAATGATTAATGATTAATGATTAATGATTA 3306
Db      3015 AGGAGCAACTGGGACTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Qy      3307 ATCAACCATCAGGTGAGAGAGACCAACAGATGATTTGATTTGAGAGAGAGATGATG 3366
Db      3061 -TCAGAGCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3119
Qy      3367 ACAAGCACTGAGCTGGGCGCACAGAGATCTGCGCAAGGCTCTCATCAAGAGAGGGA 3426
Db      3120 GCGCCCAACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3179
Qy      3427 TCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3486
Db      3180 AGAAGGCGAGCGGCGAGGTCAGGCGCACCTGAGGATGCGAGCTGTGTGTGCCCA 3239
Qy      3487 GCGACATGAAGAACAAACAGCGAGAGAAATCCAAATATCTAAATTAACGCAACGATATTG 3546
Db      3240 TGGCGTGGCGAGTGAGACAGGATGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3284
Qy      3547 GCAATCAATTAACCAACAGACATAGTGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3606
Db      3285 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3344
Qy      3607 CCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3666
Db      3345 GCGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3404
Qy      3667 TCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3726
Db      3405 CTGGGCGCGAGGCGAATGAGGTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3464
Qy      3727 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3786
Db      3465 CCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3524
Qy      3787 GCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3846
Db      3525 TGAACAACCTGTGACTCTCTGAGAGAGATCTGACCTCGAGAGAGATGATCAAGATC 3584

```

3847 CAGTGAATGCGCCCGGATTCGTACTATAAGAAATTCGATCTTAAGCCGGTACGATG 3906  
3585 CAGGAGATCGCTTCACTGAAGGCTGTCCGCCGCTGCTGCAACCGTGGACACCA 3644  
3907 ACTGCGCTTTCGCAAGATGAGGCAATTTACGATGAAAATTTCATTAATTTGAA 3966  
3645 CACAGGCCCAAGGAGGCTGTGGAGGCTGCGAAGACGTACCGCATCGTGAAGC 3704  
3967 ATTAATATTTTGAACAGCTGTATCACTATATTTTAATGATGCTTGGCAT 4026  
3705 ACAGCTGTGTGAGAGCTTCACTATCATCTGTGTCAGAGTGGCGACCTGCT 3764  
4027 TAGAAGATGATACATCTGCAACAAAGACCATCTGAGAGATTTTATATCTATGACA 4086  
3765 TTGAGGACATCTACTGAGAGAGCGAAGACATCAAGGTCTGCTGAGTACCGGACA 3824  
4087 GAATATTTACGGTATATTTCTTCTTGAATGTTATCAAGTGTGGCGCTGCTTCA 4146  
3825 AGATGTTACCTTACGCTTTCGTGAGAGATGCTCCTCAAGTGGGTGCGCTTCA 3884  
4147 AAGGTACTTCAACCAAGCGGTGTGGCTGCTGATTTGTGATTTGATGCTTCA 4206  
3885 AAGATTTCTTCAACCAAGCGGTGTGGCTGCTGATTTGCTCATCTGAGAGCTTGTGCA 3944  
4207 TCAACTTGTGCTTCACTTGTGAGCGGTGTGATTCAGCTTCAAGCTTCAAGCTATGCAA 4266  
3945 TCAAGCTGTGGCCAAAGCGCTTGGCTTGTGATGAGAGGCGCCATCAAGTCACTGCGA 4004  
4267 CGTTAAGGCACTGAGACCACTACGTGCATGTCCGATGAGAGGCGATGAGGTGCTG 4326  
4005 CTTTGCCTGCGCTGAGACCCCTGCGAGCCGTGTCAAGATTGAGGCGATGAGGGTGTG 4064  
4327 TTAATGCGCTGTACACACTATACCTGCTCATCTTCAATGTGATTTGTGTCTAATAT 4386  
4065 TTAACGCTGTGTGGCGGACCTCCATCATCATATTAAGTCTCTCTGCTGCTCATCT 4124  
4387 TTTGGCTAATTTTTCGATTAATGAGGTGTACAGCTTTTGTGAGAAATATTTAAGTGC 4446  
4125 TCTGCTCATCTTCAAGCATCACTGAGCGTGAACCTTTGCGGGAGAGTTGGAGATCA 4184  
4447 AGGACATGATGCGACGAGCTCAGCAAGATCATCAAAATGCAATGCTGCTGCGA 4506  
4185 TCAACCAAGACGAGGAGACCTGCTTGAATCATATCATGTGAAACAAGAGCGACT 4244  
4507 GCGGAACTTCA-----CGTGGTGAATTCAGCAATGAATTTGATC 4548  
4245 GTGAGTCTTCAATGTGACGTGGCAATTTGATCTGACCAAGGTGAAGGTCAACTTGA 4304  
4549 ATGATGATGACGCTATCTGTGCTTTCGAATGCGCAACCTTCAAGGCTGGAATCAAA 4608  
4305 AGTGGGGGGCGGGTACCTGCGCTTTCGAGGTGCAACATTTAAAGCTGAGTGAACA 4364  
4609 TCATGACGATGCTATCATCAAGAGAGTGAACAAGCAACCAATGTGTAAGAGACA 4668  
4365 TCATGATGAGAGCTGTACCTCAGGGGTGAGAGAGACAGCCCAAGTGGAGATCAACC 4424  
4669 TCTACATGATATTTATTTGATTTCTTCAATATTTGATCTTTTCACTCAATC 4728  
4425 TCTACATGATATTTATTTGATTTCTTCAATATTTGATTTGATTTCTTCAACCTGAA 4484  
4729 TGTTCATTTGATTTATCTGATTAATTTAATGAGCAAGAAAGCAAGGAGTGAATCAT 4788  
4485 TGTTCATTTGATTTATCTGATTAATTTAATGAGCAAGAAAGCAAGGAGTGAAGTGA 4543  
4789 TAGAATGTTTATGACAGAGATCAGAAAGATCTATATGCTATGAAAAAGTGGCT 4848  
4544 --GACATCTTCAATGACAGAGAGCAGAGAGTACTAACAAGCATGAAAGAGTGGCT 4601  
4849 CTTAAAAACCAATTAAAGCACTTCCAGACCAAGGTGCGACACACAGCAATAGCTTTG 4908  
4602 CCAAGAAACCCCAAGAGCATCCCAAGCGCCCTGTAACAGATCAAGAGGCTTCAATTTG 4661  
4909 AATATGTAACGATTAAGAAATTCATATATATATTAATGATTTGATTTGATGACATGT 4968

4662 ACATTTGACCAAGAGGCTTTCAGCTGACATCATATTTCTCATCTGCTTAAACATG 4721  
4969 TCACCATGACCTTCATGCTTACAGATGCTGCAACATATTAACGCGGTCTTACATATC 5028  
4722 TGACCATGATGATGAGACAGACACAGAGCCCGAAGAGTCAACATCTTGGCCAGA 4781  
5029 TCAATGCATATTTGATTTATTTTCACTGATGCAATGCTATTTAATAATTTGCTTAC 5088  
4782 TCAACCTGCTGTGTGGGCACTTTCACAGCGAGTATCTTCAAGATGATGCTGCTG 4841  
5089 GATATCACTATTTTATGAGCCATGAAATTTATTTGATGATGATGATGATGATGATG 5148  
4842 GCACTATTTATTTCAACCAAGCTGAAACATCTTCACTTGTGATGATGATGATGATG 4901  
5149 TCTTAACTTGTACTTACGATATTTATGAGAAATCTTGTGTGCGCAACCTGCTCC 5208  
4902 TCGTAAAGCATGTGCTTCAACATATCCAGAGTACTTCTTCTCCCGACGCTTCC 4961  
5209 GAGTGTGCTGTGCGCAAGATGAGGCGGTGCTTCACTGATGAGAGGACCAAGGCA 5268  
4962 GGTATATCGCTGCGCGCATGAGCGCATCTTCAAGCTATCGCGGCGCAAGGCA 5021  
5269 TTGGAACATGCTCTTTCGCTTGGCATGTGCTGCGCGGCGCTTCAACATCTGCTG 5328  
5022 TCCGACGCTTCTTTCGCTTGGCATGTGCTGCGCGGCGCTTCAACATCTGCTG 5081  
5329 TGTGTTCTGCTGATGATTTCACTTGTGCAATTTTGGCATGCTTCTTCAATGACGTA 5388  
5082 TGTCTTCTGCTGATGATTTCACTTCACTTCTGCAATTTTGGCATGCTTCTTCAATG 5141  
5389 AGGAAAGAGGCTTAAAGAGCTTCAACCTTCAACCTTGGCGAGAGATGATCC 5448  
5142 AGTGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5201  
5449 TGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5508  
5202 GCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5261  
5509 AGAAGCATGCGA-----TCACCCGACAGCGCAAAAGGCTTACCGGCAATGTC 5559  
5262 CGGGGCCCCCTTACGCGACCCCAACCTGCAACAGCAAGGCTCCCGGGCAACTGCG 5321  
5560 GTTCAAGGACCGTGTGAATACGTTTCTCTCATATCTGATTAAGCTTTTGAATG 5619  
5322 GGAAGCCCGCGGTGGGATCTCTTCTTCAACAGCTTCAATATCTCTTCTCATATG 5381  
5620 TTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5679  
5382 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5441  
5680 AAGAGGCTTAAACGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 5739  
5442 CGAGGCCCCCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 5501  
5740 CGAGGCGGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5799  
5502 CGAGGCGGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5561  
5800 CCGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5859  
5562 AGCAGCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5621  
5860 GTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5919  
5622 TGAATGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5681  
5920 CGCGAAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5973  
5882 GCGAATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5741  
5974 GCCCGATGAGAGGCTTACAGGCGCTTCAATGATGATGATGATGATGATGATGATG 6033

Db 5742 ACCGCTCAAGATCTCTCTACGAGCCCATCAACACGCTGCGGCGGAAGACGAGAGG 5801  
QY 6034 ACTGCCCCCGGCTTAATCCAGACGCTGCGGAAGACGAGCGCGCGC 6083  
Db 5802 TGTGGCCACGATCATCAGCGGGGCTTCGCGCGGACCTCTGCGAGCGC 5851

## RESULT 6

US-10-202-824-5

Sequence 5, Application US/10202824

Publication No. US2003017648A1

GENERAL INFORMATION:

APPLICANT: Wood, John N.

Akopian, Armen N.

TITLE OF INVENTION: Ion Channel

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZENECA Pharmaceuticals

STREET: 1800 Concord Pike, P.O. Box 15437

CITY: Wilmington

STATE: Delaware

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/202,824

FILING DATE: 26-Jul-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/669,656

FILING DATE: 24-Jun-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: PHM.70086

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-7466

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7052 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 204..6602

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-202-824-5

Query Match 14.5%; Score 944.8; DB 16; Length 7052;  
Best Local Similarity 50.9%; Pred. No. 1.1e-25;  
Matches 3060; Conservative 0; Mismatches 2667; Indels 285; Gaps 23;

QY 288 TTGAGGGCAGCTTCCCGCGGAATTGGCTCCCACTCCTCTCGAGATATGATCCCTAC 347  
Db 399 TTCTATGTTGAGCTTCCGAGAACTGCTCGGGAGCCCTGAGGAACTGAGACCTTTTC 458  
QY 348 TACAGCAATGTAAGTGTGATGTTTAAGCAAAAGAAAGATTTTTCGCTTTTCT 407  
Db 459 TACAGCACACCGGACATTCATGTGTGTAATAAAGACAGACCATTTCCAGATTCAGT 518  
QY 408 GCATCAAAAGCAATGTGATGCTCGATTCATTCGATACGTCGTGGCCATTAC 467  
Db 519 GCATTTGGGCGCTTGGCTCTTCAGTCCCTTCAACCTGATCAGAAAGACGCAATCAA 578  
QY 468 ATTCTAGTGCATTCATTTTTCCTATTCATCATCACCAATTTCTGTAAGTCATC 527  
Db 579 GTGTGTGCATTCCTGTGTTCTCATATTCAACCATCATATTCTTTGTCAACTGC--- 635

QY 528 CTGATGATTAATGCGGACAAACCCCAAGGTTGATCTAGTCACTGAGTGATTTGACCGGAATC 587  
Db 636 ---GTGTCAATGACCCGAACTGATCTTCCAGAGAAAGTGAGTACGTCTTCACTGTCATTT 692  
QY 588 TACAATTTGATGACGCTGTTAAAGTATGGCAAGAGGTTTCATTTTATGCGCGTTTACG 647  
Db 693 TACACCTTCGAGGCTCTGATTTAAGTACTGCGCAAGAGGTTTGTCTTAATGAGTTACT 752  
QY 648 TATCTTAGAGATGCAATGGAATTTGGCTGACTTCTGTAATAGCTTTAGCTTAATGTAAC 707  
Db 753 TATCTTCAGATCCGTGGAACGTGCTGACTTCACTGATCACTTCCGCTGATGTTGCT 812  
QY 708 ATGGGTAATGATTTAGTAAATCTAGACACCTTCGCAAGGTTTAAAGGCTGCGAGCGCTT 767  
Db 813 GCAGGAAATAGACCTTCGAGAAATCTGAGCCCTGCGAATTCGAGTTCTCAGACCTCTG 872  
QY 768 AAAACCGTAGCCATTGTGCGAGGCTTGAAGACCATGTCGCGCCGTCATCGAATCGGTTG 827  
Db 873 AAAACGTTTCTGTGATCCAGAGACTGAAGGTCATGTTGGAGCCCTGATCACTCAGTG 932  
QY 828 AAGAAATCTGCGGAGTGTGATTTATCTGACATGTTCTCCCTGTGCTGCTGCTTGTATG 887  
Db 933 AGGAAGCTGCGGAGCTGATCTATCTCTCAAGTCTTCTGCTGAGGCTTGTGCTGAGT 992  
QY 888 GGCCTTACAGATCTATATATGCGGCTGCTCAACGAGATGTCATCAAGATTCGCGCTGAG 947  
Db 993 GGCCTTACAGCTTTTAAAGGGAACCTTAAAGAAATGATCATGAGAACGGAACATATCC 1052  
QY 948 GGTTCCTGCGGCAATCTGACCCAGAGAACTGGGACTATCAATTCGCAATAGCTTCAT 1007  
Db 1053 CACAAGCTGACACCTCTCATCTGAAATGCGAATACATCTTCATCAAGCTGTAAT 1112  
QY 1008 TGTATTCGAGAGACGAGGACATCTCATTTCCGTTATGCGGCAATATATTCGCGGAG 1067  
Db 1113 ACGGATCCC-----TTACTGTGCGCAATGAGGCTGATGCTGCT 1151  
QY 1068 CAATGCGACGAGATTAAGTGTGCTGCGAGGGGTTTGTCCGAATCCGAATTAATGAGTAC 1127  
Db 1152 CATCTGCTGAGAGCTATGTCCTGAA---AATCTTCGACACCCGGAATTTTAACTAC 1208  
QY 1128 ACCAGCTTGATTCGTTGCGAATGAGGCTTCTGTCGCTTCGCGCTGATGACACAGAC 1187  
Db 1209 ACCAGCTTGATTCGTTGCGAATGAGGCTTCTGTCGCTTCGCGCTGATGACACAGAC 1268  
QY 1188 TTCTGGAGAGATGTGACACAGCTGTGTGCGCGCGCGGACCAATGACAGTGTCTC 1247  
Db 1269 TCCTGGAGAGCTGTGACAGACAGACATCCGAGCTTCTGGGAAATGTACATGTGCTTT 1328  
QY 1248 TTATATGTCATCATCTTCTAGGTTCTATCTTGTGAATTTGATTTTGGCCATGTT 1307  
Db 1329 TTCTGTGTTGATTTTCTTCTGATGCTTCTGATGCTTCAATTTGATCTTGGCCGTGTC 1388  
QY 1308 GCCATGTCGTATGACGAATTTGCAAGAGAGCCGAAGAGAGAGGCTCCGAAGAGAG 1367  
Db 1389 ACCATGCGGTATGAAGAGAGAGCCAGAGCAACATTTGCAAGATTCAGCCAGGAAATA 1448  
QY 1368 GCGATTCGTAAACGGAAGAGAGTGCAGCGCCAAAGCGCCCAAGCTGAGAGAGCGGCC 1427  
Db 1449 AAGTTTCAGAGACCTTGAAGTGTGCTGCAAGAGAAACAGAGAGTGTGCGAGCCCTGGGG 1508  
QY 1428 AATGCGAGGCTGAGCAGCAGCAGAGAGTGCAGCGCTGCGCGGAG----- 1470  
Db 1509 ATTGACACGACCTCGCTCCAGTCCCAAGTGATCACTTAACTCCCAAAAAGCCCAAT 1568  
QY 1471 -----AGGCTGCACTGCATCCGAAATGGC 1495  
Db 1569 GAGAGAGACCCAGGTTGAATCAAGGTTGTCAAGGGCTCCAGAGTGAACACAGTCA 1628  
QY 1496 CAAAGATCCGAGGTATTTCTTGATTCAGCTATGAGCTATTTGTTGGCGCGAGAGGCA 1555  
Db 1629 CCCCAATCAACCTTTACCAACAGCGCAGAGATGCTTTTCTAGGCGTGTTCAGAGAGA 1688

1556 CGATGACAAACAAGAGATGTCCA-TTCGAGCGTCA----- 1597  
Db 1669 CGCAGGCTACCGACGAGTGTGTTCCATCTCGAGGCCCGCAAGACATCTCATTT 1748  
Qy 1598 -----GGTGAAGTCGAGTCGAGCGTTATACAAAGACMACAGACCTACAGAG 1650  
Db 1749 CCTGACGGGATACCCCTGATGATGGGGTCTTTACGAGACAGAGAAAGCGTGAAGT 1808  
Qy 1651 CACACCAAGTACCAAG-----TTCGTAAGTAGACAGCAAT 1689  
Db 1809 TCCATATTGTCGAGGAGGTGCTGGGACAGAGTCCATCCGAGAGCCCATGTCCT 1868  
Qy 1690 CCTATCCTTACCTGTTTACCGTTTAAATACGAGGGAGTCAAGTATCTCAAGT 1749  
Db 1869 CAGTCCCAACCTGCGCTGAGACATGAGAGAGGAGCAGCTCGAGTCCCATGCT 1928  
Qy 1750 ACAGATAC-----GGAACGAGAGTGGCCGCTTTGTATACCGGATGAGCATGTAAGCAT 1806  
Db 1929 GAGCTTACCGTGGAGCGCTGAGAGGCCCGGACCTCGACATCAAGGAGGAGAGCTTC 1988  
Qy 1807 TGGT-----ATTGTCAATATATAGAGATGCCAGACAGCACTGCTATGCGAC 1856  
Db 1899 CTGTCTGGGCTACTTGAACGAACCTTCCGAGACAGAGGCGCATGAGGTTGTCACT 2048  
Qy 1857 GACTCGAATGCGTCAACCGCATGTCGAGAGAGATGGGCGCATATGTCGCTGAC 1916  
Db 2049 ATCATGACTTCTGTCATTTAGAGAGCTTGAAGTCTTAAGCTGAAGTCCCATCTGCTTG 2108  
Qy 1917 TATGCAATCTAGGCTCCGACACTCATCTATACCTGCACTCACTCCGATATCTAT 1976  
Db 2109 ATCAGCTTCGCTCAAGATATCTATCTGGAGTGTCCCGAAGTGAAGAGTTCAAG 2168  
Qy 1977 ACCTTCATGAGCGATCTACTCGGCGGCAATGCGCTCATGCGCTGACAGCAATGACAG 2036  
Db 2169 ATGCGCTGTTGAGCTGTGACTGACCCCTTCCGAGAGCTTACCATCACTCCCTGCACTC 2228  
Qy 2037 GAGAGCAAAATTGGCGAACCGCAACAGCAATCAATAGTGGGCGCAACAGTGGCGG 2096  
Db 2229 GTGCTGAACACCGTTTCTATGAGCGCATGAGACATGCCATGACAGATGCTTGATGCC 2288  
Qy 2097 ACCACCTGTCTGACACCAATCAACAGCTCATGCTGCACTACGAAATTTGCGCTGAG 2156  
Db 2289 ATGCTTCAAGCGGCAATGTGTTCAACGTTTTCACATGAGAGATGGCTTCAAG 2348  
Qy 2157 TGCACGAGCAAGCTGCGAAGATTAAATCAATGACATCTTTATGAGCCGTCAG 2216  
Db 2349 ATCATGCTTTCGACCCCTACTATTAATCCAGAAAGTGAATATCTTGCATGTC 2408  
Qy 2217 ACACAAACGCTGTGATATG-----AAGATGTGATGTCCTGATGACA 2262  
Db 2409 ATGCTCACCGTGAACCTTCTGAGCTGAGTCAATCCAAAGAGGCGAGCTGTGTGCTC 2468  
Qy 2263 TCATCGAACAGGCGCTGTGCGACAGTCCGAGAGCGATCGCGTGTCTCCG----- 2316  
Db 2469 CGTTCCTTAAGCTTGGACCTGACATCAAGGCGAAGAGCTTCTGTCTGCGGCTAC 2528  
Qy 2317 -----TTTACTATTTCCCAACAGAGAGATG----- 2344  
Db 2529 TTGAACGAACCTTTCGAGCACAGAGGCGCATGAGCGTTGTCAGATATGACTTCTGTC 2588  
Qy 2345 --CGAGATGGGCGAGTTCAAAGACAGAGCACTCGAAGTATCTTAAAGCATGAT 2402  
Db 2589 ATTGAGGAGCTTGAAGGTCTAAGCTGAAGTCCACCTGCTGATAGCTTGCTGAC 2648  
Qy 2403 GTGTTTGTGTGGGACTGTGCTGGGTTTGTGTAATTTCAAGAGTGGTATCGCTC 2462  
Db 2649 AAGTATCTGATCTGGAGTGTGCTCCCAAGTGAAGAGTTCAAGATGGCGCTGTGAG 2708  
Qy 2463 ATGCTTTGATCCCTTGTGAGCTCTTATCAAGCTGTGCAATTTGTGCAACAGATG 2522  
Db 2709 CTGCTGATGACCCCTTTCGAGAGCTTACCATCAACCTCTCTCATCTGTGTAACAGCTC 2768  
Qy 2523 TTCAATGGAATGATTCACAGATATGAAACAGAGATGAAACCGTGTCTCAAGATGCGC 2582

Db 2769 TTCAATGGAATGATTCACAGATATGAAACAGAGATGAAACCGTGTCTCAAGATGCGC 2828  
Qy 2583 AACTATTTCTTACCGCCACTTTGCGATCGAGGCCACATGAAGTAAATGCGCATGAGC 2642  
Db 2829 AACTATGCTTACCGTGTTTTCAATGAGATGGCTTCAAGATCATGTGCTTGCAC 2888  
Qy 2643 CCGAAGTACTTATTCAGAGAGGCTGGAACATCTTGCACCTTATATGTTGCGCTTATG 2702  
Db 2889 CCTTACTATTTCTTCAAGAAAGTGAATATCTTGCACCTGTGATCATGTCACGTCAGC 2948  
Qy 2703 CTATGGAATGGAATCGAGGCTGAGGCTGTCAGAGGCTGTCGATTTGCTTCCCTTGCATG 2762  
Db 2949 CTCTGAGCTGAGTGCATCCAAAGAGGCGACCTGTGTGCTCTGCTTCTTACGCTTG 3008  
Qy 2763 CTGCGTGTATTCAACTGGCCAGTCTTGGCCCACTTAAATTTACTATTTGATTTGATG 2822  
Db 3009 CTGCGGCTTCAAGCTGGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3068  
Qy 2823 GAGCGACATGAGGCTTGGTATCTGATTTGATCTTGTGATCTTGTGATATCATCTTATC 2882  
Db 3069 GGAATCTAGTGGGCGCTGGGCAACCTTATCTTGGCCATCATGCTGTCTTCACTC 3128  
Qy 2883 TTGCGGATGGAATGCAATGTCGAAAGATATCATGATCAAGGACCGCTT 2942  
Db 3129 TTGCGCTGTCGAAAGACCTTCTTCAAGAGCTAGCGGTGCGCAAGGACGCTC 3188  
Qy 2943 CC-----GATGCGACCTGCGCGCTGGAATCTTCAACCGACTTATGACAGCTTCATG 2996  
Db 3189 TCGGTGGAACCGCGAGAGCTCGCTGCGCATGATGATCTTCTCATTTCTGCTG 3248  
Qy 2997 ATGCTTTCGGGCTGCTGCGGAAATGATGATGATGATGATGATGATGATGATGATGATG 3056  
Db 3249 GTGCTTTCGGAATCTCTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATG 3308  
Qy 3057 GCGATGCTC---GTGATTCCTTCTTGGGCAACCGTGTGATGCGCAATCTGTC 3113  
Db 3309 AGCCAGAAATCATCTGCTCTATCTTCTTGTGATGATGATGATGATGATGATGATGATG 3368  
Qy 3114 GTACTTAACTTTTCTTACCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3173  
Db 3369 GTGCTAACCTTTTCTTATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 3428  
Qy 3174 CCGACTGCGATTAAGATTAAGATTAATTAAGCGAGCTTCAATGATGATGATGATGATGATG 3233  
Db 3429 CCAAGATGACGCGGAGTGAACACTTGTGATGACCTGCGAGATGATGATGATGATGATGATG 3488  
Qy 3234 AAAAGTTGGGTTAAGCGTAAATTTGCTGATTTGTTCAAGTTAATACGTAACAAATGACA 3293  
Db 3489 GCGCATGCGGCGACAGAGGCGCATGCAATTAATCA-----GACGCCACTGCCGAT 3541  
Qy 3294 AATCAATTAAGTATCAACATCACTGATGAGAGCAACAGATCACTGATTTGAGC 3353  
Db 3542 CCGCTGCGCAAGGTGAGACCCAGCTGGGATGAACCCCACTCAACAGCTCAGAGC 3601  
Qy 3354 GAGAGCATGATGACAAAGATGAGAGCTGGCCAGACAGATCTGCGCGCTC 3413  
Db 3602 CAAGAACCAATGCTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3661  
Qy 3414 ATCAAGAAAGGAGTCAAGAGAGAGAGCACTGAGAGTGGCATGCGGAGATCGAGTGA 3473  
Db 3662 TCTCAGTAG-----CCCAAGAGAAATCAAGGAGCTTCACTGATTTCCACAGTGTGG 3716  
Qy 3474 TTCAAGTACCGCGCATGAGAGACAAAGAGCGAAGATCAATATCTTAAATAC 3533  
Db 3717 GTCTCTGTGCCATTTGCTGAGGGGATGATGACTGACGAGCTGAGAGATATGAGAG 3776  
Qy 3534 GCAACGATGATTTGGCACTCAATTAACCAAGACATGATGAGAGAGAGAGAGAGAGAGAGAG 3593  
Db 3777 CAGGCTTTCGAGAGCTCTGCGAG 3829  
Qy 3594 CATGAGATTTGCTTACAG 3653

Db 3830 -----GTTGCCACAGTCCAAAGTGTGAAAACCAACGAGCAGCAAGGCCA 3878  
 Oy 3654 AAGATTCGACCATTTCAAGAACGAGACCCAAAGGGGAGGCGAGACATGAGGGGCGAG 3713  
 Db 3879 GCGCTCATGATGCTCTCTAGAGACCTGGCTCCATACCTGGGTGAGCTGGAGAGAGAG 3938  
 Oy 3714 GAGAACGCGACGCGCAGCAAGAGATTTAGGTCTCGACGAGGAACTGACGAGAGAGGC 3773  
 Db 3939 GATAGCCCTCAGTCCCTGCGCGAG-----GAGTGGATGACACGAGCTCTCTGAGGCG 3992  
 Oy 3774 GAAATCGAGAGAGGCGCGCTCGACGGTATATATTATTCATGACACGACGAGATTA 3833  
 Db 3993 AGCAGCGGTGACTGCGCGAGCCGAGGAATCCTAGAGAAATCCCGAGCTGGAGAT 4052  
 Oy 3834 CTGATGAATATACGATGATGCTGCGCGATTCGATTCGATTAAGAAATTTCCGATCTTA 3893  
 Db 4053 GACCTGAGACGAGCCGATGATCTTTTCAAGAGGCTGACCTGCGCGCTGCTGCTGC 4112  
 Oy 3894 GCGGTGACGATGACTGCGGCTCTGGCAAGATGGGGCAATTTACGACTGAAACTTTT 3953  
 Db 4113 AAGGTAACTAGCAAGTCTCCTTGGGCAAGGCTGGCAGGTCGCAAGACTGCTAC 4172  
 Oy 3954 CAATTAATTGAAATTAATTTTGAACAGCTGTTATCACTATGATTTTAAAGATAGC 4013  
 Db 4173 CGCATCGTGAAGCAGCTGGTGTGAGATTTCATATCTTCATGATCTGCTCAGCAGT 4232  
 Oy 4014 TTAGCTTTGGCATTAGAAAGATGATACCTGSCCAAAAGCCCACTAGCAGATATTTTA 4073  
 Db 4233 GAGAGCGTGGCTTTGAGGATTAACCTGGAAGAGAAACCCGAGTGAAGTCCGTCGTC 4292  
 Oy 4074 TACTATATGACAGAAATATTTACGGTTAATCTTCTTGGAAATGTTAATCAAGTGTG 4133  
 Db 4293 GAGTACACTAGCAGAGTTCACCTTCATCTGCTTTGAGATGCTGCTCAAGTGGGTA 4352  
 Oy 4134 GCGCTGGCTTAAAGTGTACTTCAACGCGGAGTGGTGGCTCGATTTGATGATGTC 4193  
 Db 4353 GCGTATGCTTCAAAAGATTTTTCACCAATGCTGGTGTGGCTGGACTTCTCATTTGTG 4412  
 Oy 4194 ATGGTATGCTTATCAACTTGTGCTTCACTGTTGAGCTGGTGTGATTTCAAGCTTTC 4253  
 Db 4413 AAGATCTCCGACAAACCTCATAGCGAAGATCTTGAATTCGACGTGGCGTCCATC 4472  
 Oy 4254 AAGATATGGAAGCTTAAGAGCACTGAGACCACTAGTGCATGTCGCGGATGAGAGGC 4313  
 Db 4473 AAGGCCCTTGGACTCTCCGCTGCGCTCGACCGCTGGGGCTGTCTCATTTGAAGGC 4532  
 Oy 4314 ATAGGAGTGGTGTATGAGCTGTGTACAGCTATACCGTCACTCTTCAATGTGCTATTG 4373  
 Db 4533 ATGAGGATGATGTGATGCTCTGTGGGCGCATCCCTTCATCAATGAGTCTCTC 4592  
 Oy 4374 GTGTGTCTAATATTTTGGCTAATTTTGCATAATGAGGTGTACAGCTTTTGTGAAAA 4433  
 Db 4593 GTCTGCGTCACTTCTGCTCATCTTCAGCATGAGGCGTGAACCTCTTCGCGGAGAA 4652  
 Oy 4434 TATTTTAAGTGGAGACATGAAATGACAGAGCTGACGACGAGATCATACAA----- 4488  
 Db 4653 TTTTTCAGAGTGGTGTGACACCAAAATTAACCATTTTCAAGTGAATTCGACATGCTG 4712  
 Oy 4489 -----ATCGAATGCTGCGAGAGCGAGAACTACAGGTGGGTGAATTTCA 4532  
 Db 4713 AATTAACAGTCCGAGTGTCAATTAACAGACACCGGCGACTTCTTCTGGGTCAAGTTC 4772  
 Oy 4533 GCAATGAATTTTCATGATGATGAGTACGCGTATCTGTGCTTTTCAAGTGGCGACTTC 4592  
 Db 4773 AAGGTCAACTTTCAGCAAGTGTGAGTACCTGCACTTCTTCAGTGGCGAACTTC 4832  
 Oy 4593 AAGAGCTGATCAATATGAAAGATGAGATGATTCATGACGAGGTGAGCAAGCA 4652  
 Db 4833 AAGAGCTGATGACATATATATGACAGCTGTGATTCGAGAGATCAACAGTCAAGCT 4892  
 Oy 4653 ATTCGTGAAGACGACATCTACATGATTTATATTTCTTCAATCATATTTGATTC 4712  
 Db 4893 AACTGGAGAACAACTTGTACATGTACTGTACTGCTGCTTTCATCATATTTTGGTGGC 4952

Oy 4713 TTTTCACTCATCTGTTCATTTGTGTATTCATTTGATTAATTTTATGACAAAGAA 4772  
 Db 4953 TTTCTTCACTGATATCTTGTGTGGGTCAATATCGCAACTTCAACCAAGAGAAAA 5012  
 Oy 4773 AAGAGGTGATCATTTGAATGTTCAATGACAGAGATCGAAGAAAGTACTATATGCT 4832  
 Db 5013 AAGCTAGAGG---CCAGACATCTTCAACAGAGAGAGAGAGAGAGTACTACATGCC 5069  
 Oy 4833 ATGAAAAAGATGGGCTTAAATAAATTAAGCAATTCAGACCAAGGTGGCAGCA 4892  
 Db 5070 ATGAAAGAGTGGGTCCAGAGAAACCCAGAGGCCATCCAGCGCCCTGAATATAGTAC 5129  
 Oy 4893 CAAGCAATGCTTTGAAATATGTAACCAATTAAGAAATTCGATATTAATGATATTC 4952  
 Db 5130 CAAGGCTTGTGTGATCATGTCAGCAGGCAAGGCTTTGACATCATCATATGCTTC 5189  
 Oy 4953 ATTTGCTGAACATGTCACATGACCTTCATCGTTACGATGCTGCGACACGTATTAAC 5012  
 Db 5190 ATCTGCTCAATATATACCATGATGATGAGAACCCAGCAGAGGGGAGAGAGACG 5249  
 Oy 5013 GCGTCTAGACTATCTCATGATGCAATTTGTTATTTTCAATTCCGATGCTATTA 5072  
 Db 5250 AAGTTCGGGCAAGATCAACAGATTCTTGTGGCGCTTTCACGGGAGGTGTGATG 5309  
 Oy 5073 AAAATATTTGCTTTACGATATCACTATTTTATGAGCCATGGAATTTATTTGATGATGA 5132  
 Db 5310 AAGATGTTGCGCTGCGACGATCACTTCAACAGCGCTGGAAGCTGTTCACTTCA 5369  
 Oy 5133 GTTGTCACTTTATACCATCTTAGGTCTTGACTTACGATATTAATGAGAA-----AGTAC 5186  
 Db 5370 GTGTGATCTGTCCATTTGGAGTCTGCTGTTTTCGCAATCTTAAGTCACTGAGAAAC 5429  
 Oy 5187 TTGTGTGCGGACCTGCTCGAGTGTGTGTGGGCAAGTGGGCGGTCTCTTGA 5246  
 Db 5430 TACTTCTCCCGACGCTCTCCGGGTATCCGTGCGCAGGATGCGCGCATCTTCAAG 5489  
 Oy 5247 CTGTGAAGGGAGCCAAAGGGCAATGCGACATGCTCTTGGCGTGGCATGTGCTGCG 5306  
 Db 5490 CTGATTCGACAGCAAGAGGATTTGACAGCTGTCTTCCCTCATATATGCTCCGCCC 5549  
 Oy 5307 GCGCTGTTCAACATCTGCTGCTGCTCTGTCGTGATGATTCATCTTGGCAATTTTGGC 5366  
 Db 5550 GCGCTTTCACATAGGCT 5609  
 Oy 5367 ATGTCTTCTTATGACGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5426  
 Db 5610 ATGGCCAGCTTGTCTTACGCTGTGACGAGGCGGATGACGACATGTTCAATTTCAAG 5669  
 Oy 5427 ACCTTTGGCAAGCATGATCTGCTCTTTCAGATGTCAGCTCAAGCCGTTGGATGAGT 5486  
 Db 5670 ACCTTTGGCAAGCATGCTGTGCTGTCTTTCAGATGTCAGCTCAAGCCGTTGGAGG 5729  
 Oy 5487 GTATGAGCGCATTTATCAATGAGAGAGATGGA-----TCCACCCAGACGAGC 5537  
 Db 5730 CTCTCAGCCCATCTTCAACAGGGGCTCTCTTACGAGCCCAACCTGCGCAACAGC 5789  
 Oy 5538 AAGGCTATCCGGGCAATTTGTGTTCAAGGACCGTGTGAATTAAGTTCTCTCTCATAC 5597  
 Db 5790 AAGGCTCCCGGGGAACTGCGGAGCCCGGCGGTGGGATCATCTTCTTCAACCACTAC 5849  
 Oy 5598 CTAGTTAATAGCTTTTGTATGATTTAATATGATCATTTGCTCTCATCTCGAAGACTAT 5657  
 Db 5850 ATATCATCT 5909  
 Oy 5658 AGTCAGGCAACGAGGAGCTGCAAGAGGCTTAAACCGAGCACTACGACATGATCTAT 5717  
 Db 5910 AAGTACGCAACGAGGAGAGACAGAGCCCTGAGGAGAGAGCACTTTCAGATGTTCTAT 5969  
 Oy 5718 GATATCTGAGAGAAATTTGATTCGAGAGGAGCCAGATCACTATGATGATGCTGCTCC 5777  
 Db 5970 GAGACCTGGAGAAAGTTCAGCCGAGAGCCACCAATTCATTTGCTTCTGCTCTCA 6029

```
OY 5778 GAATTCCTGAGCTAGTGGAGCCCGCTGCGATCCAAACCGAAGTACAGATC 5837
DB 6030 GACTTCGGGACAGCCTCTCCGGCCCTTGAATCCCAACCAACGAAATATTA 6089
OY 5838 ATATCGATGACATATCCCATCTGTCGCGTGAACCTCATGTATCGGACATCTCGAC 5897
DB 6090 ATCCAGATGACCTGCGCTGTGTCCCGGGATTAAGATCCATCTGTGACATCTTTT 6149
OY 5898 GCCCTTACGAAAGACTTTTTCGCGGGAAGGCAATCCGATAGAGAGAGCGGTGAGTT 5957
DB 6150 GCCTTCACAAAGACGTCTTGGAGAAATCCGGGGAGTTGACTCCCTGAAAGCAATATG 6209
OY 5958 GGTGAG-----ATAGCGCGCCCGCCGATACGAGGGCTAGAGCCGCTCATCAG 6011
DB 6210 GAAGGAAGTTATGGCAGCAATCTTCCAAAGATCTTAAAGCAATGCAACACC 6269
OY 6012 CTGTGCGCTGACGCTGAGAGTACTGCGCGGCTTAATCAGACGCTGCGAAGAC 6071
DB 6270 CTCGGGTGAGAGCAGGAAGACCTCTCAGCAGATTCATTAAGAGGCTTACCGAGCTAC 6329
OY 6072 AAGCGCGCGCGC 6083
DB 6330 ATGCTGCACCGC 6341

RESULT 7
US-10-297-022-40
; Sequence 40, Application US/10297022
; Publication No. US20030216310A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: THORNTON, Michael
; APPLICANT: WALIA, Nalinder K.
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: LAL, Preeti
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BRUNS, Christopher M.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: SANJANWALA, Madhu S.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: HAFALIA, April
; APPLICANT: GREENE, Barile D.
; APPLICANT: KHAN, Farrah A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: LU, Dyrng Aina M.
; APPLICANT: HILLMAN, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0109 PCT
; CURRENT APPLICATION NUMBER: US/10/297,022
; PRIOR APPLICATION NUMBER: 60/208,424; 60/209,001; 60/210,588; 60/212,335; 60/213,747;
; PRIOR FILING DATE: 2000-05-26; 2000-06-01; 2000-06-08; 2000-06-16; 2000-06-22; 2000-0
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 6027
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030216310A1 6355991CB1
US-10-297-022-40

Query Match 14.4%; Score 941; DB 17; Length 6027;
Best Local Similarity 51.6%; Pred. No. 1,16-250;
Matches 3003; Conservative 0; Mismatches 2425; Indels 387; Gaps 22;

OY 190 AGAAAAACAAAGAAATCCGATATGATGACGAGAGAGATGAAAGTCCACACCGG 249
DB 95 AAAGGCAAGAAATCCCAACACCAAAAGATGACGAGAAATGCCCCAAGCCAA 154
OY 250 ATCTACACTTGAACAGGGTGTCCAAATCTGTTCATGATGAGGAGCTTCCGCGG 309
DB 155 ATAGTGAAGTGAAGTGAAGAAAGAACTTCATTT---ATTATGAGAGACATTCCTCAG 211
OY 310 AATTGGCTCCACTCTCTGTGAGATATCATCTCTTACTACAGCAATGTACTGACTTCG 369
DB 212 AGATGGTGTGAGAGCCCTGTGAGAGCCTGAGACCTCTACTATATCAATAGAGACTTTTA 271
OY 370 TAGTTGTAAGCAAGAAAGATATTTTGGCTTTTCTGATCAAAAGCAATGTGATGC 429
DB 272 TAGTATGATTAAGGAGAGAGCCATCTTCGGTTCAGTGCACCTTGCCTGTACATTT 331
OY 430 TCGATTCATTCATCCGATAGTGTGTGCGCATTTACATTTAGTGCATCATTTATTT 489
DB 332 TAACCTCCCTCAATCTCTTATGAAATAGCTATTAAGATTTTGTATCATTCATTTATCA 391
OY 490 CCTTATTCATCATCAACCAATTTCTGCACTGCAATCTGTATGATATATGCCGACACGC 549
DB 392 GCATGCTAATATATGTGACTATTTTGAACAACTGTGTATATACATGATGATACCTC 451
OY 550 CCAC---GGTTAGTCCAGTGAAGTGAATTTACCGGATTTACATTTGAATGATGCTG 606
DB 452 CTGATGGAACAAAGATGAGATGACCTTCAAGAGAAATATATCTTTGAAATCACTTA 511
OY 607 TTAAGTATGAGCAAGAGTTTCATTTTATGCGGTTTACGATCTTAGAGATCATGGA 666
DB 512 TAAATATTTATGCAAGGGGATTCGTTTAAAGATTTTACTTCTCGGATCATGGA 571
OY 667 ATTGGCTGACTTGTGTATATAGCTTTAGCTTATGTGACCATGCGTATATATAGTGA 726
DB 572 ACTGCTCGAATTCACGTCAATTCATTTGGTGTACGACAGATTTGTGACCTGGCA 631
OY 727 ATCTAGAGCCCTGCGAAAGTTTGGGTGCTGCGAGGCTTAAACCGTAGCATTTGTC 786
DB 632 ATGCTCGGCAATGAGAACATTCAGAGTTCTCGAGCATGGAACGATTTCACTATTC 691
OY 787 CAGGCTTGAAGCAATGCGCGCCGCTCATGATGATGAGTGAAGATCTGCGCATGGA 846
DB 692 CAGGCTTGAAGCAATGCGCGCCGCTCATGATGATGAGTGAAGATCTGCGCATGGA 751
OY 847 TTATCTGACATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
DB 752 TGATCTGACATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
OY 907 GCGTGTCCAGGAGATGATCAAGAAAGTTCCGCTGAGACGCTTGGGGCAATCTGA 966
DB 812 GCAACTGAGAGATTAATGTATGATGATGATGATGATGATGATGATGATGATGATG 871
OY 967 CCGACGAGA----- 975
DB 872 GTATAGAAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
OY 976 -----ACTGGACTATCAATGCAATGCAATGCTCAATTTGATTTCCGAGAGAGGCA 1029
DB 932 AGTTTGAAGTGAAGTCAATATATCAATGATGATGATGATGATGATGATGATGATGAT 991
OY 1030 TCTCATTTCCGTATGCGGCAATATATCCGGTGGGCGGAGATGAGACGATTAAGTGT 1089
```

Db 992 TAGATGACTACTATATGTGAAAAATAGCTCTGATGACAGGCGCAATGTCCAGAGGATATATGT 1051  
 Qy 1090 GCGTGGAGGGGTTTGGTCCGAATCCGAATTTATGCTTACACAGCTTCATGTTGGAT 1149  
 Db 1052 GGTGTAAG---CTGTGTAAGATCCCAATTTATGCTTACACAGCTTCATGTTGGAT 1108  
 Qy 1150 GGGCTTCTGTCCGCTTCGCGCTGTATGACACAGGACTTCTGGAGGATCTGTACAC 1209  
 Db 1109 GGGCTTTTGTCTTGTCTTGTCTGATGACTCAGGACTTCTGGAGGATCTTATCAAC 1168  
 Qy 1210 TGGTGTGGCGCGCCGACCATGTGCAATGTCTTATGATCATCTTCTG 1269  
 Db 1169 TGCATTAGCGTGTGCGGAAAAGTACATGATTTTGTATGTCATTTTCTTGG 1228  
 Qy 1270 GTTCATTCTATCTTGTGAATTTGATTTTGGCATTTGTGCGATGTGTATGACGAATTC 1329  
 Db 1229 GCTCATTTCTATTAATTAATTTGATCTGTGCTGTGTGGCATGTGCTACAGAGACAGA 1288  
 Qy 1330 AAGAGAGCGCGAAGAAAGAGAGCTGCGCAGAGAGCGGATACGTGAAGCGGAAAG 1389  
 Db 1289 ATCAGGCGCACTTGAAGAAAGAGAGACAGAAAGAGCGCG---AATTTGAGAGATGAT 1344  
 Qy 1390 CTGCGCGCGCGCAAGGCGCAAGCTGAGAGGCGGCAATGCGCAGGCTCAGGACAG 1449  
 Db 1345 GAACAGCTTAAAGCAAC-----AGGAGGAGCTCAGCAGGAG 1384  
 Qy 1450 CGGATGCGGCTGCGCGCGAGAGAGCTGCACTGCACTCGGAATGCGCAAGTCCGACGT 1509  
 Db 1385 CAACGGCAATGCTCTGAGCAATTTCCAGAGAGCCAGTGCAGAGGAGGCTCTCAGACA 1444  
 Qy 1510 ATTCTTGATCAGCTATGAGCTATTTGTTGGCGCGAGAAAGGCGCAAGTGAACAACA 1569  
 Db 1445 GCTCATCTGAAGCGCTTAAAG---TTGATTTCAAGAGCTTAAAGAAAGAAATGAG 1502  
 Qy 1570 AAGAGAGATGTCATTCGAGCGTGGAGGTGAGAGTGGAGTGGAGGCTTATCAAA 1629  
 Db 1503 GAGAGAAAGAAACAGAAAGAGAGCTGTGGGGAAGAGAAAGATGAGATGATTTCCA 1562  
 Qy 1630 GACAAACGAGACCTTACCAAGACACCAAGCTACCAAGTTCTGTAAGTGAACAAGCAT 1689  
 Db 1563 AATATCTGAATCTGAGAGAGCATCAGAG-----GAAAGTTTGTGCTTCTC 1610  
 Qy 1690 CCTTATCTTACCTGTTCACCGTTTAACTAATGACAGGAGTACATGATTTTCAAGAT 1749  
 Db 1611 CATTTAAGGAAACGATTTGACATTAAGAAAGATAC-----TCTTCCACACCC 1660  
 Qy 1750 ACAAGATACGGAACGAGCTGTGCGCTTGTGTATACCGGTGAGCGATGTAGCCATTGG 1809  
 Db 1661 AGTCTTTGTGAGCATCGTGGCTCCCTATTTTCAACAGGCGAAATAGACAGAAAGCC 1720  
 Qy 1810 TATTTGTAACATATCAGATGCGCAGACACTTGCCTTATGCGAGCATCTCGAATGCC 1869  
 Db 1721 TTTTCACTTTAGAGGCGAGCAAGAGATGTGGATGTGAAAGCACTTGGCAGATGATG 1780  
 Qy 1870 TCACCCCGATGTCCGAGAGAGATGGGCGCATATAGTCCCGTATCTATGCGCAATTAG 1929  
 Db 1781 AGCAGACGACTTTGAGGATTAAGAGAGCGGTAGAGATCTTGTTTGTGCGCGAGAC 1840  
 Qy 1930 GCTCCCGACACTCATCTGTATACCTGCACTAGTCGCCAATATCTGTATACCTCACATGCG 1989  
 Db 1841 ACGGAGAGAGACGGAACGCAACCTGAGTCAAGCAGATAGGTCAI-----1885  
 Qy 1990 ATCTACTGCGCGCATGGCGCTCATGGGCGTCAAGCAATGACCAAGAGAGCAAAATTGC 2049  
 Db 1886 -----CTCGAGTCTGGCAGTGT 1904  
 Qy 2050 GCAACCGCAACACGCAATCATCATGATGGCGCGCACCAATGGCGGACCACTGTCTGG 2109  
 Db 1905 TCCAGCGAATGAGAGATGACAGCACTGTGATTTGCAATGTGTGTCTTGTGTGG 1964  
 Qy 2110 ACACCAATCACAGCTGATCATCGCACTTACGAATTTGGCTGTGAGTGCAGGACGAG 2169  
 Db 1965 TGAACCTTCACTTCTTACATCGCTGTGTGACAGCTTCTGCAAGAGGTGAATATA-----2019

Qy 2170 CTGCGAAGATTAAACATCATGACAACTCTTTTATGAGCCCGTCCAGACAAACGCTGG 2229  
 Db 2020 -----GATAAGCCAGCTACTGAGAAATGAAACCAACTGAAA 2059  
 Qy 2230 TTGATATGAAGATGATGATGATGCTGAAATGACATCATGAAACAGCGCTGTGGCGACA 2289  
 Db 2060 CTGAATATGAAAGAAAGAGTCAAGTCTTTCCAGTTCATGAGACTTTCTAGAAAGATC 2119  
 Qy 2230 GTGCGCAAGGATGCGGCTGTCTCCGTTTACTATTTCCCAACAGAGACATGACAGG 2349  
 Db 2120 CTCCCAAGGCAAGCAATGAGATAGCCAGCATCTTAACAATACAGTGAAGAAC 2179  
 Qy 2350 ATGGCGCACGTTCAAAAGCAAGGACCTGAAGTATCTCAAGGAGCATGATGATTT 2409  
 Db 2180 TTGAAGAAATCAGGCAAGAAATGCCACTGTGTGAT---AATTTTCCAACATATCT 2236  
 Qy 2410 GTGTGTGGGACTGTGTGCTGCTGTTGTAATTTCAAGAGTGGGTATCGCTCATGCTCT 2469  
 Db 2237 TATCTGGGACTGTCTCCATATTTGTTAAAGTAAACATGTGTCAACCTGTGTGA 2296  
 Qy 2470 TCGATCCCTTGTGAGCTCTTATCAGCTGTGTGATTTGTGTCAACGATTTTCAATG 2529  
 Db 2297 TGAACCAATTTGTGACCTGCGCATCACCATCTGTATGTCTTAATATCTCTTTCAATG 2356  
 Qy 2530 CAATGATCACAGATATGAAACAAGAGATGGAACGCGTGTCAAGATGCACTATT 2589  
 Db 2357 CCATGAGACATTAACATGACGACCATTTCAATTAATGTCTTACATGAGAACTTGG 2416  
 Qy 2590 TCTTACCGCGCACTTTGCGCATCGAGCGCACCATGAAGCTAATGCGCATGAGCCCAAGT 2649  
 Db 2417 TATTCATCTGGATCTTTACAGCAAAATGTTCTGAAATATTTCCATGATCTCTTACT 2476  
 Qy 2650 ACTATTTCCAGAGAGGCTGGAACATCTTGCATTTATCTGTGCGCTTATGCGATGG 2709  
 Db 2477 ATTAATTTCCAAAGAGCTGGAATATCTTGAAGGTTTATGACGCTTACCTGTG 2536  
 Qy 2710 AACTGGGACTGAGAGGATGCAAGGCTGTGCGTATGCGTATGCGTCTTGTGATGCTGCTG 2769  
 Db 2537 AACTGTGACTGCGCAATGTGGAAGATTAATCTGTCTCCGTTCAITTTGATGCTGCGAG 2596  
 Qy 2770 TATTCAACTGCGCAAGTCTTGGCCCACTTAATTTACTCATTTGATTAAGAGCGA 2829  
 Db 2597 TTTTCAAGTTGGCAAAATCTTGGCCCAAGTTAAATGCTTAATAAGATCATCGGAAT 2656  
 Qy 2830 CCATGGGCGCTTGGGTATCTGACATTTGTACTTATGCAATGCTTATCATCTTGTGCGG 2889  
 Db 2657 CCGGGGGGCTCTGGGAAATTTAACCTGTCTTGGCCATCATGCTTCAITTTTGGCG 2716  
 Qy 2890 TGAATGGAATGCAACTGTTCGGAAGAAATTAATGAA---TCACAGAGCCGCTTTCGG 2946  
 Db 2717 TGGTGGGCAATGAGAGCTTTTGTGTAAGATTAAGAAATGTGTGTGCAAGATGCGCAATG 2776  
 Qy 2947 ATGCGCACTGCGCGCTGGAATCTTACCGACTTTATGCAAGCTTCAATGCTGTGCTC 3006  
 Db 2777 ATGTCAACTCCACCGCTGCAATGAATGACTTCTTCACTCTTCCGATTTGTGTTC 2836  
 Qy 3007 GGGTGTCTGCGGAGAAATGATGAGTCCATGATGAGGAGTCAATGATGAT---GGGCGATG 3063  
 Db 2837 GCGTGTGTGTGGGAGTGAATGAACATGATGAGGAGTGTGATGAGTGTGCTGTCAAG 2896  
 Qy 3064 TCTGTGCAATTCCTTCTTGTGCGCACCGTGTGATGCGCAATCTTGTGTGTTAACTC 3123  
 Db 2897 CCATGTGCTTACTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2956  
 Qy 3124 TTTTCTTACCTTGTCTTTTGTCCAAATTTGGCTCATCTAGCTTATGAGGCGGACCTGGCG 3183  
 Db 2957 TCTTCTGCGCTTGTCTTGTGAGCTCATTTTAAGTGAACAACCTTGAAGCACTGATGATG 3016  
 Qy 3184 ATTAAGATGCAATTAATTAATGACGAGCGCTTCAATGGAATGCGCATTTTAAAGTTGGG 3243  
 Db 3017 ATTAATGAATGAATTAATCTTCAAAATTTGCTGTGATGATGACAAAGAGATGATTAAG 3076

OY	3244	TTAAACGGTAATTTCTGCTATGTTCTCAAGTTAAATAGCAAAATTTGACAAATTCAAATCA	3303
Db	3077	TGAAAAGAAAATATATGATATTTATTCACAGCTCTCTATTAGAAACAAAGATTTT	3136
OY	3304	GTGATCAACCATCAGGTGAGAGAACCAACAGATCAGTTGGATTGTGAGCGAAGCATG	3363
Db	3137	ATGAAATTTAAACCTTGATGATCTTAAACAAAGAAAGACAGTTGTATGTCCATCA--	3193
OY	3364	GTGACAAAGAACTGGAGCTGGGCGACAGCAGATCTCGCCGACGGCTCATCAAGAG	3422
Db	3195	-----TACAGCAAAATTTGGGAAAGATCTTGACTATTTTAAAGATGTAAATGG	3244
OY	3424	GGATCAAGAGACAGACGAACTGGAGGTGCGCATGGGGATGGATGAAATTCAGATAC	3483
Db	3243	AACTACAAAGTGTATAGAACTGGGACGAG-----	3277
OY	3484	ACGGCGATGAGAAACAAACAGCCGAAGAAATCCAAATATCTTAATATACGACATGA	3543
Db	3273	-----TGTTGAAAATATCAATATATGTAAGAAAGATTACAT	3303
OY	3544	TTGGCACTCAATTAAACCAACGAACATATGCTGGAACACGAGCTTAAACATAGAGTT	3603
Db	3309	GTCAATTCATTAACACCCAGCTTACTGTGACTGTACCAATTTGCTGATAGAGA-----	3363
OY	3604	TGTCTTTCAGGACGACACATGCGCAGATTAATCAATATGTGTGCCATTAAGAAATCGAC	3663
Db	3363	-----ATCTGACTTTGAAAATTTTAAACACGGAAGACTTTATATGATGATCTGG	3413
OY	3664	CATTCAAGGACGAGACCAACAGGGCAGCGCGAGACGATGAGGGCGAGAGAACCGC	3722
Db	3416	AAGAAAGCAAGAGAACTGATATGAAGCAGTACCTCATCAGABGTAGACTGTGACA	3477
OY	3724	ACGCCAGAAAGAGATTATGGTCTCGACGAGAACTGGAACGAGAGGGCGAATCGAG	3783
Db	3476	TCGGGCACTGTAGAGAAACAGCCCGTAGTGAACCTGAGAAACTCTGGA-----	3522
OY	3784	AGGGCCCCCTGCAGCGGTATATCATTTATTCATGACACAGACGAGATATATCTCATGAT	3844
Db	3529	-----	3528
OY	3844	ATCCAGCTGATGTCGCCCGCATTCGTACTATTAAGAAATTTCCGATCTTAGCCGGTGA	3903
Db	3529	--CCAGAGCTTGTTCACTGAGAGTTGTGTACAAAGATTCAGAGTTGTCAATCAATG	3586
OY	3904	ATGACTCCCGTTCTGCGAAGAGTGGGCAATTTACGACTGAAAATTTTCATTAATTTG	3963
Db	3587	TGGAAGAGGACGAGAGAAACATGTGTGAACCTGAAAGACGCTGTTCCGAAATAGTTG	3644
OY	3964	AAATATTAATTTTGAACACGCTGTATCATATGATTTTAATGATAGCTTACGTTGG	4023
Db	3647	AAACATTAACGTGTTTGAGACTTCATGTTTTCATATTTCTCTTGATGTGGTGTCTGG	3708
OY	4024	CATTAGAGATGTATCTGCGACAAACCAATCTCGAGATATTTTATATCTATAG	4083
Db	3707	CATTGGAAGATATATATATGATCAGCAAGACGATTAAGACGATGTGGAATATGCTG	3766
OY	4084	ACAGATATTTACGGTTATATTTCTCTTGGAAATTTATATCAAGTGTGGCGCTCGGCT	4143
Db	3767	ACAAGTTTCTACTTACATATTTTCATCTTGGAAATCTCTTAAATGGGTGGATATGGCT	3822
OY	4144	TCCAAAGTACTTACCAACGCGTGTGTGGCTCGATTTGCTGATGTCATAGTATGCG	4203
Db	3827	ATCAACAATATTTTCCACATGCTGTGTGTGGCTGACCTTCTTAATTTGTGATGTTTTCAT	3888
OY	4204	TTATCAACTGTGGTCTTCACTGTGTGAGCGTGTGATTCACACCTTCAAGCTATGCG	4263
Db	3887	TGTTAGTTTAAACAGAAATGCTTTGGTTACTCAAACTTGAACCTCAAAATCTTCA	3946
OY	4264	GAACCTTAAAGACCTGAGACCACTACGTGCATGTCCCGTATGCGAGGGCAATGAGGCTCG	4322
Db	3947	GGACACTAAGAGCTTGAGACCTCTTAAGCCTTATCTCGATTTGAAGAGATGAGGTTAG	4006
OY	4324	TGCTTAATGCGCTGCTACAGCTATACCGTCCATCTTCAATGTGCTATTTGTTGTCTTAA	4383

D	4007	TTGTGAATGCCCCCTTTTAGAGCAATTCATCATCATATGATATGCTTCTGCTTGTCTTA	4066
Q	4384	TATTTTGGCTAATTTTGGCCATAATGGGTGTACAGCTTTTGTCTGGAAAAATATTTTAAGT	4443
D	4067	TATTTGGCTAATTTTTCAGCATTATGGGCGTAAATTTGTTGTCTGGCAAAATCTACACT	4122
Q	4444	G---CGAGACATGATATGGCACGAAGCTCAGCCACGAGATCATACAAATGGCAATGCTT	4500
D	4127	GTATTTAACACCAACTGTGTACAGGTGTGACATCGAAGACGTGAATATCATCTGATTT	4186
Q	4501	GC-----GAGACGAGACTACAGTGGGTAAATTCACCAATGATTTTG	4545
D	4187	GCTTAAACCTAATAGAAAGAAATGAGCTGCTCGATGGAAAAATGTAAAGTAACTTTG	4246
Q	4546	ATCATGTAGTAAACCGCTATCTGTGCTTTTCCAAGTGGCCACTTCAAAAGCTGATAC	4605
D	4247	ATTAATGTAGAATTTGGGTATCTCTCTTTGCTTCAAGTTGCCACTTCAAGAGATGATGG	4306
Q	4606	AAATCATGAACGATCTATTCGATTCAAGAGGTGGACAGAACCAATTTGTGAACGA	4665
D	4307	ATATATGTATGACAGCACTGTATTCAGAAATGTAGAACTCAGCTAGTATGAAAGAA	4366
Q	4666	ACATCTACATGATTTATTTGCTATCTCATCATATTTGGATTCCTTTTTCACACA	4722
D	4367	GTCGTACATGATCTTACTTTGTTATTTTTCATCATCTTTGGGTCCTTTCACCTTGA	4422
Q	4726	ATCTGTCATTGTGCTTTATTCATTGTATATTTTAATGACAAAGAAAAAGCAGGTGAT	4785
D	4427	ACCTGTTATTTGGTGTATCATATGATATTTCAACACG---AGAAAAAGAAATTTGGAG	4485
Q	4786	CATTAGAAATGTTCAAGACAGATCGAAAAAGTACTATATGTATGTAAAAAGATGG	4844
D	4484	GTCAAGACATCTTTATGACAGAAAGACAGAAAGAAATCTATATGCAATGAAAAAATTAG	4544
Q	4846	GCTCTAAAAACCATTAABCCATTCGAACCAAGTGGCGACAAACCAATATAGCT	4900
D	4544	GATCGAAAAAACCGAAAAAGCTTATCCTGCACAGGAAACAAATTCGAAGAAATGATCT	4603
Q	4906	TTGAATATGTAAACGATAGAAATTCGATATATCATATATGTTATTCATTGGTCTGAACA	4965
D	4604	TTGACTTGTATACAGACAGACTTTTTCATATGACATATATATATCTCATCTGTCTTAACA	4665
Q	4966	TGTTTACCAGTACCCTCGATCGTTACGATGCGTGGACACGATATACCGCGTCTTGAAT	5025
D	4664	TGTCACAAATGATGGTGGAAACAGATGACGAGATGAATATGTGCTACATTTTGTCAAC	4722
Q	5026	ATCTCAATGCGATATTCGTATTTTCAAGTTCGAAATGTCATTAATAATATTCGCTT	5085
D	4724	GCATCTAACTGTGTCTCATTTGTGCTATTTACGAGAGTGTGATCTGAACCTATCTTC	4783
Q	5086	TACGATATCATATTTTATGAGCCATGGAATTTATTTGATGTAGTATGTCATTTTAT	5145
D	4784	TACGCAATTATATTTTACATTTGATGGAATATTTTGTATTTTGTGTGTCTATTTCTCT	4843
Q	5146	CCATCTTAGTCTTGTACTTGAACGATATTTACGAAAGTACTTGTGTGCGCCAGCCCTGC	5205
D	4844	CCATTTGTATGTATGTTCTTGTCCGAGCGTATAGAAAAAGTATTTGTGTGCCCCTACCTGT	4903
Q	5206	TCCGATGTGTGCGTGTGGCGAAAGTGGGCGGTGCTTTCGACTGTGTAAGGAGCGAAG	5265
D	4904	TCCGATGTATCCGCTCTGTGATGGAATGGCCAAATCTACGCTCATACAAAGAACCAAGG	4963
Q	5266	GCATTTGGACACTGTCTTGGCGATGTGGCATGTGCGTGGCGGCGCTGTCAACATCTGCG	5322
D	4964	GGATTCGACGCTGCTCTTGTCTTGAATGATGTCCTTCTGCGGTGTTTAACATCGGCG	5022
Q	5326	TGCTGCTGTTCTGTGATGTTCAATCTTTGGCATTTTCCGATGTGCTTCTTCAACGACG	5385
D	5024	TCTTAATCTTCTTATGTATGTTCAATCAAGCAATCTTTGGGATGTCCAACTTTGCTATG	5083
Q	5386	TGAAGAGAGAGCGCATTTACGACGCTTACAACTTCAGACCTTTTGGCCAGACATGA	5445



QY 3550 ACTCAATTAACCAACCAACATAGACTGGAACAGAGCTAAACATAGAGGTTGTCT 3609  
 Db 3366 GTCCAGCAAGCAAGCAAGAAATCCACCTG--TGTCCGCTGGCCAGAGCCCTCCGAT 3423  
 QY 3610 TACAGAGCAAGCAAGCTCCAGCATTTAACTCATATGTAAGCCATAAGATGACCATTC 3669  
 Db 3424 TCCAGGACTGGA----GCCAGGTGTCAAGCACTCCTACTGAGGCCAGAGCCAGTGC 3479  
 QY 3670 AGAGCAAGCAAGCAAGGAGGAGGAGGAGATGAGAGGAGGAGAGAGGAGGAGGAGG 3729  
 Db 3480 ATCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3539  
 QY 3720 GCAAGAGGATTTAGGTTCTGCAAGAGACTGCAAGAGAGGAGGAGGAGGAGGAGGAGG 3789  
 Db 3540 GA-----CCCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3583  
 QY 3790 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3849  
 Db 3584 CCAACACCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3643  
 QY 3850 CTGATGCTGCGCCGATTCGTAATTAAGAAATTTCCGATCTTACCGGAGGAGGAGGAG 3909  
 Db 3644 AGGAGCTGCTTACGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3703  
 QY 3910 CGCCGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3969  
 Db 3704 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3763  
 QY 3970 AATAATTTTGAACAGCTGTTATCACTATGATTTTATAGTATGAGTATGAGTATGAG 4029  
 Db 3764 GCTGGTGGAGACATTCATCATCTTCAATGATCTCACTCAGGAGGAGGAGGAGGAGG 3823  
 QY 4030 AAGATGTACATCTGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4089  
 Db 3824 AGGAGATCTACCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3883  
 QY 4090 TATTTACGATTAATTTCTTTGGAATGTTAATCAAGTGGAGGAGGAGGAGGAGGAGG 4149  
 Db 3884 TGTTCACATATGCTTGTGCTGAGATGCTGCTCAAGTGGAGGAGGAGGAGGAGGAGG 3943  
 QY 4150 TGTACTTACCAAGCGGTGAGTGGCTGATTTGCTGATTTGCTGATTTGCTGATTTG 4209  
 Db 3944 AGTACTTACCAAGTGGTGGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGAT 4003  
 QY 4210 ACTTGTGCTTCACTTGTGAGAGTGGTGTATCAAGCTTCAAGCTTCAAGCTTCAAG 4269  
 Db 4004 GCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4063  
 QY 4270 TAAAGAGCACTGAGCACTAGAGTGCATGCTCCGATGAGGAGGAGGAGGAGGAGGAGG 4329  
 Db 4064 TGCCTGAGCTCCGCTCTGAGAGCTTGTCAAGTTCAGTTCAGTTCAGTTCAGTTCAG 4123  
 QY 4330 ATGCGCTGTGTAAGAGTATACCTGCTCATCTTCAATGCTATGCTATGCTATGCTATG 4389  
 Db 4124 ATGCGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4183  
 QY 4390 GGTCTATTTTGGCAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4449  
 Db 4184 GGTCTATTTTGGCAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4243  
 QY 4450 ACATGA-----ATGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4503  
 Db 4244 ACAGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4303  
 QY 4504 AGAGCGAGAGACTAGC-----GTGGTGAATTCAGCATGATTCATGATTCATGATTC 4551  
 Db 4304 AGTCTTGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4363  
 QY 4552 TAGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4611  
 Db 4364 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4423  
 QY 4612 TGAAGATGCTATGATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4671

Db 4424 TGTATGAGCTGTGAGACTCCAGGGGATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 4483  
 QY 4672 ACATGATTTAATTTGGTATTTCTTCAATCATATTTGATTCCTTTTCACTCAATCTGT 4731  
 Db 4484 ACATGATCATCATTTTGTCAATTTTCAATCATCTTTGGGTCTTTTCTTCACTCAATCT 4543  
 QY 4732 TCATTTGTTATATGATTAATTTTATATGAGCAAAAGAGAGGAGGAGGAGGAGGAGGAG 4791  
 Db 4544 TTATTTGTTATATGATTAATTTTATATGAGCAAAAGAGAGGAGGAGGAGGAGGAGGAG 4600  
 QY 4792 AAATGTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4851  
 Db 4601 ACATTTCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4660  
 QY 4852 AAAAAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4911  
 Db 4661 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4720  
 QY 4912 TAGTACCGATTAAGAAATTTGATTAATCATATTTATTTATTTATTTATTTATTTAT 4971  
 Db 4721 TTGTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4780  
 QY 4972 CCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5031  
 Db 4781 CCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4840  
 QY 5032 ATGCGATTTATGATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5091  
 Db 4841 ACCTGCTTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4900  
 QY 5092 ATCACTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5151  
 Db 4901 ACTACTTCTTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4960  
 QY 5152 TAGGCTTTGATTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5211  
 Db 4961 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5020  
 QY 5212 TGTGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5271  
 Db 5021 TCATCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5080  
 QY 5272 GGAATGCTTTTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5331  
 Db 5081 GCAAGCTGCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5140  
 QY 5332 TGTTCCTGATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5391  
 Db 5141 TCTTCTGCTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5200  
 QY 5392 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5451  
 Db 5201 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5260  
 QY 5452 TCTTTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5511  
 Db 5261 TCTTTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5320  
 QY 5512 AAGATGAGG-----TCGACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5562  
 Db 5321 GGGGCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5380  
 QY 5563 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5622  
 Db 5381 GCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5440  
 QY 5623 TTAATATGATGATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5682  
 Db 5441 TCAACATGATGATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5500  
 QY 5683 AGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5742

Db 5501 AGCCCTGAGTGAAGACGACTTCATATGTTCTTATGATGATCTGGAGAAATTTGACCCAG 5560  
 QY 5743 AGGGCAACCAAGTATACAGCTATGATCAGCTGTCCGAATTCCTGACGTATGAGACCC 5802  
 Db 5561 AGGCCACTGATTTATGATGATTTGGTCTGTCTGACCTTTGCGACGCGCTGTGACG 5620  
 QY 5803 CGCTGAGATCCAAACCGAAGATGACAGATCATGATCATGAGATATGACATATCCATCTGTC 5862  
 Db 5621 CACTCGGATTCGCAAGCCCAACCAATGAGCTCTCAACATGAGACTGCGCCATGATGA 5680  
 QY 5863 GGGTACCTCATGATCTGGGTCAGATCTCTGACGCGCTTATGAGAAAGCTTTTGGCCG 5922  
 Db 5681 GTGGGAGCGCATTCATTTGATGATGATCTTTTGGCTTTCACCAAAAGGCTCTGGGG 5740  
 QY 5923 GGAAGGCAATCCGATAGAGAGACGGGTGAGATTGATGAG-----ATAGCGCGCGCC 5976  
 Db 5741 AGTCTGGGAGATGAGAGCGCTGAGATCCAGATGAGAGAGATTGATGAGCGCAACG 5800  
 QY 5977 CGGATACGAGGCGCTACGAGCGCTCTCATCAACGCTGTGGCGCTACGCGTGAAGATGAT 6036  
 Db 5801 CATCAAGATCTCTTACGAGCCCATCAACCACTCCGCGCGCAAGACGAAAGAGTGT 5860  
 QY 6037 GCGCCCGGCTAATCCAGCAGCGCTGGCGAAGCAAGCGCGCGCG 6083  
 Db 5861 CGGCGATGTTATCCAGAGAGCTTCGCGAGGCACTGCTGCAACGC 5907

## RESULT 9

US-09-896-994-1  
 ; Sequence 1, Application US/09896994  
 ; Publication No. US20030074024A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ken Stokes  
 ; Jos e Morissette  
 ; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
 ; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1 is  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WordPerfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/896,994  
 ; FILING DATE: 02-Jul-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/514,907  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul K. Legaard  
 ; REGISTRATION NUMBER: 38,534  
 ; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6048 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-896-994-1  
 Query Match 14.4%; Score 940.2; DB 10; Length 6048;

Best Local Similarity 55.4%; Pred. No. 1,8e-250;  
 Matches 2052; Conservative 0; Mismatches 1583; Indels 72; Gaps 9;

QY 2413 TGTGGAGCTGTGTTGGGTTTGGTTGAAATTTGAGAGTGGGTATGCTGATCGTTTCG 2472  
 Db 2087 TCTGGGAGTGTGCGCCGCTGTGTGATGTCCATGACAGAGATGAAATGGTGGTATGAG 2146  
 QY 2473 ATCCCTTGTGAGCTGTTTCATCAGCTGTGTGATGTTGGTCAACGATGTTCAATGGCA 2532  
 Db 2147 ACCCGTTTACTGACCTCACCATCACTATGTGTGATGATGATCACTCTTCAATGCGCC 2206  
 QY 2533 TGGATCACCAGATATGAAACAGAGATGAAACGGGTCTCAAGAGTGGCACTAATTTCT 2592  
 Db 2207 TGGAGACTACAAACATGACATGAAATGAGAGATGTTGAGAGTGGAAACTGTCT 2266  
 QY 2593 TCACGGCACTTTTGGCATGAGGCGCACCATGAGTAAATGGCCATGAGCCCCAGTACT 2652  
 Db 2267 TCACAGGGATTTTTCACAGCAGAGATGACCTTCAGATCAATGCCCCCTGACCCCTACT 2326  
 QY 2653 ATTTCCAGAGAGGCTGGAAACATCTTCGATTCATATGCTGAGCCCTATGCTATTGGAAC 2712  
 Db 2327 ACTTCCACAGGCTGGAAACATCTTCGATTCATATGCTGATTCATCTTACCTCATATGAGC 2386  
 QY 2713 TGGGACTCGAGGAGTGTCCAGGCTGTCCGTAATGCGTTCCTTTCGATGCTGCTGTAT 2772  
 Db 2387 TGGGCTGTCCCGCATGAGCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2446  
 QY 2773 TCAAATGCGCAAGCTTTGGCCCACTTAATTTACTGATTTGATGATGAGACGACCA 2832  
 Db 2447 TCAGCTGCGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2506  
 QY 2833 TGGGCGCTTGGGTAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2892  
 Db 2507 TGGGCGCTTGGGTAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2566  
 QY 2893 TGGGAATGCACTGTTGCGAAAGATTTATCATGATGATGATGATGATGATGATGATGAT 2952  
 Db 2567 TGGGCAATGCACTGTTGCGAAAGATTTATCATGATGATGATGATGATGATGATGATGAT 2623  
 QY 2953 ACTGCGCGGCTGGAGCTTCCACGCTTATGATGATGATGATGATGATGATGATGATGATG 3012  
 Db 2624 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2683  
 QY 3013 TGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3069  
 Db 2684 TGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2743  
 QY 3070 GCATTCCTTCTTCTTGGCCACCGTTGTATGCGCAATCTTGTGTACTTAATCTTTCT 3129  
 Db 2744 GCTGCTGCTGCTTCTTCTTGTGTATGATGATGATGATGATGATGATGATGATGATGAT 2803  
 QY 3130 TAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3189  
 Db 2804 TGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2863  
 QY 3190 ATACGATAAATATAGCGAGCGCTTCATGATGATGATGATGATGATGATGATGATGATG 3249  
 Db 2864 AGATGAAACACCTCCAGCTGCGCTGCGCGCGAGATGATGATGATGATGATGATGATGAT 2923  
 QY 3250 GTAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3309  
 Db 2924 GGAACCACTGGGATTTCTGTGTGTGTCTCTGTGGGACCGGCC-----TC 2268  
 QY 3310 AACCATGAGTGAAGAGACCAACCAATGATGATGATGATGATGATGATGATGATGATGAT 3369  
 Db 2969 AGAAGCTCGAGCTTGGCCGAGGCGGAGGCGAGCTGCGCACTGATGATGATGATGATGAT 3028  
 QY 3370 ACGAATGAGCTGAGGCGACGACGAGATCTGCGCAAGGCTTCTATCAGAGGAGATCA 3429  
 Db 3029 CCGCGCACCCCAAGAGACGAGAGAGGCTCTCCACCCCAAGAGAAACACAGTTTGAGG 3088  
 QY 3430 AGGAGCAGACGCACTGAGAGTGGCCATGCGGGATGAGATGAGATTCAGATTCAGCGCG 3489

3089 AAGCGACCAACGAGGCCAGGCCCGGCGGATCC-----AGAGCGCG 3133  
Qy 3490 ACATGAAAGAACCAAGCCGGAAGAAATCCAAATATCTAAATACCAAGATGATTTGCA 3549  
Db 3134 TGTGTGTCCTCATCTGTGTGCGGAGTCAAGACAGATGACCAAGAAAGATGAGAGA 3193  
Qy 3550 ACTCAATTAACCAACCAAGACATATAGTGAACAGAGCTAAACCATAGAGTTGTCT 3609  
Db 3194 ACAGCTGGGACCGAGAGAGATCCAGACAGACAGAAATCCAGCTGTGTCCGCT 3253  
Qy 3610 TACAGACGACGACCTGCCAGATTAATCTATATGTAGCCATAAGATGACCATTTCA 3669  
Db 3254 GGGCCAGAGGCCCTCCGATTCAGAGCTGAGCCAGGTGTCAGCAGCTGCTCTCTG 3313  
Qy 3670 AGAGAGAGAGCCCAAGGCGAGCCGCGAGATGAGAGGCGAGAGAAAGCCGACCCA 3729  
Db 3314 AGGCGGAGCGCATGTCATCTCAGCGCAGCTGCGGACAGATGAAAGCCGACCCG 3373  
Qy 3730 GCAAGAGATTTAGTCTCGACGAGAACTGACGAGAGGCGAATGCCAGAGGGCC 3789  
Db 3374 CCCCAGGCTGGGTGAGACCCAGAGGACATTTGCTCCGAGGGCAGCAGACAGCATGA 3433  
Qy 3790 CGCTCGACGATATCATTTATTCATGCAACGAGAGATATCTCGATGATATTCAG 3849  
Db 3434 CCAACACCGCTGAGCTCTGAGAGAGATCCCTGACCTGGCCAGATGTCAGAGCCAG 3493  
Qy 3850 CTGATTCCTCCCGGATTCGATATTAAGAAATTTCCATCTTACCGGTGACGATGCT 3909  
Db 3494 AGGACTGCTTCACTGAAAGGCTGTGTCCGCGCTGTCTGCTGTGCGAGCACACAC 3553  
Qy 3910 CGCGCTTGGCAGAGATGGGCAATTTACGATGAAACCTTTCAATTAATGAAATA 3969  
Db 3554 AGGCCCCAGGAGGCTGTGTGGCGGTGGCGAAGACCTGCTACCAATCGGGAGCA 3613  
Qy 3970 AATATTTGAAACAGCTGTATCACTATGATTTTATGATAGTACTTATGCGATTAG 4029  
Db 3614 GCTGGTGAAGCATTCATCATCTTCATGATCTCACTCAGCAGTGAAGCGCTGCTCG 3673  
Qy 4030 AAGATGACATCTGCGCAAGAAAGCCCATCTGCGAGATTTTATATATATGACAGAA 4089  
Db 3674 AGGACATCTACCTGAGAGGAGGAGAACCATCAAGGTTCTGCTGATGATGCGCAAGA 3733  
Qy 4090 TATTTAGGTTATATCTTTCTTGAATGTTAATCAAGTGTGGCGCTCGGCTCAAG 4149  
Db 3734 TGTTCACATATGTCTTGTGCTGAGATGCTGCTAAAGTGGTGGCTTCAAGCTTCAAGA 3793  
Qy 4150 TGTACTTCAACGACGCTGTGTGTGCTGATTTGCTGATTTGCTATGCTTATCA 4209  
Db 3794 AGTACTTCAACGATGCTGTGTGTGCTGATCTTCTCATGTGAGAGTCTCTGTGCTCA 3853  
Qy 4210 ACTTGTGCTTCACTTGTGAGCTGTGTGATTCAGACCTTCAAGACTATGCGACGT 4269  
Db 3854 GCTGTGTGGCAACACCTGTGGCTTTGGCGAGATGGGCCCATCAAGTCACTGCGAGCGC 3913  
Qy 4270 TAAAGACGTCAGACCACTAGCTGACATGCTCCGATGACAGGCGTAGGGTCTGCTTA 4329  
Db 3914 TGGCGACCTGCTGTCTGAGAGCTGTGTACGATTTGAGGGCAATGAGGGTGGTCA 3973  
Qy 4330 ATGCGCTGTACAAGCTATACGCTCATCTTCAATGTGCTATTTGCTATATTTT 4389  
Db 3974 ATGCTCTGTGGGGCCATCCGCTCATATGAGAGTCTCTCTGCTCATCTTCT 4033  
Qy 4390 GGTATATTTTGGCAATATGAGTGTAGCTTTTGTGCAAAATATTTTAAAGTCGAG 4449  
Db 4034 GGTCTATCTTCAAGCATATGAGGCGTGAACCTTTTGGCGGAATTTGGAGTGCATCA 4093  
Qy 4450 ACATGCA-----ATGCGACGAACTCAGCAGAGATATACCAATATGCGATGCTGCG 4503  
Db 4094 ACAGAGAGAGGAGACTTGTCTTTGAACCTACCATGTGAAACAAAGAGCCAGTGTG 4153  
Qy 4504 AGAGGAGAACTACAC-----GTGGGTGAATTCAGCAATGAAATTCATCATCAG 4551  
Db 4154 AGTCTTGAACCTGACCGAGAAATTTTACTGACCAAGGTGAAGTCAATTTTGAACAG 4213

Qy 4552 TAGGTAAGCGGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGGCTGATACAAATCA 4611  
Db 4214 TGGGGCGGGTACTGGCCCTTCTGACAGTGGCAACTTTAAAGCTGTGATGACATTA 4273  
Qy 4612 TGAAGATCTATGATTCAGAGAGGTGACAAGCAACCAATTCGTGAAGCAATCT 4671  
Db 4274 TGTATGACGCTGTGACTCCAGGGGGTATGAAGAGACCTCAGTGGGAATACAACTCT 4333  
Qy 4672 AATATATTTATTTTGTATTTCTTATCATATTTGATCTCTTTTCACTCAATCTGT 4731  
Db 4334 ACATGATATCATTTTGTCTATTTTCACTTTTGTGGGTCTTTTCTTCACTCTGAACTCT 4393  
Qy 4732 TCAATTTGTATATGATTAATTTTATGCAAAAGAAAGAAAGAGAGATGATTAAG 4791  
Db 4394 TTATTTGTATATGATTAACCTTCAACCAAGAAAGAAAGTATGAGGGGCGAG--G 4450  
Qy 4792 AATGTTATGACAGAAAGATCAGAAAGTACTTAATGCTATGCAAAAGATGGGCTCTA 4851  
Db 4451 ACATCTTATACAGAGAGAGAGAGAAAGTACTTAATGCTATGAAAGCTGGGCTCA 4510  
Qy 4852 AAAAACTTAAAGCCATTCAGAGCCAGGTGGCCAGCAAGCAATGCTTTTGA 4911  
Db 4511 AGAAGCCAGAGCCCATCCAGCGCCCTGAACAAAGTACAGGGCTTCAATTTGACA 4570  
Qy 4912 TAGTACCGATTAAGAAATTCATATATATATTTATTTATTTGCTGAAACATTTCA 4971  
Db 4571 TTGTGACCAAGAGCCCTTGTACGTCACATCATGTTTCTGATCTGTGAATATGAGA 4630  
Qy 4972 CCATGACCTCGATGTTATGATGCTGAGCAGGTATTAAGCGGCTCTAGACTATCTCA 5031  
Db 4631 CCATGATGCTGAGACAGATACCAAGTCTGTGAAATTAACATCTTGGCCAAAGATCA 4690  
Qy 5032 ATGCGATATTTGATGATTTTCAATTCAGTGTCTATTAATAATTCGCTTTACAT 5091  
Db 4691 ACCTGCTTGTGGCCATCTTCAAGCGAGTATGTCAGAGTGGCTCCGCGCC 4750  
Qy 5092 ATCACTATTTATGAGCGATGAAATTTATTTATGATGATGTTGCTATTTATCATCT 5151  
Db 4751 ACTACTTCTTACCAACAGCTGGAATATCTTGTGATGCTGTGCTTCTTCAATCG 4810  
Qy 5152 TAGGCTTGTACTTAGGATTTATGAGAGTATTCGAGTCTGTGCGCGACCTGCTCGAG 5211  
Db 4811 TGGGACGCTGCTCTCGGACATCATCAGAAAGTACTTCTTCCCGACGCTTTCGAG 4870  
Qy 5212 TGTGCGTGTGCGAAAGTGGGCCGTGTCTTCACTGTGTAAGAGAGCCAAAGGCAATTC 5271  
Db 4871 TCATCCGCTGGCCGAATAGGCCGATCTCAGACTGATCGAGGGGCCAAAGGGATCC 4930  
Qy 5272 GGAACCTGCTTTGCGGTGGCCATGTGCGTCCGCGCTGTTCACATCTGCTGCTGCG 5331  
Db 4931 GCAAGCTGCTCTTGGCCCTCATGATGTCCGCTGCGCTCTTCAACATCGGGCTGCTGCG 4990  
Qy 5332 TGTCTGTGATGATCATCTTTGCAATTTTGGCATGTGTCTTATGACGAGGAAG 5391  
Db 4991 TCTTCTGTGATGATCATCTTCACTCATCTTTGCAAGGCGCAACTTGTATGTCAAGT 5050  
Qy 5392 AGAAGAGCGGATTAAGACGCTTCAACCTTCAAGACCTTTGGCAGAGCATGATCTGCG 5451  
Db 5051 GGGAGGCGGATGAGAGACATGTTCAACTTCCAGACCTTGGCAAGCATGTGCTGCGC 5110  
Qy 5452 TCTTCAAGATGTCAGCTCAGCGGTGGATGTGTATCTGAGCGCATTTCAATGAGG 5511  
Db 5111 TCTTCAAGATCAGCAGCTGCGCGGTGGATGTGCTCTTCAAGCGCATCTCTCAACCTG 5170  
Qy 5512 AAGGATGGA-----TCCACCGACAGCGCAAGAAAGGTATCGGGGCAATGTGTT 5562  
Db 5171 GGGCGCTTACTGCAACCCCATCTTGGCCCAAGAAATGCTTGGGGGAGATGCGGGA 5230  
Qy 5563 CAGGACCGTGAATACGTTTCTCTCATCATCTTATATATGAGCTTTTGTATGATTA 5622  
Db 5231 GCCAGCGGTGGGATCTCTCTTCAACAGCTATCATCATCTTCTCTATCTGCTG 5290

QY	5623	TTATATAGTACATTCGTCTCAATTCTCCGAGACTTATAGCAGGCCACCGAGGACCTGCAAG	5682
Db	5291	TCAACATATACATTCGCCATCATCTCTGGAGAACTTCAGCTGTGCCACGAGAGAGACACCG	5350
QY	5683	AGGCTCTAACCGACGACGACTACGACATGTACTATAGATCTGTGCGACCAATTGCATTCGG	5742
Db	5351	AGCCCTGAGTAGAGAGACGACTTCATATATGTTCTATAGATCTGTGGAGAAATTTGACCCAG	5410
QY	5743	AGGGCACCCAGTACATACGCTATGATACGCTGTCCGAAATTCCTGGACGTATCTGGAGCCCC	5802
Db	5411	AGGCCACTCACTTTATTTAGATATTCGGTCTCTGTCTGACTTTTGGCCGACGCCCTGTCTGAGC	5470
QY	5803	CGCTGCAGATCCACAACCGAACAGTACAAGATCATATCGATGAGCATACCATCTGTCTC	5862
Db	5471	CATCTCCGTATCGCCAGAGCCCAACCGATATACCTCATCAACATGGACTCTGCCCATATGCGA	5530
QY	5863	GCGGTGACCTTATGTATCTGCGTCCACATCTCTCGACGCCCTTACGAAAGACTTCTTTTGGC	5922
Db	5531	GTTGGGACCCGATCCATTCATGTGACATCTTCTTTGCCCTTACCCAAAAGGGTCTCTGGGGG	5590
QY	5923	GGAAGGCAATCCGATAGAGAGACGGGTGAGATTGTGAG-----ATAGCGGCCCGCC	5976
Db	5591	AGTCTGGGGAGATGGAAGCCCTCTGAAGATCCAGATGAGAGAGAAATTCATATGGCAGCCAAAC	5650
QY	5977	CGGATACGGAGGGCTACGAGGCCGTCTTCATCAACGCTGTGCGCTGTACGCTGAGAGACT	6036
Db	5651	CATCCAAAGATCTCTACGAGGCCCATACACACCACTCCGGCCGACAGCACAAGAGGTGT	5710
QY	6037	GCGGCCGGCTATCCAGACAGCCCTGCGGAAAGCCAAAGCGCGCGCGC	6083
Db	5711	CGGCGATGTTATCCAGAGAGCCTTCCGAGGACCTTCTGTCAACGC	5757

RESULT 10  
 US-10-685-237-1  
 Sequence 1, Application US/10685237  
 Publication No. US20040236377A1  
 GENERAL INFORMATION:  
 APPLICANT: Kenneth B. Stokes  
 Jos,e Morissette  
 TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL  
 SENSING BY CARDIAC PACEMAKERS THROUGH  
 GENETIC TREATMENT  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP  
 STREET: One Liberty Place - 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 6.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/685,237  
 FILING DATE: 14-Oct-2003  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/514,907  
 FILING DATE: 08-Feb-2000  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul K. Legard  
 REGISTRATION NUMBER: 38,534  
 REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO. 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6048 bases

Query Match	14.4%	Score 940.2	DB 18	Length 6048
Best Local Similarity	55.4%	Pred. No. 1.8e-250		
Matches 2052	Conservative 0	Mismatches 1563	Indels 72	Gaps 9
QY 2413	TTGTGGACGTGTGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTAATCCCTCATGCTCTTCG			2472
Db 2087	TCGTGGAGATGCTGCCCGCTGCTGATGTCATCAAGCGAGGAGATGAATGGTGTCTCATGG			2146
QY 2473	ATCCCTTCGTGAGCTCTTATCATACGGTGGGATGTGGTCAACAGATGTCATGAGCAA			2532
Db 2147	ACCGCTTACTGACCTCACATCACTATGTGTCATCTGACTCAACACTCTTCAATGGGCG			2206
QY 2533	TGATTCACCAAGATATGAACAGAGAGATGGAACGCGTCTCAAGATGGGCACTATTTC			2592
Db 2207	TGGAGCACTACACATGACAAAGTAATTCAGAGAGATGCTGAGGTGGAAACCTGGTCT			2266
QY 2593	TCACCGCACCTTTGCCATCGAGGCGCAACATGAAGCTAATGCGCATGAGCCCAAGTACT			2652
Db 2267	TCACAGGAGATTTTCACAGCAGAGATGACCTTCAAGATCATATGCCCTCGACCCCTACTACT			2326
QY 2653	ATTTCGAGAGAGGCTGGAAACATCTTGCATCTTCATATCGTGGCCCTATCCGTATTGGAAC			2712
Db 2327	ACTTCCAAACAGGCTGGAAACATCTTGCACAGCAATCATCTCATCTTACGCTCATGAGC			2386
QY 2713	TGGAGACTCGAGGGGTGTCAGAGGTCTGCCGATATGCGTCCCTTCGATTTGCTGCTGAT			2772
Db 2387	TGGGCTCTGTCCCGATAGACACTTGTGCTGCTGCTCTCTTCCGCTGTGGGGTCT			2446
QY 2773	TCAAACTGGCCAACTCTTGGGCCCACTTAAATTTACTCATTTTCGATTATGGAGCACCA			2832
Db 2447	TCAGCTGGCCAAATCATGAGCCCACTGAAACACATCATCAATGATCATCGGAATCTAG			2506
QY 2833	TGGGCGCTTTGGGTAATCTGACATTTGTACTCTTGATATATCTTCATCTTTGGCGGTA			2892
Db 2507	TGGGGGCACTGGGGAACTGACATCTGTGTGCTAGCCATCATCTGTGTTATCTTGTCTGTGG			2566
QY 2893	TGGGAATGCACTGTTCGGAAGAATATATCATGATCAACAAGACCGCTTTCGGATGGCG			2952
Db 2567	TGGGCACTGACCTTTTGGCAAGACTACTCTGAGCTGAGGGAACAGGACTCA---GGCC			2623
QY 2953	ACTGCGCGCTGGAACCTTCAACGACTTTATGCAACAGCTTCATGATGATGCTTCCGGGTGC			3012
Db 2624	TGCTGCTCGCTGTCACATGATGACTCTTTTCAATGCTTCTTATCATCTTTCGGCATATCC			2683
QY 3013	TCGTGCGGAAGATGATGAGTTCATGTGGGACTGCAATGTAGCT---GGCGATGTCTGT			3065
Db 2684	TCGTGTGAGAGTGTGATCGAGACCAATGTGGGACTGCAATGTAGAGTGTCCGGGGCAGTCATAT			2743
QY 3070	GCATTTCCCTTCTTGTGGCCACCGTGTGCATCCGCAATCTGTGTGTTTAACTTTTC			3129
Db 2744	GCTGCTGTGTCTTGTGTTGTATTAGGTCATTTGGCACTTGTGTCTCTGAATCTCTTCC			2803
QY 3130	TAGGCTGCTTTTGTCCAAATTTTGGCTCATCTTACCTTATCAGCGCCGACTGCGCATTAAG			3189
Db 2804	TGGCTCTGTCTCTAGCTCTTTCAGTGTGAGCAACACTCAGCGCCCTGTGATGAGACAGAG			2863
QY 3190	ATACGAATAAATAGCCGAGGCTTTCATGCAATGTGCGCATTTAAAGTTGGGTTAAGC			3249
Db 2864	AGATGAACAACCTCCAGCTGGCCCTGCGCGCATCCAGAAGGGGCGCTGCGCTTGTGTCAAGC			2923
QY 3250	GTAATATTGCTGATTTGTTCAAGTTAATAGCTAACTTGAACAAATCAATTAAGTATC			3309
Db 2924	GGACCACTGTGGAATTTGTCTGTGTGTCTCTGCGGCAACCGGCC-----TC			2968
QY 3310	AACCATGAGTGAAGAGCAACAACAGATTCAGTTTGGAGCGAAGAGCATGTGACA			3369
Db 2969	AGAAAGCCGACCCCTTGGCGGCCCAAGGGCCAGCTGCCAGCTGCATTTGCCACCCCTTACT			3028

QY 3370 ACGAATGAGCTGGGCGACAGAGATCTGCGGAGCGCTCATCAAGAGGGATCA 3429  
Db 3029 CCCCACACCCCAAGAGCGAGAGAGTCCCTCCACCCGCAAGAAACAAGTTGAGG 3088  
QY 3430 AGGAGCAGACGCACTGAGGTGGCCATCGGGATCGAGTGAATTCAGATACAGGCG 3489  
Db 3089 AAGCGAGCAACAGGCGGACGCGGAGATCC-----AGAGCGCG 3133  
QY 3490 ACATGAAGAACAAAGCCGAAGAAATCCAAATATCTAATATACGACAGATGATGCA 3549  
Db 3134 TGTGTGTCCTTCCTGTGGCGAGTCAAGATGACCAAGAGAGATGAGAGA 3193  
QY 3550 ACTCAATTAACCAAGCAAGCAATTAAGCTGGAACAGAGTAAACATAGAGTTGTCT 3609  
Db 3194 ACAGCTGGGCGACGAGAGAGAGTCCAGACAGACAGAAATCCAGCTGTGTCCGGCT 3253  
QY 3610 TACAGAGCAGACGACTGCGACATTAATCTATATGTAAGCATAAGATCAGCATTC 3669  
Db 3254 GGGCCAGAGGCTCTCGGATTCAGAGACCTGGAAGCAGGTGTCAAGGACTGCTCTCTG 3313  
QY 3670 AGAGAGAGACCAAGGCGAGCGCCGAGAGATGAGGGCGAGAGAAAGCGGACGCA 3729  
Db 3314 AGGCGAGGCGCAGTCAATCTCAAGCCGACTGCGCAGCAGTGAAGCGGAACCCGAG 3373  
QY 3730 GCAAGAGGATTTAGTCTCGACGAGAACTGGAAGGCGGCGAATGCGAGAGGCGC 3789  
Db 3374 CCCCAGGCTGGGTAGACCCAGAGAGAGAGTGTCTCGAGGCGAGCAGACAGATGA 3433  
QY 3790 CGCTGACGAGTATCATTTATTCATGCAACAGAGAGATATCTCATGATATTCGAG 3849  
Db 3434 CCAACACGCTGAGTCTCTGAGAGAGATCCCTGACTTGGCCAGATGTCAAGAGCCAG 3493  
QY 3850 CTGATTCGCCCGCATTCGTATTAAGAAATTTCCATCTTACCGGTGACGATGACT 3909  
Db 3494 AGGATGCTTCACTGAAGGCTGTGTCCGCGCTGTCTGCTGTGCGGTGACACACAGC 3553  
QY 3910 CGCGCTTGGCAAGATGGGGCATTTTACGATGAACCTTTCAATTAATGAAATTA 3969  
Db 3554 AGGCGCCAGAGAGGTGTGTGGCGGTGGCAGAGCTGCTACACATCGTGGAGCA 3613  
QY 3970 AATATTTGAAACAGCTGTATCATATGATTTATGATGATGATGATGATGATGATG 4029  
Db 3614 GCTGTTGAGAGATTCATCATCTTCATGATCTCAAGAGTGAAGCGCTGCGCTTCG 3673  
QY 4030 AAGATGACATCTGCGCAAAAGACCCATATGCGAGATATTTATATATATGACAGAA 4089  
Db 3674 AGGACATCTACCTAGAGAGCGAGAGACATCAAGGTTCTGCTGATGATGCGCAGAA 3733  
QY 4090 TATTTACGCTATATTTCTTTGGAATGTTAATCAAGTGTGGCGCTCGGCTTCAAG 4149  
Db 3734 TGTTCATATATGCTTCTGTGAGATGCTGCTAAGTGGTGGCTTACGCTTCAAGA 3793  
QY 4150 TGTATTCACCAACGCTGTGTGTGCTGATTTGATGATGATGATGATGATGATGATG 4209  
Db 3794 AGTACTTACCAATGCTGTGTGTGCTGATCTTCTATGATGATGATGATGATGATG 3853  
QY 4210 ACTTGTGCTTCACTTGTGAGCTGTGTGATCAAGCTTCAAGATATGCGAAGT 4269  
Db 3854 GCTGTGTGGCAACACCTGTGGCTTGTGCGAGATGGGCCCATCAATGACATCGGAGC 3913  
QY 4270 TAAAGCAGTGAACCTAGTGTGATGCTCCGATGACAGGCGATGAGGGGTGCTGTA 4329  
Db 3914 TGTGTGACCTCGTCTCTGAGAGCTGTGTCAAGATTGAGGGCAATGAGGGGTGCTCA 3973  
QY 4330 ATGCGCTGTGTAAGAGTATACGCTCATCTTCAATGTGCTATGTGTGCTAATATTT 4389  
Db 3974 ATGCGCTGTGTGGGCGCATCCGCTCATATGAAAGTCTCTCTGCTCATCTTCT 4033  
QY 4390 GGTCAATTTTGGCAATATGAGGTGTGACGCTTTTGTGGAATAATATTTTAAAGG 4449  
Db 4034 GGTCTATCTTCAAGCATATGAGGCGTGAACCTTTTGGCGGAAAGTTTGGAGGTGATCA 4093

QY 4450 ACATGA-----ATGCGAGAACTCAGCGACGAGATCATACCAATTCGCAATGCTGCG 4503  
Db 4094 ACCAGACAGAGGAGACTTGTCTTGAATCTACCATGTGAACAACAAGGCCAGTGTG 4153  
QY 4504 AGAGGAGAACTTAC-----GTGGGTAAATTCAGCAATGAAATTTGATCATG 4551  
Db 4154 AGTCTTGAACCTGACCGGAGAAATTTGATGTGACCAAGGTGAAGTCAACTTGAACAG 4213  
QY 4552 TAGGTAAAGCTATCTGTGCTTTTCAATGTGCGCACTTCAAGGCTGTGATCAATCA 4611  
Db 4214 TGGGGGCGGGTACCTTGCCCTTCTGCAAGTGTGCAAACTTTAAGCTGTGATGACATTA 4273  
QY 4612 TGAACGATGTATCATGATTCACAGAGGTGGAACAAGCAACAATGTGTAAGCAATCT 4671  
Db 4274 TGTATGAGCTGTGACTTCAGGGGTATGAAAGACCTTCAGTGGAAATCAACTCT 4333  
QY 4672 ACATGATTTAATTTGATTTCTTCAATATTTGATTTGATTTTCACTCAATCTGT 4731  
Db 4334 ACATGTATCATATTTTGTATTTTCAATCTTGTGATTTTGTGATTTTCACTGACCTCT 4393  
QY 4732 TCATTGCTTATCTTGTATATTTTATGACAAAGAAAGAAAGAGAGATGATTAAG 4791  
Db 4394 TTATGTGTGATCATCTTGAACAATTCACCAAGAAAGAAAGTTAGGGGCGCAG--G 4450  
QY 4792 AAATGTATGACAGAGATCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 4851  
Db 4451 ACATCTTATGACAGAGAGAGAGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 4510  
QY 4852 AAAAACAATTAAGGCAATTCACAGAGCCAGGTGCGACCAAGCAATATGCTTTGAA 4911  
Db 4511 AGAAGCCCGAGAGCCATCCAGCGCCCTGGAACAAGTATCAGAGGCTTCAATTTGACA 4570  
QY 4912 TAGTACCGATTAAGAAATTCATATATATATATATATATATATATATATATATAT 4971  
Db 4571 TTGTGACCAACAGGCTTTTACGTCACATCATGTTCTGATCTGTTGAATATGAGTA 4630  
QY 4972 CGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5031  
Db 4631 CCAATGATGTGAGACAGATTAACAAGTCTGAAAGAAATCAATCTTGGCAGAGATCA 4690  
QY 5032 ATGCGATATTTGATTTATTTTCAAGTCCGATGCTATTAATAATATATGCTTTACAT 5091  
Db 4691 ACCTGCTTTGTGGCCATCTTCAAGGCGAGTATGTCAAGCTGCTGCTGCTGCTGCTG 4750  
QY 5092 ATCACTATTTATGAGCCATGAAATTTATGATGATGATGATGATGATGATGATGATG 5151  
Db 4751 ACTACTACTTCAACAACAGCTGGAATATCTTCACTTGTGTGTGTCTCTTCCATCG 4810  
QY 5152 TAGCTTGTATCTTGAAGATTAATTAAGAGTACTTGTGCGCGGCGCTGCGAG 5211  
Db 4811 TGGGACGTGTCTCGGACATCAACAGAAAGTACTTCTTCCCGAGCGCTTTCGAG 4870  
QY 5212 TGTGTGCTGTGCGAAGTGTGGCGGTGCTTCACTGTGTAAGGAGCCAGGCGATTC 5271  
Db 4871 TCATTCGCTGTGGCGAATAGGCGGATCTTCAAGATATTCAGAGGCGCCAGAGGAGATC 4930  
QY 5272 GGAACGTGCTTGTGGCGTGAATGTGCTGCGGCGCTGTTCAATCTGCTGCTG 5331  
Db 4931 GCAAGCTGTCTTGTGGCTTCAATGATGTCCCTGCGCTTCAACATCGGCGTGTGCG 4990  
QY 5332 TGTTCCTGTGATGATTAATCTTGTGCAATTTTGGAGTGTGCTTCAATGAGGAG 5391  
Db 4991 TCTTCTGTGATGATTAATCTTCACTCACTTGTGAGAGGCAACTTGTATGATCAAGT 5050  
QY 5392 AGAAGGCGGATTAAGAGCTTCAACATTCAGAGCTTTGGCAGAGCATGATCTGCG 5451  
Db 5051 GGAAGGCGGATGAGAGATGTTCAACTTCAGAGCTTGGCAACAGATGTGCTGCG 5110  
QY 5452 TCTTTCAGATGTGAGCTGAGCGGCTTGGAGTGTGATCTGAGCGCATTAATGAGG 5511  
Db 5111 TCTTTCAGATGACCAAGCTGCGCGCTGGAATGTGCTTCAAGCGCATCTCTCAACACTG 5170  
QY 5512 AAGCATGGA-----TCACCGGACAGCGACCAAGGCTATCCGGGCAATGTGTGTT 5562



Db 2224 GGACACACTGGGATTTCTGTGTGCTCTGCGGCAACCGGC-----TC 2968  
 Qy 3310 AACCATCAGGTGAGAGCAACCAAGATCAGTTGGATTGAGCGAAGACATGCTGCA 3369  
 Db 2869 AGAAGCCCGCAGCCCTTCCCGCCCGCAGGCGCAGCTCCAGCTGCTCCACCCCTCTACT 3028  
 Qy 3370 AGCAACTGAGAGCTGGGCGCAGACGAGATCTCGCGAGCGGCTCATCAAGAAAGGGGATCA 3429  
 Db 3029 CCCCCCAACCCCGAGAGCGAAGAGTGCTCCCAACCGCGAAGAAACACAGTTTGAAG 3088  
 Qy 3430 AGAGCAGACCGCAACTGAGAGTGCGCATCGGAGATCGGATGGAATTCACGATACAGCGCG 3489  
 Db 3089 AAGGAGACCAACAGAGCCAGGGCACCCCGGGGATCC-----AGACGCG 3133  
 Qy 3490 ACATGAGAACACAAAGCCGAGAAATCTAATATACGACGACGATGATGGCA 3549  
 Db 3134 TGTGTGTCCTCATGCTGTGCGCGAGTCAGACACAGATGACCAAGAAAGAGATGAGAGA 3133  
 Qy 3550 ACTCAATTAACCAACCAACCAATAGATGAGAACAGACTAAACATAGAGTTGTCT 3609  
 Db 3194 ACAGCTGGGACGAGAGAGAGATCCAGCAAGCAGAGAAATCCAGCTGTGTCCGCT 3253  
 Qy 3610 TACAGACGACGACACTCCAGACTTAATCACTATGTAGCCATPAAGATGACCATTC 3669  
 Db 3254 GGCCTAGAGGCGCTCCGATTCAGAGACTGAGAGCGAGGTGTACGCACTGCTCTCTG 3313  
 Qy 3670 AGACAGAGAGCCACAAAGGCGAGCGCGAGAGATGAGAGGCGAGAGAGCGGCA 3729  
 Db 3314 AGGCGGAGGCGAGTCATCTCAGGCGGAGCTGCGGCGACAGTGAAGCGGACCCGAG 3373  
 Qy 3730 GCAAGAGAGATTTGCTCTGACAGAGAACTGACAGAGAGGCGAAATGCGAGAGGGCC 3789  
 Db 3374 CCCCAGGCTGCGGTGAGACCCAGAGAGCAGTTGTCTCGAGGCGGACACACAGCATGA 3433  
 Qy 3790 CGCTGACGAGATATCTATTATTCATGACACAGAGATATCTCGATGATATTCAG 3849  
 Db 3434 CCAACACCGCTGAGCTCTGAGAGCAGATCCCTGACTGCGCAGAGATGTCAAGACCCAG 3493  
 Qy 3850 CTGATGCTGCGCCGAGTTCTGACTATAAGAAATTTCCGATTTAGCCGAGTACGATGCT 3909  
 Db 3494 AGAGCTGCTCAGTAAGAGCTGTGTCCGCGCTGTCCCTGTGTGCGGTGACACACAC 3553  
 Qy 3910 CGCCGTTCTGCGAAGGATGCGGCAATTTAGACAGTGAATCTTTCAATTAATGAAATA 3969  
 Db 3554 AGGCGCCAGGGAAGGTCTGTGTGCGGTGCGCAAGACCTGTACCAACATCTGAGACCA 3613  
 Qy 3970 AATATTTGAAACAGCTGTATCTATGATTTTAATGAGTAGCTTAGCTTTGAGATTAG 4029  
 Db 3614 GCTGTTCGAGACATTCATCATCTTCATGATCTACTCAGCAGTGAAGCGCTGCGCTTGC 3673  
 Qy 4030 AAGATGACATCTGCAACAAAGACCACTACTGAGAGATTTTATTAATATGACAGAA 4089  
 Db 3674 AGGACATCTACTAGAGAGGGAAGAACATCAAGTTCTGCTTGAAGTATCCGACAGAA 3733  
 Qy 4090 TATTACGTTAATTTCTTTGGAATTTAATCAAGTGTGCGCTGCGCTTCAAG 4149  
 Db 3734 TGTTCACATATGTCCTTGTGTGAGATGTCTCAGATGAGTGTGAGTGTGAGTGTGAG 3793  
 Qy 4150 TGTACTTCAACCAAGCGGTGTGTGTGCTGATTTGAGATGTGATGTGATGCTTATCA 4209  
 Db 3794 AGTACTTCAACCAAGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3853  
 Qy 4210 ACTTGTGCTTCACTTGTGTGAGTGTGTGATTTCAAGCTTCAAGATATGCGAACT 4269  
 Db 3854 GCTGTGTGCGCAACACCTTGTGCGCTTGTGCGAGATGCGGCCATCAAGTCACTGCGAGCG 3913  
 Qy 4270 TAAAGACATGAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4329  
 Db 3914 TGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3973  
 Qy 4330 ATGGCTGTGTAAGATATACCTGCTCACTTCAATGTGCTATGTGTGCTAATATTTT 4389

Db 3974 ATGCGCTGTGTGGGCGCATCCGCTCATCAATGAAGTCTCTGCTGCTCATCTTCT 4033  
 Qy 4390 GGTATATTTTGGCATATAGGTGTACAGCTTTTGTGTGAAATATTTTAAGTCGAG 4449  
 Db 4034 GGTCTATCTTCAAGATCATGAGGCGTGAACCTTTTGGGGAATTTTGGGAGTGCATCA 4093  
 Qy 4450 ACATGA-----ATGGACGGAAGCTCAGCCAGCATATCACTAATGTGCAATGCGCTGCG 4503  
 Db 4094 ACCAGACAGAGGAGACTGCTTGTGAATCACTACATCTGTGAACACAGAGCCAGTGTG 4153  
 Qy 4504 AGACGAGAACTACAC-----GTGGGTGAATTCAGCAATGAATTTGCATCATG 4551  
 Db 4154 AGTCTTGAATTTACCGGAGAAATGTATGACCAAGGTGAAGTCAACTTGAACAAG 4213  
 Qy 4552 TAGGTAAAGGTATGTGCTTGTTCATAGTGGCACTTCAAGGCTGTGATCAATCA 4611  
 Db 4214 TGGGAGCGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4273  
 Qy 4612 TGAAGATGCTATGATTTCAAGAGGTGACAGCAACCAATTCGTGAACCGAATCT 4671  
 Db 4274 TGTATGAGCTGTGAGCTCAGGGGATGAGAGAGAGCTCAGTGGAAATACACCTCT 4333  
 Qy 4672 ACATGATATTAATTTGATTTCTTCAATCATATTTGATCTTTTCACTCATCTGT 4731  
 Db 4334 ACATGATATCTATTTGTATTTTCAATTTTCAATCTTTGGTCTTTTCACTGAACTCT 4393  
 Qy 4732 TCATTGTGTATATGATTAATTTAATGACAAAGAAAGAAAGAGGTGATCATTTAG 4791  
 Db 4394 TTATGTGTGATCATTTGACAACTTCAACCAAGAAAGAAAGTGTGAGGCGGAG--G 4450  
 Qy 4792 AATGTTTATGACAGAAAGATCAGAAAGTACTAATGCTATGAAAGATGAGGCTCTA 4851  
 Db 4451 ACATTTTATGACAGAGAGAGAGAAAGTACTAATGCTATGAAAGATGAGGCTCTCA 4510  
 Qy 4852 AAAACCATTTAAAGCATTCAGAGCAAGGTGCGCACCAAGACATATGCTTTGAA 4911  
 Db 4511 AGAAGCCCGAGAAACCATCCAGGCGCCCTGAACAGTACAGGCTTCAATTTGACA 4570  
 Qy 4912 TAGTACCGATTAAGAAATGATTAATCATTTATTTATTTATTTGCTGAAATTTCA 4971  
 Db 4571 TTGTGACCAAGAGGCTTTGACCTCACATCATTTGCTGATGCTGCTGAATATGAGA 4630  
 Qy 4972 CCATGACCTCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5031  
 Db 4631 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4690  
 Qy 5032 ATGCGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5091  
 Db 4691 ACCTGCTCTTTGTGCGCATCTTCAAGCGAGTATTTGATGATGATGATGATGATGATGAT 4750  
 Qy 5092 ATCACTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5151  
 Db 4751 ACTATCTTCAACCAAGCTGGAATATCTTCAAGCTTGTGATGATGATGATGATGATGATGAT 4810  
 Qy 5152 TAGGTCTTGTACTAGGATATTTAGAGAAATGATGATGATGATGATGATGATGATGATGAT 5211  
 Db 4811 TGGGCACTGTGCTCTGAGATCATTCAGAAATCTTCTTCCCAAGCTCTTCCGAG 4870  
 Qy 5212 TGTGTGCTGTGAGAAAGTGGGCGGTGCTTCTGATGATGATGATGATGATGATGATGATGAT 5271  
 Db 4871 TCACTGCTGTGCGCAATGAGCTGATCTTCAAGCTGATGATGATGATGATGATGATGATGAT 4930  
 Qy 5272 GAGACGTCTTGTGCGGTGCGCATGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 5331  
 Db 4931 GACAGCTGCTTGTGCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4990  
 Qy 5332 TGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5391  
 Db 4991 TCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5050  
 Qy 5392 AGAAGAGCGGATTAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 5451  
 Db 5051 GGGAGGCTGGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5110

Qy	5452	TCCTTACGATCTCGACGCGTACCGGTTGGAGTGGTCTGAGCGCCATTATTCATGAG	5511
Db	5111	TCCTTCGATACCAACGCTCGGCTGGGCTGGAGTGGCTCTCAGCCCACTCTCAACACTG	5170
Qy	5512	AAGCATGCGA-----TCCACCCGACAGCCGACAAAGGCTATCCGGGCAATTGTGGT	5562
Db	5171	GGCGGCGCTCATCGGAGACCCCACTCTGCCCAACAGCAATGGCTCTCGGGGGGAGCTGGCGGA	5230
Qy	5563	CAGGACCGTTGGAAATAAGTTTCTCCTCTCATACCTAGTATAAGCTTTTGTAGTATA	5622
Db	5231	GCCGACCGTGGGAGTCTCTTCTTCACACCTATCATATCATATCTCTTCTCATCGTGG	5290
Qy	5623	TTAATATGATCATTTGCTGTCACTTCTCGAAGACTATATGTCAGGCGCACCGAGGACGTGCAG	5682
Db	5291	TCAACATGTATCATTTGCCATCATCTCGAGGAATTCTCAGCGTGGCCACGGAGGAGACACG	5350
Qy	5683	AGGGCTTACCGAGAGACGACTACGACATGTACTATGAGATCTGGCAGCAATTCCATCCGG	5742
Db	5351	AGCCCTGAGTGAAGAGACGACTTCGATATGTCTTATGAGATCTGGGAGAAATTGACCCAG	5410
Qy	5743	AGGGACCCAGTATACATGACTATGATGACTGTCTGCATTTCTCGAATTCCTGAGCGTATCGAGCCCC	5802
Db	5411	AGGCGACTCATGTTTATTTAGTATTCGGTCTGTCTGACTTTGGCCGAGCGCCTGTCTGAGC	5470
Qy	5803	CGCTGCAGATCCACAAACCGAACAAGTACAAAGATCATATCGATGAGACATACCATCTGTCTC	5862
Db	5471	CATCCCGTATCGCCAGAGCCCAACGATAAACCTCATCAACATGAGACTCTGCCCATGTGGA	5530
Qy	5863	GCGGTGACCTCATGTACTGCTGGGTCCGACATCCCTCGAGCGCCCTTACGAAACACTTTTGGC	5922
Db	5531	GTTGGGAGCCGATCCATTCATGTACATGAGCATCTCTTTGCTTCAACAAAGGCTCTGGGGGG	5590
Qy	5923	GGAAGGGCAATCCGATAGAGAGAGCGGGTGAATTTGTAG-----ATAGCGGCGCCGCC	5976
Db	5591	AGTCTGGGGAATGAGACGCCCTGAAGATTCAGATGAGAGAGAAAGTTTATGCAAGCGCAAC	5650
Qy	5977	CGGATACGGAGGGCTACGAGCGCCGTCTCATCAACGCTGTGGCGTCAAGCTGAGAGTACT	6036
Db	5651	CATCCAAATCTCTCATCGAGGCCATCAACACACACTCCGGCGGACGACAAAGAGGTGT	5710
Qy	6037	GCGGCGCGCTAATCCAGACGCGTGGCGAAAGCAAGAGCGCGCGGC	6083
Db	5711	CGGCCATGTTATCCAGAGAGCTTCCGAGAGCACTCTGTCGAACGC	5757
RESULT 12			
US-09-840-125-3			
Sequence 3, Application US/09840125			
Patent No. US20020061524A1			
GENERAL INFORMATION:			
APPLICANT: Splawski, Igor			
APPLICANT: Keating, Mark T.			
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND			
FILE REFERENCE: 2323-155			
CURRENT APPLICATION NUMBER: US/09/840.125			
CURRENT FILING DATE: 2001-04-24			
PRIOR APPLICATION NUMBER: 09/634,920			
PRIOR FILING DATE: 2000-08-09			
PRIOR APPLICATION NUMBER: 60/147,488			
PRIOR FILING DATE: 1999-08-09			
NUMBER OF SEQ ID NOS: 4			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 3			
LENGTH: 6048			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1) .. (6048)			
US-09-840-125-3			

	Query Match	14.4%	Score 939.4	DB 9	Length 6048	
	Best Local Similarity	55.7%	Pred. No. 3.1e-250			
	Matches 2064	Conservative	0	Mismatches 1571	Indels 72	Gaps 11
Oy	2413	TGTGGGACTGTGTCTGGGGTTTGGTTGAATTCAGAGAGTGGGTATCCGCATCGTCTTCG	24722			
Db	2087	TCTGGGAGTGCTGCCGCTGTGGATGTCCATCAAGCAGGGAGTGAATTGTGTGATCATGG	2146			
Oy	2473	ATCCCTTCGTGAGCTCTTCAACGCTGTGTCATTTGGTTCACACGATGTTCATGGCAA	2532			
Db	2147	ACCCTTTACTGACCTCACATCATCTATGTGTCATCTGACTCAACACTCTTTCATGGCGC	2206			
Oy	2533	TGATTCACAACGATATGAACAAGGATGGAAACGCGGCTCAAGAGTGGCAACTAATTC	2592			
Db	2207	TGGAGCACTAACATGACAGTAATTCAGAGAGATGCTGCAAGTGGAAACTGGTCT	2286			
Oy	2593	TCACCGCACCTTTGCCATCGAGGCCACATGAGATTAATGGCCATAGGCCCAAGTACT	2652			
Db	2267	TCAAGAGGATTTTACAGCAGAGAATGACTTTCAAGATCATTTGCCCTGACCCCTACTACT	2326			
Oy	2653	ATTTCAGAGAGGCTGGAAACATCTTGCATTCATTATGCTGGCCCTATTCGTATTGGAAC	2712			
Db	2327	ACTTCGAACAGGGCTGGAAACATCTTGCACAGCATCATCTGATCTTAAAGCTCATGAGC	2386			
Oy	2713	TGGGACCTGAGGGGTGCCAGGCTGTGTCGATTTGGCTTCCTTTCGATTCGTGCTGTAT	2772			
Db	2387	TGGGCTGTGCTCCGATGAGCACTTTGTGGGTGCTGCTCTTTCGCTGTGCGGCTCT	2446			
Oy	2773	TCAAACTGGCCAATCTTTGGGCCACACTTAATTTACTCATTTTCGATTATGGGACGCAACA	2832			
Db	2447	TCAAGCTGGCCAATCATATGGGCCACCTTGAAACACTCATCAAGATCATGGGAACTCAG	2506			
Oy	2833	TGGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTATCATCTTTCGCTGGTGA	2892			
Db	2507	TGGGGGCACTGGGGAAACCTGCACTGTGTGTAGCATCATCTGTTTCATCTTTGCTGTGG	2566			
Oy	2893	TGGGAATGCAACTTTTGGGAAAGAAATATCATGATCAACAAGAACCGTTTTCCGATGGCG	2952			
Db	2567	TGGGCAATGACACTTTTGGCAAGAACTACTGGAGCTGAGAGGAAAGGACTCA--GGCC	2623			
Oy	2953	ACCTGCGCGCTGGAACTTCAACGCACTTTATGACACACTTCATGATGTTTCCGGGTGC	3012			
Db	2624	TGCTGCTCTCGCTGGCAATGATGATGACTCTTTCAATGCTTCTTAATCATCTTCGCAATCC	2683			
Oy	3013	TCTGCGGAGAAATGATGCAATGCAATGTGGGACTGTCATGTACGT--GGCGAATCTTCGT	3069			
Db	2684	TCTGTGGAAGATGATGCAAGACATGTGGGACTGCAATGAGAGTGTGGGGCAATCATTAAT	2743			
Oy	3070	GCATTCCTCTTTTGGGCAACGCTGTTCATTCGGCAATCTTTGGTACTTAACTTTTCT	3129			
Db	2744	GCCCTGCTGTCTTCTTCTTGTATTATGTGTCATTTGGCAACTTGTGTCTTGATTTCTTCC	2803			
Oy	3130	TAGCCTTGCTTTTGTCCAAATTTTGGCTCATCTACTACTATAGCGCGCACTGCCGATAAGC	3189			
Db	2804	TGGCTTGTGCTCTAGCTCTTCACTGTCAGACAACTCAACAGCCCTGATGAGACAGAG	2863			
Oy	3190	ATACGAATTAATAATGACCGAGGCTTTCATGCAATTTGGCCGATTTAAAAGTTGGTTAAGC	3249			
Db	2864	AGATGAACAACCTCCAGCTGGCCCTGGCCCGCATCAGAGGGGCGCTGGCTTGTCAAGC	2923			
Oy	3250	GTAATATTTGCTGATTTTTCAGATTAAATAGTAAACAAATTGACAAATCAATTAATGATATC	3309			
Db	2924	GGACCACTGTGGATTTTGTG----TGTGTCTCTCGGCAACCGGCTCAGAAAGCCCGC	2978			
Oy	3310	AACCATCAGGTGAAGAGCAACAACGATTCAGTTTGGAGGAGAGAGCATGTGTACA	3369			
Db	2979	AGCCCTTGGCGCCAGGGCCAGCTGCCAGCTGATTTGCCAATCTTATCTCCGCCAACC	3038			
Oy	3370	ACGAATCTGAGCTGGGCCACGACGAGATCTCTGCCGACGGCTTCATCAAGAGGGGATCA	3429			
Db	3039	CCCGAGACGAGAGAGGTGTCTCCACACCGGAGAAACAAGTTTAGAGAGGCGAGCA	3098			
Oy	3430	AGGAGCAGACGCACTGAGAGTGGCCATCGGGGATCGAATGAAATTCAAGATACAGGCG	3489			

Db 3099 ACCAGGCGAGGCGACCCCGGGG---ATCCAGAGCGCGTGTGTGCGCATGCTGTGGC 3155  
 Qy 3490 ACATGAAGAACACAGCCGGAAGAAATCCAAATATCTAAATACGACATGATTTGCA 3549  
 Db 3156 CGAGTCAGACACAGATGACCAAGAAAGATGAGAGAACACCTGTGGGACCGAGAGAGA 3215  
 Qy 3550 ACTGAATTAACCAAGACATATAGCTGGAAACAGAGTAAACATAGAGTTGTCT 3609  
 Db 3216 GTCCAGACAGACAGAAATCCAGCCTG--TGTCCGCTGGCCCAAGAGCCCTCCGAT 3273  
 Qy 3610 TACAGAGACGACACTGCGACATTTAACTCATGTAGCCATTAAGATCAGCACTTCA 3669  
 Db 3274 TCCAGACCTGGAGCGAGGTGCA-----GCGACTGCTCTCTCG 3313  
 Qy 3670 AGGACGAGAGCCACAGGCGACGCCGAGACGATGAGGGCGAGAGAAAGCCGACGCCA 3729  
 Db 3314 AGGCGGAGGCGCAGTCACTCTCAGCGCGACTGGCGACGATGGAAGCGGAAACCCCAAG 3373  
 Qy 3730 GCAAGAGATTTAGTCTCCAGCGAGAACTGGACGAGAGAGGCGAATCCGAGAGGGCC 3789  
 Db 3374 CCCCAGGCTGCGGTAGACCCCAAGAGACATTTGCTCCGAGGGCGACACAGACATGA 3433  
 Qy 3790 CGCTGACGCTGATATCATTTATTATGACACAGACGAGATATATCTGATGATATCCG 3849  
 Db 3434 CCAACACCGCTGAGCTCTGAGACAGATCCCTGACTCGGCCAGATGTCAGAGACCCAG 3493  
 Qy 3850 CTGATTTGTCGCCGATTCGTATCTATTAAGAAATTTCCGATCTTACCGGTGACGATGCT 3909  
 Db 3494 AGGATGCTTCACTGAAGGCTGTGTCCGGCGCTGTCCCTGTGTGGGAGACACACAC 3553  
 Qy 3910 CGCGCTTCGCGACAGATGGGGCAATTTACGACTGAAAATTTCAATTAATGAAAATA 3969  
 Db 3554 AGGCCCCAGGAGAGGTGTGTGGCGGTGCGCMAACCTGCTACACATCTGGGAGCA 3613  
 Qy 3970 AATATTTGAAACACCTGTTATCACTATGATTTATGATGATTTAGCTTAGCTTTGGCATTAG 4029  
 Db 3614 GCTGTTGAGACATTTCACTCATCTGATGATCTTCACTGACAGTGGAGCGCTGGCTTCG 3673  
 Qy 4030 AAGATGATCATCTGCGACAAAGACCATATGCGAGATATTTATATATATGACAGAA 4089  
 Db 3674 AGGACATCTACCTTAGAGAGGAGGAGACCATCAAGTTCTGTGATATGCGACAAAG 3733  
 Qy 4090 TATTTACGCTTATATTTCTTTGGAATGTTATCAAGTGTGTGGCGCTCGGCTTCAAG 4149  
 Db 3734 TGTTCACATATGTCCTGTGTGAGATGTGCTCAAGTGGGTGCTTACGCTTCAAGA 3793  
 Qy 4150 TGTACTTACCAACGCGTGTGTGCTGATTTGCTGATTTGTCATGATGCTTATCA 4209  
 Db 3794 AGTACTTACCAATGCTGTGTGTGCTGCTGCTGCTCATGCTGCTCTCTGTGCTCA 3853  
 Qy 4210 ACTTGTGCTTCACTTGTGTGAGCTGTGTGATTAAGCCCTTCAAGACTATGCGAAGCT 4269  
 Db 3854 GCTGTGTGGCAACACCTGGGCTTTGGCGAGATGGGCCCATCAAGTCACTGGGAGCG 3913  
 Qy 4270 TAAAGACACTGAGACCACTAGTGCATGTCCGATGAGGGGCAATGAGGCTGTGTTA 4329  
 Db 3914 TGCCTGCACTCCGTCTCTGAGAGCTGTGTCAGATTTGAGGGGCAATGAGGGGTGTGCA 3973  
 Qy 4330 ATGGCTGTGTCAAGCTATACCGTGCATCTTCAAGTGTCTATGATGTGTCAATATTT 4389  
 Db 3974 ATGGCTGTGTGGCGCCATCCGCTCATATGAAAGTCTCTCTGTGCTCATCTTCT 4033  
 Qy 4390 GGTAAATTTTGGCAATATGAGTGTACAGCTTTTGTGCGAAATATTTTAAGTCGAG 4449  
 Db 4034 GGTCTATCTTCAAGATCATGGCGTGAACCTCTTTGGCGGAAAGTTTGGAGGTGCATCA 4093  
 Qy 4450 ACATCA-----ATGGACGAACTCAGCCACGAGATCATACCAATGCAATGCTGCG 4503  
 Db 4094 ACCGACGAGGAGGAACTTGTCTTTGAACTACCATGTGAAACAAAGAGCCAGTGTG 4153  
 Qy 4504 AGAGGAAACTACAC-----GTGGTGAATTCAGCATGGAATTTGATCATG 4551

Db 4154 AGTCTTGAACCTGACCGGAGAAATTTACTGGACCAAGGTGAAGTCACTTGAACAAG 4213  
 Qy 4552 TAGGTAAAGCTATTTGTGCTTTTTCAGATGGGCCACTTCAAGGCTGATTAACAATCA 4611  
 Db 4214 TGGGGCGGGGTACCTTGCCCTTCTGCAAGTGGCAACATTTAAGCTGTGATGACATTA 4273  
 Qy 4612 TGAAGATGCTATGATTCAGAGAGGTGACCAAGCAACCAATGTGTAAGCAATCT 4671  
 Db 4274 TGTATGACTGTGACTTCAGGGGGTATGAAGACACCTTCAGTGGAAATACACCTCT 4333  
 Qy 4672 ACATGATTTATATTTGATTTCTTCAATATTTGATTCCTTTTTCACACTCACTGT 4731  
 Db 4334 ACATGTATCATTTTGTATTTTTCATCATCTTTGGCTTTTTCACCTTCACTGT 4393  
 Qy 4732 TCATTTGTGTTATCTTGAATATTTTAATGACAAAGAAAGAGAGTGTGATTTAG 4791  
 Db 4394 TTATGTGTCACTATTTACAACTTCAACCAAGAAAGAAAGTTAGGGGGCCAG---G 4450  
 Qy 4792 AAATGTTATGACGAAATGACAAAGAAAGTAACTATTAAGTAAAGAAAGTGGCTGTA 4851  
 Db 4451 ACATCTTATGACAGAGAGCAAGAAAGTAACTATTAAGTAAAGAAAGTGGCTGTA 4510  
 Qy 4852 AAAAACTTAAAGCCATTTCCAGACCAAGGTGGCGACCAAGCAATAGCTTTGAAA 4911  
 Db 4511 AGAAGCCCCAGAGCCATCCAGCGCCCTGAAACAATACAGGGCTTCAATTTGACA 4570  
 Qy 4912 TAGTAACGATPAAGAAATTCATATATATATATATATATATATATATATATATAT 4971  
 Db 4571 TTGTGACCAACAGGCTTTGACGTCACATCATGTTCTGATCTGTTGAATATGTTGA 4630  
 Qy 4972 CCATGACCTCGATGTTAGATGTGTGGACAGCTAATAGCGGCTCTTACATCTTCA 5031  
 Db 4631 CCATGATGTGTGAGACAGATGACCAAGTCTGAAAGAAATCAACATTTGGCAAGATCA 4690  
 Qy 5032 ATGCGATATGTGATTTTTCAGTTCCGATGCTATTAATAATATTTCCCTTACAT 5091  
 Db 4691 ACCTGCTTTGTGGCCATCTTCAAGGCGAGTATGTCAAGTGGCTGCTGCCGCC 4750  
 Qy 5092 ATCACTATTTATGAGCCATGAAATTTATTTATGATGATGATGATGATTTATTCATCT 5151  
 Db 4751 ACTACTTACTACCAACAGCTGAAATATCTTCACTGCTGTGTGTGATCTCTTCATCG 4810  
 Qy 5152 TAGCTCTGATCTTGAAGATTTATTCAGAGTCTTGTGTGCGGACCCCTGCTCGAG 5211  
 Db 4811 TGGGACGTGTCTCTGGACATCATCCAGAAATCTTCTTCCCGACGCTCTTCAG 4870  
 Qy 5212 TGTGCGGTGTGCGAAGATGGGCGGTGTCTTCACTGTGAAGGAGCCCAAGGCAATTC 5271  
 Db 4871 TCATCCGCTGTGCGGAAATGAGCCGATCTTCAAGCTGATCCGAGGGGCAAGGGGATCC 4930  
 Qy 4931 GCACGCTGTCTTTGCCCTTCAATGATGCTGCGCTGCTTCAACATCGGGCTGTGCG 4990  
 Qy 5332 TGTTCCTGTATGTTACTTTTGGCATTTTGGCATGTGCTTTCATGACAGTGAAG 5391  
 Db 4991 TCTTCTCTGTATGTTACTTCACTCATCTTTGGCATGCGCAACTTGTGCTTATGCAAGT 5050  
 Qy 5392 AGAAGAGCGGATTAAGACGCTTCAACCTCAAGACTTTGGCGAGAGCATGATCTGCG 5451  
 Db 5051 GGGAGGCTGGATGAGACATGTTCAATCTTCAAGCTTGTGCGCAACGATGCTGTGCG 5110  
 Qy 5452 TCTTCAAGATGCAAGCTGACCGGTTGGAGTGTGTAAGTGAAGCCATTAATGAAG 5511  
 Db 5111 TCTTCAAGATCAACAGCTGCGCGGTGGAGTGTGCTTCAAGCCCATCTCAACACTG 5170  
 Qy 5512 AAGATGGA-----TCCACCCAGACGCAACAAAGCTATTCGGGCAATTTGTGTT 5562  
 Db 5171 GCGCGCCCTACTGCGACCCCACTGTGCCCAACAGCAATGTGCTTCGGGGGAGCTGGGGA 5230  
 Qy 5563 CAGGACCGTGAATATAGTTTCTCTCATACCTAGTATATAGCTTTTGAATGTTA 5622  
 Db 5231 GCCAGCGGTGGGATCTCTTCTTCAACACTTACATCATCTCTCTCTCATGTGG 5290



Db 3216 GTCCAGCAGAGAGAGATCCCACTG--TGTCGGCTGGCCAGAGCCCTCCGGAT 3273  
Qy 3610 TACAGACGACGACCTGCCAGCATTAATGATGTAAGCAATGAATGACCATTTCA 3669  
Db 3274 TCCAGGACCTGAGCAGAGTGTCA-----GCGACTGCTCTCTCTG 3313  
Qy 3670 AGGAGAGAGCAGCAGAGGCGCCGAGAGATGAGAGGAGAGAAAGCCGACGCA 3729  
Db 3314 AGGCGGAGGCGAGTCATCTCAGGCGGAGCGAGAGAGTGAAGCCGAAACCCGAG 3373  
Qy 3730 GCAAGAGATTTAGTCTCGACGCAATGAGAGAGAGGCGAATGCCAGAGAGGCGC 3789  
Db 3374 CCCAGGGTGGGGTGAAGAGCCCAAGAGAGCAGTTGTCGAGAGGAGCAGCAGAGAGCA 3433  
Qy 3790 CGCTGACGCGTATATCAATTAATTCAGCAGAGAGATATCTCGATGAATATCCAG 3849  
Db 3434 CCAACACCGCTGAGCTCTGAGAGAGATCCCTGACCTCGGCAAGATGTCAAGAGCCAG 3493  
Qy 3850 CTGATGCTGCGCCGATTCGATTAATAAATTTCCATCTTGACCGGTCGACGATGACT 3909  
Db 3494 AGGACTGCTTACGTAAGAGCTGTGTCCGCGCTGTCTGTGCGGTGACACACAC 3553  
Qy 3910 CGCCGTTCTGCGCAAGATGGGCAATTTACGACTGAAATCTTTCAATTAATGAAATA 3969  
Db 3554 AGGCCCCAGGAGAGGTCTGGTGGGCGGTGGCCAGACCTGCTACCAATCGTGAAGACA 3613  
Qy 3970 AATAATTTGAAACAGCTGTATCACTATGATTTTAATGATAGCTTACCTTTGGCATTAG 4029  
Db 3614 GCTGGTTCGAGACATTCATCATCTTCATGATCTCAGAGAGTGAAGCGCTGGCCTTGG 3673  
Qy 4030 AAGATGATCTGTGCGACAAAGACCAATCTGAGAGATTTTATATCTATATGACAGAA 4089  
Db 3674 AGGACATCTTACCTGAGAGAGGAGAGACCATCAAGGTTCTGTTGAGATGCCAGAA 3733  
Qy 4090 TATTTACGTTATATTTCTTTGGAATGTTAATCAAGTGGTGGCGCTCGGCTTCAAG 4149  
Db 3734 TGTTCACATATGTCTTGCTGTGAGATGCTGTCTCAATGAGGTGGCTTACGCTTCAAGA 3793  
Qy 4150 TGTACTTCAACCAAGCGGTGTGTGTGCTGATTTGCTGATTTGATGATCTGCTTATCA 4209  
Db 3794 AGTACTTCAACCAAGCGGTGTGTGTGCTGATTTGCTGATTTGATGATCTGCTTATCA 3853  
Qy 4210 ACTTCGTTGCTTCACTTGTGAGAGCTGTGTATTCAGGCTTCAAGCTTATGGAAGT 4269  
Db 3854 GCTGTGTGGCCAAACCCCTGGGCTTTGCGAGATGGGCCCATCAAGTCACTGGGAGCG 3913  
Qy 4270 TAAAGACCTGAGACCACTAGTGCATGTCCTCCGATTCAGAGGCGATGAGGTCGTGTTA 4329  
Db 3914 TGGCTGACCTCCGTCCTCTGAGAGCTGTGTACATTTGAGGGCATGAGGGTGGTGTCA 3973  
Qy 4330 ATGCGCTGTGACAGATTAACCTTCATCTTCAATGTGCTATGTGTCTAATATTTT 4389  
Db 3974 ATGCGCTGTGAGGCGCATCCGTCATCAATGAAGTCTCTCTGCTGCTCATCTTCT 4033  
Qy 4390 GCGTAAATTTTCCATATGAGGTGTACAGCTTTTGTCTGGAATAATTTTAAGTCCAGG 4449  
Db 4034 GCGTCACTTTCAGATCATGAGGCGTGAACCTTTTGGCGGAAAGTTTGGAGGTGCATCA 4093  
Qy 4450 ACATGATG-----ATGGCAGAAAGCTCAGCGACAGAGATCATACCAATGCGATGCGTGC 4503  
Db 4094 ACCAGACAGAGGAGAGCTTGCCTTTGAACATACATGTGAACAAAGAGCCAGTGTG 4153  
Qy 4504 AGAGCGAAGACTTACAC-----GTGGGTGAATTCAGCAATGAATTTGATCATG 4551  
Db 4154 AGTCTTGAACCTTGAACGGAGAAATTTACTGGAACCAAGTGAAGTCAATTTGACACG 4213  
Qy 4552 TAGGTAAAGCGTATCTGTGCTTTTCCAAAGTGGCCACTTCAAGAGCTGTGATCAATCA 4611  
Db 4214 TGGGGGCGGGTACCTGGCTTTCTGAGGTGGCAACATTTAAAGGCTGATGACATTA 4273  
Qy 4612 TGAAGATGCTATGATTCAGAGAGGTGACAAAGCAACATTCGTGAAGCAATCT 4671

Db 4274 TGTATGAGCTGTGGAGCTCCAGGGGGTATGAAGAGACGCTCAGTGGGATTAACAACCTCT 4333  
Qy 4672 ACATGATTTATATTTGGTATTTCTTCAATCATATTTGGATCTTTTTCACATCAATCTGT 4731  
Db 4334 ACATGATCATCTATTTGTCAATTTTCAATCATCTTTGGGTCTTTTTCACCTGAACTCT 4393  
Qy 4732 TCAATGGTATATGATTAATAATTTTATGCAAAAGAAAGAGAGGATCATTTAG 4791  
Db 4394 TTATTTGGTATATTTGACATTTCAACCAAGAGAAAGAGTGAAGGGCCAG---G 4450  
Qy 4792 AATGTTTATGACAGAGATCAGAAAAATGTAATTAATGCTATGAAAAAGTGGGCTCTA 4851  
Db 4451 ACATCTTCATGACAGAGAGAGAGAAAGTACTCAATGTCATGAAGAAAGCTGGGCTTCA 4510  
Qy 4852 AAAAACCTTAAAGCCATTTCCAGAGCCAGAGTGGCCAGCAAGCAATATCTTTGAAA 4911  
Db 4511 AGAAGCCCGAAGAACCCATCCAGGCGCCCTGAACAAATACAGGGCTTCAATTTGACA 4570  
Qy 4912 TAGTAAACGATTAAGAAATGATTAATATATTTATTTATTTGCTGAAAGTGTCA 4971  
Db 4571 TTGTGACCAAGAGAGCTTTGACGTCACATCATATTTTGTATCTGCTGAATATGTGA 4630  
Qy 4972 CCATGACCTTCGATCTTATGAGATCGTGGACAGATTAACGCGGTCTCTAGACTATCA 5031  
Db 4631 CCATGATGTGAGAGACAGATGACCAAGTCCCTGAAGAAATCAACATCTTGGCCAAAGTCA 4690  
Qy 5032 ATGCGATATTCGATATTTTCACTTCCGATTCGAATGTCTATTAATAATTTGCTTTAGAT 5091  
Db 4691 ACCTGCTTTTGTGCGCATCTTCAAGAGGTATATTTGTCACAGCTGCGCTGCGCC 4750  
Qy 5092 ATCACTATTTTATGAGCAATGAAATTTATTTGATGATGATGATTTATTCATCT 5151  
Db 4751 ACTACTTCTTCAACCAAGCTGTAATATCTTGACTTGTGTGTATCTCTTCAATCG 4810  
Qy 5152 TAGTCTTGTACTTATGAGATTTATGAGAAGTACTTGTGTGCGCCGACCTGTCTCGAG 5211  
Db 4811 TGGGCACTGTGCTCTCGAGACATATCCAGAAAGTACTTCTTCCCGAGCGCTTTCGAG 4870  
Qy 5212 TGTGTGCTGTGCGAAGAGGCGGTGTCTTTCAGCTGTGTGAAGAGAGCCAGGCGATTG 5271  
Db 4871 TCATCCGCTGTGCGCGAATAGGCGCATCTTCAAGATGATCCAGGGGCGCAAGGGGATCC 4930  
Qy 5272 GGAACGCTCTTGTGCGGTGGCCATGTGCGGCGGCGGCTTCAACATCGCGTGTGCG 5331  
Db 4931 GCACGCTGTCTTGTGCGCTCATGATGTCCTGCTGCTTCAACATCGCGTGTGCG 4990  
Qy 5332 TGTCTGTGATGATGATCTTGTGCAATTTTGGCATGTGCTTTCATGACGATGAAG 5391  
Db 4991 TCTTCTGTGATGATGATCTTGTGCAATTTTGGCATGTGCTTTCATGATGAAGT 5050  
Qy 5392 AGAAGAGGCGATTAAGAGCTTCAACTTCAAGACCTTTGGCCAGAGATGATCTGCG 5451  
Db 5051 GGGAGGCTGTGATGAGAGATGTTCAACTTCCAGACCTTCCAGCAAGCATGTGCTGCG 5110  
Qy 5452 TCTTCAATGTGAGAGTGGCGGCTTGGATGAGTGAACGCAATTAATGAAG 5511  
Db 5111 TCTTCAATGTGAGAGTGGCGGCTTGGATGAGTGAACGCAATTAATGAAG 5170  
Qy 5512 AAGCATGCGA-----TCACCCGACAGCGCAAGGCTATCCGCGCAATTTGGT 5562  
Db 5171 GCGCGCTTACTGAGACCCCACTGTGCCAAACAGCAATGTGCTGCGGGGAGAGCGGGA 5230  
Qy 5563 CAGGACCGTTGATTAAGTTCTCTCTCTCATATCTAGTTAATAGCTTTTATATGTTA 5622  
Db 5231 GCGCGAGCGTGGGATCTCTCTTTCACACCTTCAATCATCTCTCTCTCATATGCGG 5290  
Qy 5623 TTAATATGATCATGCTGTGATCTTGAAGAACTATATGAGGCGCCAGAGAGAGTGAAG 5682  
Db 5291 TCAATATGATCATGCTGTGATCTTGAAGAACTATATGAGGCGCCAGAGAGAGAGCAG 5350  
Qy 5683 AGGCTTAAACGAGAGAGACTTACAGATGATGATGATGATGATGATGATGATGATGATG 5742  
Db 5351 AGCCCTGAGAGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 5410



QY 3370 ACGAAGTGGAGCTGGCCACGACGAGATCTGCGGAGCGGCTCATCAAGAGGGGATCA 3429  
Db 3189 CCCAGAGCGAGAGAGGTGCTCCACCCGACGAGAAACAGTTTGAGAGAGGAGACA 3248  
QY 3430 AGAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGAGTGAATTCAGATACAGCGCG 3489  
Db 3249 ACCAGGCGAGGACCCCCGGGGG---ATCCAGAGCCGTGTGTGTGTGCCATTCGTGTGGC 3305  
QY 3490 ACATGAGAACACACAGCCGAAAGAAATCCAAATATCTAAATPACGAAAGATGTCGA 3549  
Db 3306 CGAGTCAGACACAGATGACCAAGAGAGATGAGGAAACAGCTGGGACAGAGAGAGA 3365  
QY 3550 ACTCAATTAACACACAGACATATGACTGAAACGAGACTAAACCATAGAGTTGTCT 3609  
Db 3366 GTCGACGACGACGAGATCCAGCTG---TGTCGGCTGGCCGAGGCGCTCCGGAT 3423  
QY 3610 TACAGACGACGACACTGCCAGCATTTAATGATGTAGCCATPAGATGACCATTCGA 3669  
Db 3424 TCCAGGACCTGAGGCGAGGTGCA-----GCCACTGCTCTCTG 3463  
QY 3670 AGGACGAGACGACAGGCGACGCGGACGAGATGAGGGCGAGAGAAAGCGGACGCGCA 3729  
Db 3464 AGGCGGAGGCGAGTGCATCTCAGGCGGACGAGTGGGAAAGCGGAAACCCGAG 3523  
QY 3730 GCAAGAGAGATTTAGTCTGACGAGAACTGACGAGAGGCGGAAATGCGAGGGCC 3789  
Db 3524 CCCCAGGTGGGCTGAGACCCGAGAGGACAGTGTCCGAGGGCGACACAGACATGA 3583  
QY 3790 CGCTGACGAGTATCATTTATTCATGACACGACGAGATATCTCGATGATATTCAG 3849  
Db 3584 CCACACCGCTGAGCTCTGAGGACGATCCGACCTGGCCAGATGTCAGAGACCGAG 3643  
QY 3850 CTGATGCTGCGCGGATTCGATCTATPAGAAATTTCCGATCTTAGCCGCTGACGATGCT 3909  
Db 3644 AGGACTGCTCACTGAGAGGCTGTGTCCGCGCTGCTGCTGAGGCTGACACACAC 3703  
QY 3910 CGCGCTCTGCGACGAGATGGGGCAATTTACGATGAAACCTTTCAATTAATGAAATA 3969  
Db 3704 AGGCGCCAGAGAGGCTGTGGCGGTGGCGAGACCTGCTACCAATCGTGGACCA 3763  
QY 3970 AATATTTGAAACAGCTGTATCATCTATGATTTTATGATGAGTGTAGCTTTGGCATTA 4029  
Db 3764 GCTGCTGACACATTAATCATCTTCAATGATCTTACTAGAGTGGAGCGCTGGCTTGG 3823  
QY 4030 AAGATGACATCTGCGACAAAGACCCATATGACAGATATTTTATATATGACAGAA 4089  
Db 3824 AGGACATCTACTAGAGAGGCGAAACATCAAGGTTCTGCTGAGATGCGGACAAAG 3883  
QY 4090 TATTTACGTTATATTTCTTTTGAATGTTAATCAAGTGTGGCGCTCGGCTTCAAG 4149  
Db 3884 TGTTCACATATGTTCTGTGTGAGAGTGTCTCAAGTGGTGGCTTACGCTTCAAGA 3943  
QY 4150 TGTACTTCAACACGCGTGTGTGTGCTGATTCGATTTGTAATGTATGCTATCA 4209  
Db 3944 AGTACTTCAACCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4003  
QY 4210 ACTTGTGCTTCACTTGT 4269  
Db 4004 GCGTGTGGCGCAACCCCTGGGCTTTGGCGAGATGGGCGCCATCAAGTCACTGGGAGCG 4063  
QY 4270 TAAAGACACTGAGACCACTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4329  
Db 4064 TGGCTGACTTCCGTCTGTGAGCTCTGTACGATTTGAGGGGATGAGGGTGTGTGTGCA 4123  
QY 4330 ATGGCTGTGTACAGTATACCTGATCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGT 4389  
Db 4124 ATGGCTGT 4183  
QY 4390 GGTCTATTTTTCATATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4449  
Db 4184 GGCTCATCTTCAAGATCATGGGGGTGAACCTTTTGGGGGAGATTGGAGGTGTGTGTCA 4243

QY 4450 ACATGA-----ATGGCAGAAAGCTCAGCCAGAGATCATACCAATGCAATGCGCTGCG 4503  
Db 4244 ACCAGACAGAGAGAGACTTGGCTTGTGAATCACCATGTGTAAACAAAGAGCCAGTGTG 4303  
QY 4504 AGAGGAGAACTTAC-----GTGGGTGAATTCAGCAATGAATTTGATCATG 4551  
Db 4304 AGTCTTGAATCTTGACCGGAGAAATTTGATCTGAGCAAGAGTGAAGTCACTTTGACAAAG 4363  
QY 4552 TAGGTAAAGGCTATGT 4611  
Db 4364 TGGGGGCGGGTACTTGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4423  
QY 4612 TGAAGATGTATGATTCAGAGAGGTGGAACAGCAACCAATTCGTGAAGCAATCT 4671  
Db 4424 TGTATGACCTGTGTGCTTCCAGGGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4483  
QY 4672 ACATGATTTTATTTGT 4731  
Db 4484 ACATGATCATCTATTTGT 4543  
QY 4732 TCATTTGT 4791  
Db 4544 TTATTTGT 4600  
QY 4792 AATGTTTCATGACAGAGATGAGAAAGTACTATTAATGTTATGTTAAGATGGGCTCTA 4851  
Db 4601 ACATCTTATATGACAG 4660  
QY 4852 AAAACATTTAAAGCAATTCAGAGACCAAGGTGGCGACCAAGCATATGCTTTTGAAG 4911  
Db 4661 AGAGGCCGAG 4720  
QY 4912 TAGTAAAGGATTAAGAAATTTGATTAATCATTAATGTTATGTTGTGTGTGTGTGTGT 4971  
Db 4721 TTGTGACCAAG 4780  
QY 4972 CCATGACCTGATCGTTAAGATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5031  
Db 4781 CCATGATGTGTGAGACAGATATCAAGAGTCTGTGAAATTAACATCTTGGCCAAAGATCA 4840  
QY 5032 ATGCGATTTCTGATTAATTTTCAATTCAGATGCTTAAATTAATTCGCTTTACAT 5091  
Db 4841 ACCTGCTCTTGT 4900  
QY 5092 ATCACTATTTATTTAGCCATGAGATTAATTTATGATGATGATGATGATGATGATGATG 5151  
Db 4901 ACTACTTCTTCAACAGAGCTGGAATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4960  
QY 5152 TAGGTCTTGTATGAGATTAATTCAGAGAGTCTTGTGTGTGTGTGTGTGTGTGTGTGT 5211  
Db 4961 TGGGCACTGTGTCTTGT 5020  
QY 5212 TGT 5271  
Db 5021 TCACTCCGCTGT 5080  
QY 5272 GGAACATGCTTGT 5331  
Db 5081 GCACTGT 5140  
QY 5332 TGT 5391  
Db 5141 TCTTCTGT 5200  
QY 5392 AGAAGAGGAGCAATTAAGAGT 5451  
Db 5201 GGAAGAGGAGCAATTAAGAGT 5260  
QY 5452 TCTTTCAGATGT 5511  
Db 5261 TCTTTCAGATGT 5320  
QY 5512 AAGATGT 5562

Db 5321 GGGCCGCTTACTGCGACCCCACTCTGCCCCAAGCAATGGCTTCGGGGGGAATCGCGGA 5380  
Qy 5563 CAGCGACCGTTGGAAATACGTTTCTCTCTCATACCTAGTTATAGCTTTTGAATGTA 5622  
Db 5381 GCCACCGCGGCGATCTCTCTCTTCAACCACTACATCATCTCTTCTCATGCTG 5440  
Qy 5623 TTAATATGATATGCTGCTCATCTCTGAAACATATGTCAGGGCACGGAGAGCTGCAAG 5682  
Db 5441 TCAACATGATATGCTGCTCATCTCTGAAACATATGTCAGGGCACGGAGAGAGCA 5500  
Qy 5683 AGGGTCTAACCGACGACGACTACGATGATGATGATGATGATGATGATGATGATGATG 5742  
Db 5501 AGCCCTGATGAG 5560  
Qy 5743 AGGGCAACCAAGTACATACGCTATGATGATGATGATGATGATGATGATGATGATG 5802  
Db 5561 AGGCCACTGAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5620  
Qy 5803 CGCTGAGATCCGACCAACGGAACGAAAGATGATGATGATGATGATGATGATGATGATG 5862  
Db 5621 CACTCGATATCGGCAAGCCCAACCAAGTAAAGCTTCAATCAACATGAGACTGCGCATG 5680  
Qy 5863 GCGGTACCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5922  
Db 5681 GTGGGAGACCGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 5740  
Qy 5923 GGAAGGCAATCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5976  
Db 5741 AGCTGGGGGAGATGAG 5800  
Qy 5977 CGGATACGAGAGGAG 6036  
Db 5801 CATCAAGATCTCTTACAGAGCCATCAACACACATCTCGGGCCAGACGAGAGAGAG 5860  
Qy 6037 GCGCCCGGCTTAATCAGACAGCGCTGGGAAAGCAAGGCGCGCGC 6083  
Db 5861 CGGCGATGATATCCAG 5907

RESULT 15  
US-10-333-191-1  
; Sequence 1, Application US/10333191  
; Publication No. US20030235838A1

GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
; FILE REFERENCE: 2323-154-II  
; CURRENT APPLICATION NUMBER: US/10/333,191  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/US01/22639  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,738  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0

SEQ ID NO 1  
; LENGTH: 8491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (151)..(6198)  
; NAME/KEY: misc feature  
; LOCATION: (1)..(8491)  
; OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 14.4%; Score 939.4; DB 17; Length 8491;  
Best Local Similarity 55.7%; Pred. No. 3,9e-250;

Matches 2064; Conservative 0; Mismatches 1571; Indels 72; Gaps 11;  
Qy 2413 TGTGGAGACTGTGTGGGTTTGGTTGAATTTGAGAGTGGGTATGCTCATGCTTGG 2472  
Db 2237 TGTGGAGAGTGTGCGCGCTGTGATGTCCATCAAGAGAGAGAGAGAGAGAGAGAGAG 2296  
Qy 2473 ATCCCTTGTGAGCTTCTCATCAAGCTGTGATGATGATGATGATGATGATGATGATG 2532  
Db 2297 ACCGCTTACTGACCTCACCATCATATGTGATGATGATGATGATGATGATGATGATG 2356  
Qy 2533 TGGATCACCAGATATGAAAGAGAGATGAAAGAGAGATGAAAGAGAGATGAAAGAGAT 2592  
Db 2357 TGGAGCATACAAATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2416  
Qy 2593 TCAAGCCACTTGTGATGAG 2652  
Db 2417 TCAAGAGATTTTCAAG 2476  
Qy 2653 ATTTCAAG 2712  
Db 2477 ACTTCAAG 2536  
Qy 2713 TGGAGCTGAG 2772  
Db 2537 TGGAGCTGTCCGCGATGAG 2596  
Qy 2773 TCAAACTGAG 2832  
Db 2597 TCAAGCTGAG 2656  
Qy 2833 TGGAGCTTGTGGATATGAG 2892  
Db 2657 TGGAGGAG 2716  
Qy 2893 TGGAGATGAG 2952  
Db 2717 TGGAGATGAG 2773  
Qy 2953 ACTTGGCGGCTGAG 3012  
Db 2774 TGTGCTGCTGAG 2833  
Qy 3013 TGTGCGAGAGATGAG 3069  
Db 2834 TGTGAG 2893  
Qy 3070 GCATTCCTTCTTCTTGTGAG 3129  
Db 2894 GCTGTGCTGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2953  
Qy 3130 TAGCTTGTGTTTGTGCAATTTTGTGCTCATGATGATGATGATGATGATGATGATGATG 3189  
Db 2954 TGGCTTGTGCTGAG 3013  
Qy 3190 ATACGAATAAATAG 3249  
Db 3014 AGATGAACAACCTCCAG 3073  
Qy 3250 GTAAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3309  
Db 3074 GAGACCACTGGAGATTTCTGC-----TGTGTCTCTGCGGACCGGCTCAGAGAGAGAG 3128  
Qy 3310 AACCATCAGTGAAG 3369  
Db 3129 AGCCCTTGTGCGGCGAG 3188  
Qy 3370 AGCACTGAG 3429  
Db 3189 CCGAG 3248  
Qy 3430 AG 3489  
Db 3249 ACCAGGCGAG 3305



```
Db      5441 TCAACATGTACATTCATCATCATCTTGGAGACTTCAGCGTGGCCACGAGAGAGACACCG 5500
QY      5683 AGGGTTAAACGACGACGACTACATGACATGATCTGGACGCAATTGATCCGG 5742
Db      5501 AGCCCTTGAGTAGGAGGAGCTTCGATATGTTCTATGAGATCTGGAGAAATTTGACCCAG 5560
QY      5743 AGGGCACCCAGTACATACGCTATGATCAGCTGTCGGAATTCCTGAGAGTACTGAGACCCC 5802
Db      5561 AGGCACTCAGTTATTAGTATTCGGTCTGTGACTTGGCGAGGCCCTGTGAGC 5620
QY      5803 CGCTGAGATCCACAACCGAACAGTACAGATCATATCGATGACATACCCATCTGTC 5862
Db      5621 CACTCGTATCGCCAGCCCAACAGATAGCCTCATCAACATGAGACTGGCCCATGTGA 5680
QY      5863 GCGGTGACCTCATGTACTGGGTGACATCTCTGAGCGCCTTACGAAAGACTTTTGGCG 5922
Db      5681 GTGGGGACCGCATCCATTGCATGACATCTCTTGTGCACAAAGGGTCTGCGGG 5740
QY      5923 GGAAGGCAATCCGATAGAGAGACCGGTGAGATTGTGAG-----ATAGCGGCCCGGC 5976
Db      5741 AGTCTGGGAGATGACGCCCTGAGATCCAGATGAGAGAAATTCAATGGCAGCCACC 5800
QY      5977 CGGATACGAGGGGCTACGAGCCCGTCTCATCAAGCTGTGCGCTCAGCGTGAGAGTACT 6036
Db      5801 CATCCAAAGATCTCTGAGAGCCCATACACACCACTCCGGGCGCAAGCAAGAAAGGTGT 5860
QY      6037 GCGCCCGGCTAATCCAGCAGCGCTGCGAAAGCAAGGCGCGCGGC 6083
Db      5861 CGGCCATGTATTCCAGAGAGCCTTCGCGAGGCACCTGCTGCAACGC 5907
```

Search completed: May 9, 2005, 18:46:07  
Job time : 3473 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 03:49:57 ; Search time 18835 Seconds  
(without alignments)  
13162.335 Million cell updates/sec

Title: US-08-554-424-7  
Perfect score: 6513  
Sequence: 1 TCTAGACGTGGCGCATAG.....ACGCGATTATGCTAGA 6513

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 60479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_est3.*
4:	gb_est4.*
5:	gb_est5.*
6:	gb_est6.*
7:	gb_est7.*
8:	gb_est8.*
9:	gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787.6	12.1	4675	3 AK083220	Mus muscu
2	776.6	11.9	5943	9 AY416499	AY416499 Homo sapi
3	696.8	10.7	5666	9 AY416501	Mus muscu
4	677.8	10.4	5710	9 AY416500	AY416500 Pan trogl
5	406.8	6.2	673	4 BM632901	BM632901 B729409
6	334.6	5.1	866	4 B1729409	B1729409 B17006875
7	327	5.0	537	4 B1509823	B1509823 B170021A
8	321.4	4.9	829	7 CUS27280	CUS27280 UI-M-HB0-
9	312	4.8	2802	3 AK032187	AK032187 Mus muscu
10	310.4	4.8	928	5 BQ715936	BQ715936 AGENCOURT
11	302	4.6	502	4 CUS01326	CUS01326 B17006875
12	301.2	4.6	771	9 CUS01326	CUS01326 B17006875
13	292.2	4.5	1777	3 BC029489	BC029489 Homo sapi
14	288	4.4	768	6 CUS20657	CUS20657 UI-M-G10-
15	281.6	4.3	688	6 CUS20657	CUS20657 UI-M-G10-
16	280.4	4.3	866	9 CG766052	CG766052 TC848.2 D
17	280.4	4.3	908	5 BQ946179	BQ946179 AGENCOURT
18	279.6	4.3	911	5 CUS27280	CUS27280 UI-M-HB0-
19	271.6	4.2	760	5 BX876821	BX876821 BX876821
20	271	4.2	718	6 CUS04204	CUS04204 UI-M-GV0-
21	263	4.0	816	5 BQ444145	BQ444145 UI-M-EX0-
22	262.4	4.0	694	7 CUS457096	CUS457096 UI-M-HN0-
23	256.6	3.9	735	4 B1488967	B1488967 603021693
24	254.8	3.9	665	2 BB653350	BB653350 BB653350

25	254.2	3.9	778	1 AU035605	AU035605 AU035605
26	250.4	3.8	674	4 BG42331	BG42331 602374246
27	245.4	3.8	751	5 BU226444	BU226444 603946353
28	244.2	3.7	561	2 BF076296	BF076296 225823 MA
29	242	3.7	618	2 BB622500	BB622500 BB622500
30	241.8	3.7	582	5 BP202326	BP202326 BP202326
31	240.6	3.7	568	6 CB616190	CB616190 AMGNUTC:N
32	240.6	3.7	673	7 CR538717	CR538717 DKF2P459P
33	239.2	3.7	819	7 CR847292	CR847292 969918 MA
34	238.4	3.7	544	2 BF323267	BF323267 ma38e08.
35	238.4	3.7	639	9 CR189953	CR189953 Forward B
36	238.4	3.7	1237	9 CL650204	CL650204 CH213-280
37	235	3.6	610	1 AL588672	AL588672 AL588672
38	234.2	3.6	821	7 CO425057	CO425057 UI-M-HU0-
39	232.8	3.6	763	6 CA358980	CA358980 631834 NC
40	232	3.6	583	5 BP202296	BP202296 BP202296
41	230.8	3.5	547	2 BF470392	BF470392 UI-M-BH3-
42	230.6	3.5	537	7 CR537070	CR537070 DKF2P459E
43	229.8	3.5	676	5 BU115795	BU115795 603138772
44	225.2	3.5	881	9 CUS42775	CUS42775 CH240.424
45	225	3.5	606	6 CB581383	CB581383 AMGNUTC:C

## ALIGNMENTS

RESULT 1	AK083220	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
	AK083220		Mus musculus adult male hippocampus cDNA, RIKEN full-length	AK083220	AK083220.1	GI:26101130	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning				
			enriched library, clone: C630029C19 product: sodium channel, voltage-gated, type VIII, alpha polypeptide, full insert sequence.						2	Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
									3	Shibata, K., Itoh, M., Aizawa, K., Nagakura, S., Sasaki, N., Carninci, P., Komano, H., Akiyama, J., Nishi, K., Kishimura, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsumoto, M., Ozawa, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer				
									4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	Functional annotation of a full-length mouse cDNA collection				
									5	Nature 409, 685-690 (2001)					
										The FANTOM Consortium and the RIKEN Genome Exploration Research					

TITLE Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 4675)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohse, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fanom.gsc.riken.jp/  
 Location/Qualifiers

FEATURES  
 source  
 1. 4675  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM DB: C630029C19"  
 /db\_xref="taxon:10090"  
 /clone="C630029C19"  
 /sex="male"  
 /tissue\_type="hippocampus"  
 /clone\_lib="RIKEN Full-length enriched mouse cDNA library"  
 /dev\_stage="adult"  
 <1. 3589  
 /note="putative sodium channel, voltage-gated, type VIII, alpha polypeptide (MGI:103169, GBNM\_01123, evidence: BLASTN, 99%, match=3589)"  
 misc\_feature

ORIGIN  
 Query Match 12.1%; Score 787.6; DB 3; Length 4675;  
 Best Local Similarity 55.2%; Pred. No. 6.4e-193;  
 Matches 1962; Conservative 0; Mismatches 1369; Indels 223; Gaps 13;  
 2580 GGCACATATTTCTTACCGCCACCTTGGCATGAGGCCACCAATGAAGCTAATAGGCCATG 2639  
 Db 7 GGGACACCTGGTGTCTCACTGGGATCTTCAACGCGGAATGTTCTTGAAGCTCAATAGCCATG 66  
 QY 2640 AGCCCAAGTACTATTTCCAGAGAGGGCTGAGACATCTTCACTTATTCATGAGCCCTTA 2699  
 Db 67 GATCCCTACTATTTACTTCCAGAGAGGGCTGAGACATTTTGAACGATTTATTCGCTCCCTC 126  
 QY 2700 TCGCTATTTGAGCTGGGACTCGAGGTGTCTCAGGGTCTGTCCGTTATGCTTCTTTCGA 2759  
 Db 127 AGTTTATGAGCTGGGCTTTCAGAGAGTGGAGGGGCTCTCAATGCTGCGATCTTTCCGA 186  
 QY 2760 TTGCTGGGTATTTCAACATGCGCAAGTCTTGGCCCACTTAAATTTATTCATTTGATT 2819  
 Db 187 TTGCTCGAGTCTTCAATTTGGCCAAATCTTGGCCCACTTGAACATGCTGATCAAGATC 246  
 QY 2820 ATGGAGCAGCAGATGGCGCTTGGGTATCTGACATTTGATCTTGCATTTATCATCTTC 2879

Db 247 ATTTGAACTCCGTTGGCGCCCTGGGACACCTGAGCTGGCTGCGCATCTTCTTC 306  
 QY 2880 ATCTTGGCGTATGAGTGAATGCACTGTTCCGAAAGAAATTAATGATA--TCACAGAGAC 2936  
 Db 307 ATCTTGGCGTATGAGTGAATGCACTGTTCCGAAAGAAATTAATGATA--TCACAGAGAC 366  
 QY 2937 CGCTTTCGAGTGGAGCTGCGCTGCGCTGGAATCTTCAACGATTTATGACAGCTTCATG 2996  
 Db 367 ATCACCACGAGAGTGAAGCTCCCGGCTGGGCAATGAACGATTTCTTCACTCCCTCC 426  
 QY 2997 ATCGTGTCCCGGCTGCTGCGGAGATGAGATGAGTCAATGAGGATGAGTATGAGT 3056  
 Db 427 ATGCTCTTCGAGTCTGTTGGGAGTGGATGAGATGAGATGAGTATGAGTATGAGT 486  
 QY 3057 GCGC--ATGCTCTGAGATTCCTCTTCTTGGCCACGCTTGTATGAGGCAATCTTGTG 3113  
 Db 487 GCGGCGCAGGCGCATGAGCTTATGCTGTTCAATGATGATGATGATGATGATGATGATG 546  
 QY 3114 GTACTTAACCTTTCTTGAACCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3173  
 Db 547 GTGCTGAATCTTATTTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 606  
 QY 3174 CCGACTGCCGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3233  
 Db 607 ACGAGCAGCAGCAGGGAATGAACA----- 632  
 QY 3234 AAAAGTTGGTTAAGCGTAAATTTGCTGATTTGTTCAATTAATGATTAATGATTAATG 3293  
 Db 633 ----- 632  
 QY 3294 AATCAATTAAGTATCAACATCAGTGAAGAGACCAACCATGATGATTTGAGC 3353  
 Db 633 -----CTGCAATATTCGTTATCCGATC 657  
 QY 3354 GAAGACATGATGACACGAACTGAGTGGCCACGACGATCTGCGCCAGCGCTTC 3413  
 Db 658 AAGAGGGGTGGCTGCGCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 717  
 QY 3414 ATCAAGAGGGATCAAGAGCAGACGCACTGAGAGTGGCCATGGGGATGAGTGA 3473  
 Db 718 CAACGGAGGCTGATGAAGTGAACCTTTAGACGAGCTGATGAAGAGGCCAATGCTC 777  
 QY 3474 TTACGATTCAGCGGACATGAAGAAACAAGCCGAAAGAAATTCATTAATATAC 3533  
 Db 778 ATGCGCAACACACCGCGCTGACATTCACAGAAACGCGATTTCCAGAAATATGAAAT 837  
 QY 3534 GCAACGATGATGGCACTCAATTAACACCAAGCAATATGATGAGACGAGCTTAAC 3593  
 Db 838 GGCACCACTAAGGGGATGCGGACAGCGCTGAGAGTACATCATGACAGAGACCA 895  
 QY 3594 CATAGAGTTTGTCTTACAGACGACGACACTGCGAGATTAATCATATGATGAT 3653  
 Db 896 -----TGTCTTCAATTAAC-----CCAACTGACCTGGGCTGCCAT 938  
 QY 3654 AAGATTCACATTAAG 3713  
 Db 939 TGTGTGGGCGAGTCT--TATTTGAGAACTCAACAGAGATTTAGCAGCGAG 993  
 QY 3714 GAGAGCGGACCGCAGAGAGAGATTTAGTCTTGAAGAGAACTGAGAGAGAGAGAG 3773  
 Db 994 TCAGACCCGAGAGGAGCA-----AAGACAACTGAGCATATCAAC 1035  
 QY 3774 GATGAG 3833  
 Db 1036 TCTCTAAG 1095  
 QY 3834 CTGAGATTAATTTATGAG 3887  
 Db 1096 CTTGAGAGATTAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1155  
 QY 3888 ATCTTACCGGTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3947

Db 1156 TGCTGCACGCTCAACATCGAGGAGGAGACTAGGCAAGTCGTGTGATCTCGGAAAAACC 1215  
 Qy 3948 AACTTTCAATTAATTTGAAATTAATTTTGAACAAGCTGTTATACATTAATTTTAAATG 4007  
 Db 1216 TGCTTCCTCATTTGGAGACACAATTTGGTTGAGACTTTCATCATTTTTCATGATTCCTGC 1275  
 Qy 4008 AGTAGCTTAGCTTTGGCATTTAGAAAGATGTACATCTGCCAACAAGACCCTACTGCAAGAT 4067  
 Db 1276 AGCAGTGAAGCCCTGCTTGGAGACATCTACATTTAGACAGAGAAACATCCGTAC 1335  
 Qy 4068 ATTTTAATATATATGAGACAGAAATTTTACCGTTATATTTCTTGGAAATGTTAAATCAAG 4127  
 Db 1336 ATCCGAGGATATGCGGACAAAGGCTTCACTACATCTTCATCTCGAAGATGTGTCTCAA 1395  
 Qy 4128 TGGTTGGGCTCGGCTTCAAGTGTATTTTCAACCAACGGGTGTGTGGCTGATTTCTGTG 4187  
 Db 1396 TGGACAGCTATGT 1455  
 Qy 4188 ATTTGATGATATGCTTATCAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4247  
 Db 1456 ATTTGAGCTGTCTTTTGTAGCTTATAGCTTATGCTTGTGTGTGTGTGTGTGTGTGTGT 1515  
 Qy 4248 GCTTCAAGACTATGCGAACCTTAAAGACCTGAGACCACTACGTGCAATGCTCCGTATG 4307  
 Db 1516 GCGATTAAGTCCCTTAAAGACCTTAAAGACCTTAAAGACCTTAAAGACCTTAAAGATTT 1575  
 Qy 4308 CAGGCAATGAGGCTGT 4367  
 Db 1576 GAAAGGATGAGGCTGT 1635  
 Qy 4368 CTATTTGGTGTCTAATATTTTGGCTAATTTTGGCATATTTGGGTGTACAGCTTTTGTCT 4427  
 Db 1636 CTGT 1695  
 Qy 4428 GAAATATATTTTAAAGTCGAGACATGAAT-----GCGACGAG 4466  
 Db 1696 GGGAAATACCACTACTGTCTTCAACGACTTCAAGAAATCCGTTGAAATGACGAGGTG 1755  
 Qy 4467 CTCAGCCACGAGATCATACAAATGCGAATGCTGTGCGAGACGAGAACTACAGTGGGTG 4526  
 Db 1756 AACAATTAACCGACTGTGAGAGCTCATGAGGCGAACACACAGAAATCCGATGGAG 1815  
 Qy 4527 AATTCAAGCATGAATTTGATCATATGATGTAACGGGTATCTGTGCTTTTCCAAATGAGCC 4586  
 Db 1816 AAGCTCAAGATCAACTTGAACAGTCCGGGACGGCTTCTGTGCTTTTCAAGTGGCA 1875  
 Qy 4587 ACCTTCAAGGCTGATTAACAATCATGACATGATGATTCATGATTCAGAGAGTGGACAG 4646  
 Db 1876 ACCTTCAAGGCTGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1935  
 Qy 4647 CAACCAATTCGTGAACGAACATCTACATGATTTATATTTTGTATTTTCAATCATATTT 4706  
 Db 1936 CAGCTGATATATGAGGCGACATCTACATGATCTACTTGTATCTATCATATCTTC 1995  
 Qy 4707 GATCTTTTTCACACTCAATCTGTTCATTTGTTTATGTTATCATTTTAAATTTTAAAGAGAA 4766  
 Db 1996 GGGCTCTTCTTCACTCACTTGTATCGATGATGATGATGATGATGATGATGATGATGATG 2055  
 Qy 4767 AAAAAAAGAGAGTGTATGAAATGTTTCAAGAGAAATCAGAAAAAGTACTAT 4826  
 Db 2056 AAAAAA-----GTTTGGAGGTCAAGACATCTTCAATGACAGAGAAACAGAAAGTACTAC 2112  
 Qy 4827 AATGCTATGAAAAAGAT-GGGCTCTAAAAAACATTAAGCCATTTCCAAAGCAAGGTG 4885  
 Db 2113 AACGCTATGAAAGGCTAGGCTCCAAAGAACCAAGAAAGCCATCCCTCCACCTTTTGA 2172  
 Qy 4886 GCGACCAACAGCAATAGCTTGAATATGTAACGATTAAGAAATTCATATATCATATAT 4945  
 Db 2173 CAATATCCAGAGATGTCTTGTATTTGTACGACGACAGACCTTCCATCTGTATAT 2232  
 Qy 4946 GTTATTCATTTGTGTGAACATGTTTCAACCATGACCTCGATGTTTACATGCTGTGACAC 5005  
 Db 2233 GATCTTATCTGCTTAAACATGTGACATGATGTGAGACAGACACAGAGACAGCA 2292

Qy 5006 GTATTAACGGGCTCCAGACTATCTCATATGCGATATTCGTATGTTATTTCAAGTCCGAATG 5065  
 Db 2293 GATGAGAAACATTTCTATCGAATTAATCTGTCTTGTGTATCTTCTTACCTGGAAGT 2352  
 Qy 5066 TCTATTAATAATTTGCTTACATATACATATCAATTTTATGAGCCATGAAATTTTATGGA 5125  
 Db 2353 TGTGCTCAAAATGTTTGTGCTTGAAGACACTATTTTCAACATGTGCTGAAACATTTTGA 2412  
 Qy 5126 TGTATGATGTTCAATTTTATTCATCTTATGATTTAGTCTTGTATCTTAAGCGATATTTATGAGA 5185  
 Db 2413 CTTTGTGTGTGTATCTTCTCATATTTGGAATGTTCTGTGCTGATATCATTTGAGAAATGA 2472  
 Qy 5186 CTGTGTGTGCGGACCTTGTCTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5245  
 Db 2473 CTGTGTGTGCGGACCTTGTCTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2532  
 Qy 5246 ACTGATGAAGGAGACCAAGGCAATTCGACACTGCTTTCGCTTGTGAGCATGTGCTGCC 5305  
 Db 2533 TCTATTAAGGAGGCGCAAGGAGATCCGACCTGTCTTGTGCTTAAATGATGTGCTGCC 2592  
 Qy 5306 GAGCTGTTCACATCTGCTGT 5365  
 Db 2593 CGCCTGTTCACATCTGCTGT 2652  
 Qy 5366 CATGTCTTCTTCAATGACCTGGAAGAGAAAGAGGAGGCTTAAACAGCTTCAACTTCA 5425  
 Db 2653 GATGTCCAATTTGCGATACGTGAAGACAGAGGCGGCAATTAATGACATGTTCAACTTGA 2712  
 Qy 5426 GACCTTTGGCAGAGCATATGATCTGTCTTTCAGATGTGCAAGTCAAGCCGCTTGGAGATG 5485  
 Db 2713 GACCTTTGGCAGAGCATATGATCTGTCTTTCAGATGTGCAAGTCAAGCCGCTTGGAGATG 2772  
 Qy 5486 TGTACTGAGCGCATTTATCA-----TGAGAAACATGCGATTCACCCGACGCA 5536  
 Db 2773 CTATCTGTGCAATCTGCAACCGCCCTGAGCTGAGCTTGAACAAGAGACCCGAG 2832  
 Qy 5537 CAAAGGCTATCCGGGCAATTTGT 5596  
 Db 2833 AAGTGGCTTCAAAAGGAGCTGTGAGAAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2892  
 Qy 5597 CCTATTAATTAAGCTTTTGTATGATTTATTAATGATTAATGATCTGTGATCTTCAAGAACTA 5656  
 Db 2893 CATCATATCTCTTCTTGTATGT 2952  
 Qy 5657 TAGTCAAGCCACCGAGACGTGCAAGAGGTCTTAACGACGACGATCAAGATGATCTA 5716  
 Db 2953 CAGGCTAGCCACAGAGGAAAGCGCGATCTCTGAGGAGAGACGATTCGAGACTTCTTA 3012  
 Qy 5717 TGAATCTGCGACGAATTTGATCTGCGAGGAGGACCCAGTATCATAGCTATGATGATGATG 5776  
 Db 3013 TGAATCTGCGAGGAAGTTGATCTGATGCGACCAAGTTCATGAGTACTGTAAGCTGGC 3072  
 Qy 5777 CGAATTCCTGAGCTATCTGAGGAGGCGCTGCGAGATCAACAAACGAAACAGATCAAGAT 5836  
 Db 3073 GCACTTTGCGAGCCCTGTGAGCATCTGCTTCCAGTACCCAGGCTCAACATGAGCT 3132  
 Qy 5837 CATATGATGACATATACCATCTGTGCGGTGATCTGATGATCTGCTGATCTGCA 5896  
 Db 3133 CATGCGCATGAGACCTGCGCATGTGAGCGGAGATGATATCACTGCTTGGACATCTTTT 3192  
 Qy 5897 GCGCTTACGAAAGACTTTTGTGCGGAGAGGCAATCCGATTAAGAGAGAGGAGT 5956  
 Db 3193 GCGCTTACGAAAGAGTCTGAGAGACAGTGGGAGATTTGACATCTGCGGACAGAT 3252  
 Qy 5957 TGTGAG-----ATAGCGGCGCGCGGATTAAGAGGAGGCTTACAGAGCCGCTTATCAAC 6010  
 Db 3253 GAGAGAGCGGCTGT 3312  
 Qy 6011 GCTGTGCGTCAAGGAGATGATGAGCCCGGCTTATTCAGACGCTGTGCGAAAGCA 6070  
 Db 3313 TCTGCGCGCAAGAGAGAGAGGTGTCTGAGGTGTCTTCAAGGTCTTCAAGGAGGAGCA 3372

QY 6071 CAAGGCGCGCGGCG 6084  
 Db 3373 CCGGCTAGGCGG 3386

RESULT 2  
 AY416499  
 LOCUS  
 DEFINITION Homo sapiens SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY416499  
 VERSION AY416499.1 GI:39772459  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 5943)  
 Authors: Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Perrier, S., Wang, G., Zheng, X.H., White, T.J., Smuts, J.J., Adams, M.D. and Cargill, M.  
 Title: Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 Journal: Science 302 (5652), 1960-1963 (2003)  
 PubMed: 14671302  
 2 (bases 1 to 5943)  
 Authors: Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Perrier, S., Wang, G., Zheng, X.H., White, T.J., Smuts, J.J., Adams, M.D. and Cargill, M.  
 Title: Direct Submission  
 Submitted: (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 Comment: This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
 source  
 Location/Qualifiers  
 1..5943  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 <1..>5943  
 /gene="SCN8A"  
 /locus\_tag="HCM5911"

ORIGIN  
 Query Match 11.9%; Score 776.6; DB 9; Length 5943;  
 Best Local Similarity 45.4%; Pred. No. 5e-190;  
 Matches 2704; Conservative 0; Mismatches 2882; Indels 368; Gaps 21;

QY 186 CGAAGAAAAAAGAAATCCGATGATGACGAGCGAGATGAAGTCCACA 245  
 Db 100 CTCAGAAACACCAAGAGCGCGATGCGGAGCGAGTGAAGACGACGACCC 159  
 QY 246 CCGATCTCACTTGAACAGGAGTGCATACCTGTTCGATTCGAGGCGAGCTTCCG 305  
 Db 160 AAGCAACACGACCTGGAAGCAGGAGAGGTTTCCCTTCATCTACGGGACATCCC 219  
 QY 306 CCGAATGGGCTCCTCCTCTCGAGATATCGATCCCTACTACAGCAATGTACTACA 365  
 Db 220 CAAGGCGGTGTGACGTTCCCTCGAGAGCTTGAACCACTACTATTGAACGAGAAACC 279  
 QY 366 TTGCGATGTTGAAGCAAGAAAGATTTTGGCTTTTCTGCATCAAAAGCAATGG 425  
 Db 280 TTGTGATTAATAACAGAGGAAAACTCTTCAGATTTAAGTGCACGCTGCTTGGAC 339  
 QY 426 ATGCTCGATTCATCAATCCGATAGTGTGAGGCAATTTAGTCAATTCATCAATTA 485  
 Db 340 ATTTTAAGTCTTTTAACTGATTAAGAAATAGCTATTAATTTTGCATCATTCATTA 399  
 QY 486 TTTTCCCTATTCATCATCAACAATTCCTCAACCTGCATCTGATGATATGCGGACA 545  
 Db 400 TTTAGCATGATCATATATGACGCTATTTGACCAACTGTATTCATGATGATTTAGTAAC 459

QY 546 ACCCCAGGTTGAGTCCACGAGTG---ATATTCACCGAATCTACATTTGATCA 602  
 Db 460 CCTCCTGACTGTGCAAGAAATGTGAGTACAGTTTCACAGGATTTATACATTTGATCA 519  
 QY 603 GCTGTTAAAGTATGAGCAGAGGTTTCAATTTATGCGGTTTACGATCTTAGAGATCA 662  
 Db 520 CTATGAAATATATTCAGAGAGTTTCTGCATTAATGAGCTTTTACCTTTTACGGGACCA 579  
 QY 663 TGAATTTGGCTGAGCTTGTGATTAATAGCTTTATGTCATGACATGGGATTAATTTA 722  
 Db 580 TGAATGTTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 639  
 QY 723 GGTATATGAGAGCCCTGCGAAGTTTGGGCTGCGAGGCTTAAACGCTAGTCAAT 782  
 Db 640 GGCATGTTTACGCTTACGACCTTTCAGGAGTACGAGGCTTTTAAATCTATTTGGTGA 699  
 QY 783 GTGCCAGGCTTGAAGACATCGTCGCGCCCTCATCATGATCGGTGAAGATTCGCGCAT 842  
 Db 700 ATCCAGGCTGTAAGACATTTGGGTGCTGATTCAGTCTGTGAAGAACTGTCAAGT 759  
 QY 843 GTGATTAATCTGACCATGTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902  
 Db 760 GTGATGATCTGACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819  
 QY 903 ATGGGCTGCTGACCGAGAAATGCAAT-----CAAGATTCCTGCTGACGATTC 953  
 Db 820 ATGGGGAACCTTCGAACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879  
 QY 954 TGGGGAATCTGACCGACGAGAACTGGAATCATCATCATCATCATCATCATCATCATCAT 1013  
 Db 880 GAAATGGAACCAAGGCTTTGATTTGGAAGATATCATCAATTAATAAATTTCTATC 939  
 QY 1014 TCGAAGACGAGGAGATCTCATTTCCGTTATCCGGAATATTCGGTGGGGAATGC 1073  
 Db 940 ACAGTTCCTGGAATGCTGGAACCTTTATCTGTGGGAACAGTTCTGATGCTGGCAATCC 999  
 QY 1074 GACGACATTTACGTTGCTGCGAGGAGTTGTGCTCCGATTCGAAATTTGCTTACACGAC 1133  
 Db 1000 CCGAGAGATATCCAGTGTATGAAG---CAGAGAGAACCCCACTATGTTATCAACAAT 1056  
 QY 1134 TTGATTCGTTGGATGAGGCTTTCTGTCGCGCTTCGCGCTGATGACACAGACTTCTGG 1193  
 Db 1057 TTTGACACTTTTATGCTGGGCTTTCTTGGCATTTATTTGCTTATGACCAAGACTATTTGG 1116  
 QY 1194 GAGATCTGATCAGAGTGTGTGCGCGCGCGGACCAATGACATGCTGTTCTTTATA 1253  
 Db 1117 GAAACCTGTATCAATTTGACTTTACGAGACGCGGGAATACATGATCTTCTGCTC 1176  
 QY 1254 GTCATATCTTCTAGATTCATCTATCTTGTGAATTTGATTTTGGCAATTTGCTCATG 1313  
 Db 1177 TTGATCATCTTTGATGCTTTCTTCTATCTGTGTAATTTGATCTTGGCTGTGGTGCATG 1236  
 QY 1314 TCGATGACGAATTTGAAAGAGGCGCAAGAAAGAGAGGCTGCGCAAGAGAGGAGATTA 1373  
 Db 1237 GCTTATGAAGAA---CAGAACTAGGCAACTGGAAGAGGCGCAAGAAAGAGGCTGGA 1293  
 QY 1374 CCGAAGCGGAAGAGCTGCGCGCGCGCAAGAGGCGCAAGAGGCTGCACTGATCCGAAAT 1432  
 Db 1294 TTTTAAAGC---AATGTTGAGCACTTTAAGAGCAACAGAAAGAGGACAGGCTGCTGC 1349  
 QY 1433 GCAGGCTCAGGACGAGCGAGTGGGCTGCGCGCAAGAGGCTGCACTGATCCGAAAT 1492  
 Db 1350 GATGGCACTTACAGAGAACTGTCTCAAGAAATGCAATGAGAGAGAGAGTGAAGAG 1409  
 QY 1493 GCGCAAGAGTCCGACATTTCTTTCATCACTATGAGCTATTTGTTGGCGCGCAAGAGG 1552  
 Db 1410 AGGAGGCTCCCTCGAGGCTTTCTGAATCTCTAAATCTCAAGCTCAAGAGTCAAGGA 1469  
 QY 1553 CAAGATGACAAACAAGAGAAAGATGTCATTTGGAAGGCTGAGAGTGGAGTCCGAGTTC 1612  
 Db 1470 AAGAGTAAAGAGAGAAAGAGAGAGAAAGAAAGAACTCTGTAAGAGAGAGAGAAAG 1529



3441 TGTGAAACAGCCTGAGGAATCTTG----- 3465  
3827 GGATATATCTGATGAATATCCAGCTGATTCGCCCCGATTCGACTATAGAAATTTCC 3886  
3466 -----GATCCAGATGCTGCTTTCACAGAGGTTGTGTCCAGGGTTCAA 3509  
3887 GATCTTAGCCGGGAGCATGACTCGCGTTCTGGCAAGATGGGGCAATTTACATGAA 3946  
3510 GTGCTCCAGGTAAACATCGAGAGAGGGCTAGCAAGTCTTGTGATCTCTGGAAAAAC 3569  
3947 AACTTTCAATTAATGAAAAATTAATTTGAAACAGCTGTATGACTATGATTTAAT 4006  
3570 CTGCTTCATCATGCTGAGACAACTGGTTTGAGACTTCATCATCATGATTCGTCT 3629  
4007 GAGTACTTACGTTTGGCATTTAGAAATGACATCGCCCAAAAGCCATCTGACAGA 4066  
3630 GAGCAGTGGGCGCTGCTTCGAGACATCTACATTTAGCAGAGAAAGCCATCGCAC 3689  
4067 TATTTATCTATGATGAGAAATTTACGGTTATCTTCTTGAAAATGTTAATCAA 4126  
3690 CATCTGSAATATGCTGACAAAGTCTTACCTATATCTTCACTCTGAGATGTGCTCAA 3749  
4127 GTGTGGCGCTCGGCTTCAAGGTGATCTTACCAAACGGGTGGTGTGCTCGATTTGCT 4186  
3750 GTGGAAGAGCTATGGCTTGTCAAGTTCTTCAACAAATGCTGGTGTGGCTGAGCTTCC 3809  
4187 GATGTCAATGATATGCTTATCAACTTGTCTTCACTTGTGGAGCTGTGTGATTC 4246  
3810 CATTTGGCTNN 3869  
4247 AGCCTTCAAGACTATGCGAAGCTTAAAGACATGAGACCACTACGTGCATGTCCGAT 4306  
3870 NNN 3929  
4307 GCAGGCGATGAGGCTGCTGTTATATGCGCTGTGTAACAACTTCACTTCAATGT 4366  
3930 NNN 3989  
4367 GCATTTGGTGTCTAATTTTGGCTAATTTTGCATTAATGGGTGACAGCTTTTGG 4426  
3990 GCTGTGGTGTCTAATTTTGGCTAATTTTGCATTAATGGGTGACAGCTTTTGG 4049  
4427 TGGAAA-----ATATTTAAGTGCAGAGACATGATGSCAGAGCTCAG 4472  
4050 GGGAAAGTACCACTACTGCTTTATAGACTTTCGAAATCCGATTTGAAATGAAGTGT 4109  
4473 CACGAGATCATCAAAATGCGAATGCTCGGAGAGCGAGAACTA-----CACGTGGGT 4525  
4110 CAACAATTAATACTGAATGTGAAAAAGCTTATGAGGGGAAACAAATACAGATTCAGTGA 4169  
4526 GAATTCAGCAATGAATTTGATCATGTAGTAAAGGATCTGCGCTTTTCCAGTGGC 4585  
4170 GAACGTGAGATCACTTGTACATGTGTGGGCAAGATACCTGGCCCTTTTCAAGTAC 4229  
4586 CACCTTCAAGGCTGATACAAATCAATGACATGCTATGATTCACAGAGGTGACAA 4645  
4230 AACCTTCAAGGCTGATGACATGTATGACAGCTGTAGATTTCCGGAAAGCTGATGA 4289  
4646 GCACCAATTCGTGAACCAACATCTACATGTATTTATTTGTGATTTCTTCAATAT 4705  
4290 GCGGCTTAATGATGAGACAAATCTACATGTACATCTATTTGTATCTTCAATCT 4349  
4706 TGAATCTTTTCACTCAATGATGCTTATGATGTTATGATGATTAATTTAATGGA 4765  
4350 CGGCTCTTCTTCACTCACTGACCTGTGATGTTGATGATGATGATGATGATGATGAT 4409  
4766 AAGAAAAAGAGCTGATCATTAAGATGTTCAATGACAGAAATCAAGAAAAAGTACTA 4825  
4410 AAGAAAAAGTGGAGG---TCAGGACATCTTCAATGACAGAAAGTAAAGTACTA 4466  
4826 TAATGCTATAAAAGATGGGCTTAAAAAACAATTAAAGCAATTCAGAACCAAGGTG 4885  
4467 CATGTGATGAAAAAGCTGGGCTCAAAAGAGCAAGAAACCAATTCCTCCGCCCTTGA 4526

4886 GGCACCAAGCAATAGTCTTTGAATAGTAACCGATTAAGAAATTCATATATCATAT 4945  
4527 CAATATCCAGAAATGCTTTGATTTGTCTACAGCAAGCTTTGACATTTGATAT 4586  
4946 GTTATTCATTTGTGAAATGTTCAACATGACCTCGATGTTTACATGCTCGGACAC 5005  
4587 GATGCTCATCTGCTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 4646  
5006 GTATACGGGCTTACATCTCAATGCAATTCGATTTTATTTTCAATTTCCGAATG 5065  
4647 GATGAGAACATCTCTACATGATTAACCTGATTTGTTATCTTCTTCACTGATG 4706  
5066 TCTATTAATAATATTCGTTTACATATCTATTTTATTTAGCAAGATTTTATTTGA 5125  
4707 TGTGCTCAAAATGTTGCTTGAAGCACTATCTTACCATTTGGCTGGAATCTTGA 4766  
5126 TGTATGATTTGATTTATTTATTCATCTTATGCTTGTATGAGATTTATGAGATTA 5185  
4767 CTTCGTTGATGATCTCTCATTTGTGGAAATGTTCTGAGATATATTAATGAGAAATA 4826  
5186 CTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5245  
4827 CTTCGTTTCCCAACCTTATTCGATCAATCCGATTTGCTGCTGCTGCTGCTGCTGCT 4886  
5246 ACTGTAAGAGGAGCAAGGATTCGACATCTGCTTTCGCTTGGCCATGCTGCTGCC 5305  
4887 TGTGATCAAAAGGCGCAAGGATTCGATCTGCTGCTTGTGCTTATGATGATGCTGCT 4946  
5306 GGGCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5365  
4947 TGCCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5006  
5366 CATGCTGCTTCAATGCAATGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5425  
5007 GATGTCAAATTTGATGATGTAAGACAGAGCTGTGATGATGATGATGATGATGATGAT 5066  
5426 GACCTTTGCGCAGAGCATGATCTGCTTTCAGATGTCAGATGACCGGTTGGAGATG 5485  
5067 GACATTTGGCAACAGATGATCTGCTGTTTCAAAATCAACACTGAGCTGTGGATG 5126  
5486 TGTACTGAGCGCATTTACA-----TGAAGACATGATCCACCGACAGCA 5536  
5127 CTGCTGCTGCCATCTTAAACCGCCCTTACATGACCTTAAAGAAACCCAG 5186  
5537 CAAAGCTATCCGGGCAATTTGTTGTTTCAAGACCGTGTGAATTAAGTTTCTCTCAT 5596  
5187 GATGCTTTAAAGGATTTGGAACCCCTCAGTGGGATCTTCTTCTTGTAAAGT 5246  
5597 CTAATGATTAAGCTTTTGTATGATTAATTAATGATCATGCTGCTGATCTCGAATCTA 5656  
5247 CATCATCATCTCTTCTTAATTTGTGTGAACATGATCATGATCATCTGAGAACTT 5306  
5657 TGTGAGGCAACCGAGAGCTGACAGAGGCTTACACGACGATACGATGATGATGAT 5716  
5307 CAGTGTAGCAACAGAGAAAGTGCAGACCTCTGATGAGATGATCTTTGAGACCTTCA 5366  
5717 TGAATCTGAGCAATGATTCGAGAGGAGCAACCGATACATAGCTATGATCAGCTGTC 5776  
5367 TGAATCTGAGAAATTTGACCCGATGACACCGATTCATTTGATGATCTGTAAGCTGG 5426  
5777 CGAATTCGTAAGCTTGAAGGCGCTGAGATTCACAAACCGAACAGTACAAGAT 5836  
5427 AAGCTTTGAGAAATGCTTGAAGATCTCTCGAGTGGCCCAAGCAAATACATTTAGCT 5486  
5837 CATATGAGATGATACCATCTGTCGGGTGACCTCATGATCTGCTGATCTCTGCA 5896  
5487 CATGCTATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5546  
5897 CGCCTTAGAAAGATCTTTTGGCGGAGAGGCAATCCGATGAGAGAGAGAGGAGT 5956  
5447 TGCCTTCAACAGCGGCTCTGAGATAGCGGAGATTTGACATCTCTCGGCGAGAT 5606

QY	5957	TGTTGAG-----A	AGAGGCGCCCGCCGGATACGAGAGGCTACAGAGCCCGCTCATCAAC	6012
Db	5607	GGAAAGGCGGTTTCGTCGATCCAAATCTCTCCAAATGTCTTACGAGCCAAATCAACAACAC	5666	
QY	6011	GCTGTGCGGTAGCGCTGACAGTA	CTGCGCCCGGCTAATCCAGACGCGCTGGCGAAACA	6070
Db	5667	ACTGCTGTGCAAGCAGAGAGAGGTATCTGCACTGTCCTCTGACGCTGCTTACCGGGAGCA	5726	
QY	6071	CAAGCGCGCGCGCG	6084	
Db	5727	TTTGGCAAGCGGG	5740	
RESULT 3				
LOCUS	AY14501		5666 bp	DNA
DEFINITION	Mus musculus SCNBA gene, VIRTUAL TRANSCRIPT, partial sequence,			
ACCESSION	AY14501			
VERSION	AY14501.1		GI:39772461	
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 5666) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtnsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 5666) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtnsky,J.J., Adams,M.D. and Cargill,M.			
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	Location/Qualifiers			
source	1..5666 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>5666 /gene="SCNBA" /locus_tag="HGM5911"			
ORIGIN				
Query Match	10.7%;	Score 696.8;	DB 9;	Length 5666;
Best Local Similarity	56.1%;	Pred. No. 3e-169;		
Matches 1278;	Conservative 0;	Mismatches 960;	Indels 39;	Gaps 4;
QY	3844	ATCCAGCTGATGTCGTCGCCCATTCGTCGATTAAGAAATTTCCGATCTTACCGCGTAGC	3903	
Db	3190	ATCCAGACGCGCTGCTTCAACGAGGGTGTGTCAGAGGTTCAAGTGTCCAGGTCAACA	3249	
QY	3904	ATGACGCGCGTTCGCGCAAGATGGGGCAATTACGACGTGAAAACCTTTCATTAATG	3963	
Db	3250	TCGAGGAAGACTAGGCAAGTCGTGTGTGATCTTCGGAAAACTGCTTCTCAATTGTGG	3309	
QY	3964	AAAAATAATATTTGAAAACAGCTGTATCACTATGATTTTAAATGATGATGCTTACCTTTGG	4023	
Db	3310	AGCACAATGTGTTTGAAGCTTCAATCAATTTTCAATGATTCCTCCTCAGAGTGGAGCCCTGG	3369	
QY	4024	CATTGAAGATGTACATCTTGCCACAAAGACCCATACATGCGAGAGATTTTATACATATGG	4083	
Db	3370	CCTTCGAGCATCTACATTTGAGCAGAGGAAGACCATCCGACCATCCTGGAGTATGCGG	3429	

OY	4084	ACAGAAATTTATACGGTTATATCTCTTTGGAAAGTTAAATCAAGTGTGGCGCTCGCT	4143
Db	3430	ACAAAGCTTCACTCACTCACTTCACTCTGGAGATGTGTCTAAATATGACACCTATGGCT	3489
OY	4144	TCAAAAGTACTTCACCAACGCGTGTGTGGCTCGATTTTCGTATGTCAATGTATATGC	4203
Db	3490	TCGTCAAGTTCTTACCAATGCTCGTGTGTGTGGACTTCTCATTTGTGGCTNNNNNN	3549
OY	4204	TTATCAACTTCGTGCTTCACTGTGTGAGCTGTGTATTCAAAGCTTCAAGCTATGC	4263
Db	3550	NN	3609
OY	4264	GAAGCTTAAAGACACTGAGACCACTAGTGTGCATGTCCCGTATGACAGGCAATGAGGCT	4323
Db	3610	NN	3669
OY	4324	TCGTTAATGCGCTGGTACAAAGCTATACCGTTCATCTTCAATGTGTCTATTTGGTGTCTAA	4383
Db	3670	TGGTGAAGCGCTTGTGTGGCGCCATCCCTTCATCATGAAGTGTCTGTGTGTCTCA	3729
OY	4384	TATTTGGCTAATTTTGGCCATAATGGGTGTACAGCTTTTGTCTGAAATATTTAACT	4443
Db	3730	TCCTTCGGCTGATTTTACGATCATGTGGCGTTAACTGTGTGTCTGGGAAATACCACTACT	3789
OY	4444	GGGAGGACATGAAT-----GGCAGCAACTCAGCCACAGATCA	4482
Db	3790	GCTTCAACGAGACTTCAGAAAATCCGGTTTCCAAATCGACGAGTGAAACAATAAACCACT	3849
OY	4483	TACCAAAATCGAAATGCGTGCAGAGACGAAACTCAAGTGGGTAAATTCAGCAATGAAT	4542
Db	3850	GTGAGAAAGCTCATGAGAGGCAACAACAAGATCCGATGGAAACGTCAAGATCAACT	3909
OY	4543	TCGATCATGTAGGTAAAGCGGTATCTGTGCTTTTCCAAATGTGCAACTTCAAAGCTCGGA	4602
Db	3910	TCGCAACGTCGGGGCAGGCTACTGCGCTTCTTCAAAGTGGCAACTTCAAAGCTCGGA	3969
OY	4603	TACAAATCATGAAGAATGCTATGCAATTCAGAGAGGTGGCAACACCAACCAATGGTGAA	4662
Db	3970	TGCACTCATGTATGACGCTGTAAATTCGAAAGCCGAGACGACGCTGATATAGAG	4029
OY	4663	GGAACATCTACATGATTTATTTTCGTATTTTTCATCATATTTTGAATCTTTTTCACAC	4722
Db	4030	GCAACATCTACATGATCTACTTCTGTCATCTTTCATCATCTTGGGCTCTTTCACCC	4089
OY	4723	TCAATCTGTTCATTTGGTGTATCTATGTATATTTTAATGAGCAAAAGAAAAGCAGCTG	4782
Db	4090	TCAACCTGTTCATGGGTCACTCATTCACAAATTCACAAACAAAGAAAAA---GTTTG	4146
OY	4783	GATCATTAAGAAATGTCATGACAGAAATATGAAAAAGTCTAATATGCTATGAAAAAGA	4842
Db	4147	GAGGTCAAGACATCTTCAATGACAGAGAAAGAAAGTACTACAGCCATGAGAAAGC	4206
OY	4843	TGGGCTCTAAAAAACCATTAAGCCCATTCACAGCCAAAGGTGGCGACCAACAGCAATAG	4902
Db	4207	TAGGCTCCAAAGAACCAAGAGGCCATCCCGGACCTTTGAACAAATATCAAGAGATTG	4266
OY	4903	TCCTTGAATATGTAACCGATTAAGAAATTCGATATATCATTTATGTATTTCAATGGTCTGA	4962
Db	4267	TCCTTGAATTCGTACCCCAACAGCCCTTTCGACATCGATCATATATCTCATTCGCTTGA	4326
OY	4963	ACATGTTCACATGACCGCTCGATGTTACATGTGGGTGGGCAAGCTATTAACCGGCTCTAG	5022
Db	4327	ACATGTGTGACATATATGTGTGAGACAGACACACAGAGCAAGCAGATGAGAACATTTCTT	4386
OY	5023	ACTATCTCAATGCGATATTCGTATGTTATTTTCAGTTTCGATGTCTATTAATAATATTCG	5082
Db	4387	ACTGATTTAATCTGTCTTGTGTATCTTCTTCACTCGAGTGTGTCTCAAAATGTTTG	4446
OY	5083	CTTACGATATCACTATTTATTTATGAGCAATGAAATTTATTTGATATGTAATGTGTCAATT	5142
Db	4447	CTTTGAGACACTACTATTTTCAACATTTGGCTGGAACATCTTTGACTTTGTGTGTCAATTC	4506

QY	5143	TATCCACTTAAGTCTTTGATCTTAAGGATATATATGAGAAAGTACTTGGTGGCCGACCC	5202
Db	4507	TCCTCAATGGGAAATGTTCTCTGGCTGATATCAATGGAAGTACTTGGTCTCCCAACC	4566
QY	5203	TGCTCCGAGTGGAGGCGCTGTGGCCAAAAGTGGGCCCGTGTCTTTCGACTGGTGAAGGAGCA	5262
Db	4567	TATTCGCGCGTCAATCCGATGTGGCCCGCATCGGGGCGCATCTTGCGCTGATCAAGGGCGCCA	4626
QY	5263	AGGGCATTCGGACAATGCTCTTGGCGTTGGCCATATGTCGTCGCGCGCGCTGTGAACATCT	5322
Db	4627	AAGGATCCCGACCCCTGCTCTTGGCTTAAATGATGTCGCGCGCGCGCTGTGAACATCTG	4686
QY	5323	GCCGCTGCTGTTCTCTGCTGATGTTCACTTTTGGCACTTTTCGGCATGTGCTTTCATATGC	5382
Db	4687	GCTCTGCTCTTCTCTGCTGATGTTCACTTTTCGATCTTTGGGATGTCCAACTTGGCGGT	4746
QY	5383	ACGTGAAGAGAAAGAGCGCATTTAAGACGTCTACAACTTCAAGACTTTGGCCAGAGCA	5442
Db	4747	ACGTGAAGAGCAAGAGCGCATTTGATATCAATGTTCAACTTTCGAGACTTTGGCAACGCA	4806
QY	5443	TGATCCCTGCTTTCATGATGTCAGCGTCAACCGGTTGGAGTGGATGCTAGACGCCATTA	5502
Db	4807	TGATCTGCTGTTTCAATCAAGACTCTGTGTGATTTGGATGGCTTACTGCTGCAATCC	4866
QY	5503	TCGA-----TGAGAAAGCATGCGATCCACCCGACGCAAAAGGCTATTCGGGCA	5553
Db	4867	TGAACCGCCCCCTGACTGCAAGCTTGGACAAGAGAGCACCCAGAAAGGCGCTTCAAAAGGG	4926
QY	5554	ATTGTGTTTCAAGCAGCGTTGGAGTAAGTTTTCCTCATATCTGATATTAAGCTTTT	5613
Db	4927	ACTCGGGAAACCTTCGCTGGGCAATCTTCTTCTTGTAAGTACATATCATCTCTTC	4986
QY	5614	TGATAGTTATTAATATGTACATTCGCTGCAATTCGAGAACTATATGTCAAGGCCACCGAG	5673
Db	4987	TGATCGTGTAAACATGATCATTTCCATCATCTTGAGAACTTCAAGGATGACCAAGC	5046
QY	5674	ACGTGCAAGAGGCTTAACGAGCAGACTTACGACATGTACTATGATATCTGAGAGAT	5733
Db	5047	AAGACGCCGATCTCTGAGCGAGGAGCAGCTTCGAGACTTCTATGAAATCTGGGAGATG	5106
QY	5734	TCGATCCGAGAGGAGCACCAAGTACATATAGCTATGATGACTGTCCGAATCTCTGACGTAC	5793
Db	5107	TTGATCTGATGCCACCAAGTTCAATCGAGTATCTGTAAAGCTGGCGCACTTTGCCGACGCC	5166
QY	5794	TGAGAGCCCGCGCTGCAATCCACAAACCGAAAGAGTACAGATATATCGATGACATAC	5853
Db	5167	TGGAGCATTCCTCTCGAGTACCCAAAGGCCAACACATCGAGCTATCGCACATGACCTGC	5226
QY	5854	CCATCTGTCGGGCTGACCTCATGTACTGCTGCGCATCTCTGACGCGCTTACGAAAGACT	5913
Db	5227	CCATGTGAGCGGAGATGTGAATCCACTGTCTTGGACATCTTTTGGCTTACCAAGGAG	5286
QY	5914	TCCTTGGCGGAGGGCAATCCGATGAGAGAGACGGGTGAGATTGGTGAG-----ATAG	5967
Db	5287	TCCTGGAGAGACAGTGGGGAGTTGGACATCTGCGGCGACAGATGAGGAGGCGATTCTGTGG	5346
QY	5968	CGGCGCGCGCGGATACGAGAGGGCTACGAGCGCGCTCATCAACGCTGTGGCGTGAAGCTG	6027
Db	5347	CGTCCAAATCTTCCAAAGATGTCTTAACGAGCTTATACACACACTTGTGGGCGCAAGCAG	5406
QY	6028	AGAGTACTTGGCGCGCGCTAATCCAGACAGCGCTGTGGCGAAAGACAAAGCGCGCGCG	6084
Db	5407	AAGAGGTGTCTGCAGTGTCTTGGACGCTGTCTTACAGGGGACACCTGGCTAGCGGG	5463

RESULT 4

AY416500 5710 bp DNA linear GSS 17-DEC-2003

LOCUS AY416500 Pan troglodytes SCN8A gene, VIRUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY416500

VERSION AY416500.1 GI:39772460

KEYWORDS GSS.

SOURCE	ORGANISM
Pan troglodytes (chimpanzee)	Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.	
REFERENCE	
AUTHORS	1 (bases 1 to 5710) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trices
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PubMed	14671302
REFERENCE	2 (bases 1 to 5710)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	location/Qualifiers
source	1..5710 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <1..>5710 /gene="SCN8A" /locus_tag="HCNM5911"
ORIGIN	
Query Match	10.4%; Score 677.8; DB 9; Length 5710;
Best Local Similarity	42.4%; Pred. No. 2.7e-164;
Matches 2513; Conservative	0; Mismatches 3043; Indels 368; Gaps 26;
QY	186 CGCAAGAAAAACAAAAGAAATCCGATATGATGACGACGACGAGATGAAGTCCACAA 245
DB	100 CTCAGAAACCAACCAAGGCCGCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 159
QY	246 CCGATCTCAACATTGAACAGGGTGTGCCAATACCTGTTGCATTGACGAGCACTTCCG 305
DB	160 NNN 219
QY	306 CCGAATTGGCCTCCATCTCTCGAGAGATATCATCCATCCATCAGCAATGTACTGCA 365
DB	220 NNN 279
QY	366 TTCGATGTTGAAGCAAGAAAGATATTTTTCGCTTTTCTGCATCAAAAGCAATGTGG 425
DB	280 TTTTGATGATTAACAGAGGAGAAACCTCTTCAGATTAGTGCCAGCCTGCTTGTAC 339
QY	426 ATGCTCATTCATTAATCCGATACGTGTGTGGCATTTACATTTAGTGCATCATTA 485
DB	340 ATTTTAAGTCTTTTAACCTGATTAAGAAATAGCTATTAAATTTTATACATTCA 399
QY	486 TTTTCCATTCATCATCAACCAATTCCTGCTCACTCATCTGATGATATGCGGCA 545
DB	400 TTTAGCATGATCATTAATGTGACATTTTGAACAACTGTGATTCATGACTTTAGTAAC 459
QY	546 AGCCCAAGGTTGAGTCCACTGAGTG--ATATTACCGGAATTTACACATTTAAATCA 602
DB	460 CCTCTGACTGTCGAGAAAGTGTGAGTACAGTTTCACAGGATTTTAATCA 519
QY	603 GGTGTTAAGATGAGCAAGAGGTTCAATTTATGACCGGTTTACATCTTAAGATGAC 662
DB	520 CTAGGAATATATTGCAAGAGGTTTTCGATAGATGGCTTTACTTTTACGGATACCA 579
QY	663 TGGATTGGCTGAGCTGTTAGTAAATAGCTTTAGTTATGTGACCATGGTATTAATTTA 722
DB	580 TGGACTGGTATGATTTGAGTGCATCATGATGGGTATATATTAACAGATTTGTAACCTA 639

Qy 723 GGTAACTAGACAGCCCTGCGAAGCTTTAGGGTGTGCGAGCGCTTAAACCGTAGCCATT 782  
 Db 640 GGCAATGTTTCAAGCTCTACGACCTTTCAAGGGTACTGAGGGCTTTGAAAACTATTTCGGTA 699  
 Qy 783 GTGCCAGGCTTGAAGACATGTCGGCCGCTCATCGAATGGGTGAAGATCTGGCGAAT 842  
 Db 700 ATCCAGGCGCTGAAGACAAATGTGGGTCCCTGATTCAGTCTGTAAAGAAACCTGCAAT 759  
 Qy 843 GTGATTAATCTGACCATGTTCTCCCTGTGCGGTGTGAGGTGGGCTACAGATCTAT 902  
 Db 760 GTGATGATCTGACAGATGTTCTGCTGAGTGTTCCTGCTTGATCGAATGANNNTTTC 819  
 Qy 903 ATGGCGGTGCTCACCGAAGTGCAT-----CAAGAAATTCCCGCTGAGCGGTTC 953  
 Db 820 ATGGGGAAACNNNNNAAACNNNTGTGTGTNTNNNCATPAAACTNNAACGNNNNNTATCTT 879  
 Qy 954 TGGGGCAATCTGACCGACGAGAACTGGGACTATACAAATCCGATATGCTCCATTGGTAT 1013  
 Db 880 GAAAAATGGCACAAAGGCTTNNATTTGANNNNNNNNNNNNNNNNNNNNNNCAAATTTCTAC 939  
 Qy 1014 TCCGAGACGAGGGGATCTCATTTCCGTTATGCGGCATATATCCGGTGGGGGCAATGC 1073  
 Db 940 ACAATTCCTGCAAGCTGTAACCTTTACTCTGTGGAAACAGTTCTGATGTGGCAATGC 999  
 Qy 1074 GACGACGATTAAGTGTGCTGCAAGGGGTTTGTGTCGAAATCCGAATTTATGCTACACAGC 1133  
 Db 1000 CCAGAGGGATCCAGATGATGAAG---CAGAGAGAAACCCCACTATGTTACACAAAT 1056  
 Qy 1134 TTGCAATTCGTCGATGGGCTTTCTGTCGCGCTTCGCGCTGATGACACAGAGCTTCTGG 1193  
 Db 1057 TTTTACACTTTTACTGCGGCTTCTTGGCATTAATTTCCCTTAATGACCAAGACTAATGG 1116  
 Qy 1194 GAGATCTGTACGACGCTGTGTGGCGCGCCGCAATGACCATGCTCTTCTTA 1253  
 Db 1117 GAAACTGTGATCAATGNNNTTACGAGCACCGGAAACATCATATCTTCTTCTGC 1176  
 Qy 1254 GTCACTCATCTTCTAGGTTCAATCTTATCTTGAATTTGATTTGGCCATGTTGCCATG 1313  
 Db 1177 TTGTCATCTTTGTGGGTTCTTTCTATCTGTGAACTTGATCTTGGCTGTGGCCATG 1236  
 Qy 1314 TCGTATGACGAATTCGAAAGAGAGCGCGAAGAGAGAGGCTGCCGAAAGAGCGATA 1373  
 Db 1237 GCTTATGAAGA---CAGAACTCAGGCAACACTGAGAGGCGAGAACAAAGAGGCTGAA 1293  
 Qy 1374 CGTGAACGGAAGAGAGCTGCCCGCCGCAAGCGGCA-AGCTGAGAGAGCGGCAATGC 1432  
 Db 1294 TTTTAAAGC---AATGTTGAGCAACTTAAAGACACAGAGAGAGGCAAGGCTGCTGC 1349  
 Qy 1433 GCAAGCTCAGGCGACAGCGATGCGGCTGCCGGAAGAGGCTGCACTGCATCCGGAAT 1492  
 Db 1350 GATGCGCACTTCACAGAGAACTGTCTCAGAAATGCCATAGAGAAAGGTGAAGAGG 1409  
 Qy 1493 GGCCAAGATCCGACGATTTCTGCAATCAGCTATGAGCTATTTGTGGCGGCGAAGAGG 1552  
 Db 1410 AGGGGGCTCCCTCGAGAGCTTCTGAAATCTTAACTCAGCTCAAGAGATGAAAGGA 1469  
 Qy 1553 CAACGATGACAAACAAGAGAGATGTCAATTCGAGAGCTGAGGTGGAGTGGAGTC 1612  
 Db 1470 AAGAAGTACGAGAGAGAGAGAGAGAGAGAGAACTCTTAAGAGAGAGAGAGAGG 1529  
 Qy 1613 GGTAGAGGTTATCAAAAGACAAACAGACACTACACAGACACCAAGCTACAAAGTTTCG 1672  
 Db 1530 GGATCCGAGAGAGGTGTTAAGTCAAGTC-----AGAAAG 1565  
 Qy 1673 TAAAGTACGACGACATCTTATCTTACCTGTTCACCGTTTAACTACGACAGGAGATC 1732  
 Db 1566 TGGNNNNAAGAGAGGCTTTCCGCTGCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1685  
 Qy 1733 ACGTAGTTCACAAAGTACAGATACAGAAAGAGACGTCGCTTTGTGTATACCGGATG 1792  
 Db 1626 NNNNNNNNNNTCACTGCTCAGACATCCAGAGC---TCGCTCTTCTCTCCGACACAC 1680  
 Qy 1793 CGATCGTAAGCATTTGGTATGTCAACATATCAGAGATGCCAGAGACACTTGCCTATGC 1852

Db 1681 AGCAAGACACATCTTCAATTCANNNNNACCTGG-----GGGTTCCGAGACCC 1730  
 Qy 1853 CGAGCATCTGAAATGCCCTCACCCCGATGTCCGAAGAAATGGGCAATAGTCCCGT 1912  
 Db 1731 GGGCTCCGAGATG-----AGTTGGCGAGTACAGACACAGACAGGTGAGGA 1778  
 Qy 1913 GTACTATGGCAATCTAGGCTCCCGACACTCATCTGATATCTCTGCAATGCCCAATATC 1972  
 Db 1779 GAGGAGGGGCGCGGAGCTCTTCTTATCTCCATCCGGGCCCGCGAGCGCCGAGAG 1838  
 Qy 1973 GTATACCTCAGATGCGATCTACTCGGCGGATGCGGCTCATGGGCGTCAACAAATGAC 2032  
 Db 1839 CTACAGCGGCTACAGCGGCTACAGCGGAGCGGCTCTCGGCACTTCCCAAGCT 1898  
 Qy 2033 CAAGAGACCAATTTGGGCAACCGCACACAGCAATCATCATGTGGGCGCACCAATG 2092  
 Db 1899 GCGGCGAGCGTGAAGGCAACAGACGCTGACCTGCAACGCGGTGTGCTCTCATTCG 1958  
 Qy 2093 CGGACCACTGTCTGACACCAATCAACAGCTGATCGGACTACGAATTTGGCT 2152  
 Db 1959 CGGCTCCGCT----- 1969  
 Qy 2153 GAGTGCACGAGCGAGCTGCAAGATTAAACATCATGACAACTCTTTATCGACCCGT 2212  
 Db 1970 -----CCCAATCGCGGGGCTCTCTCGACAGGCTPAACTGAGTGAAAT 2018  
 Qy 2213 CCAGACCAACGGTGTGATATGAAGATGTGATGCTCTGAATGACATATGAAACA 2272  
 Db 2019 TAAAGAAAGGCCCTGATCTCTTTAGTTTCCATGAGCAATTAAGCTCTCTACGGGCG 2078  
 Qy 2273 GCGCGTGTGCGACAGTGGGCAAGCATCGGCGTGTCCGTTACTATTTCCACAC 2332  
 Db 2079 GAAGGACGAATCAACAGTATATGAG-----TGTGTTAC 2114  
 Qy 2333 AGAGACGATGACGAGATGGGCGGACGTTCAAGACAGCACTCGAAGTATCTCA 2392  
 Db 2115 AAATACACTGTAGAGNN 2174  
 Qy 2393 AGGCATGATGTGTTTGTGTGGGACTGTGCTGTGGTGTGTTAAATTTCAAGAGTG 2452  
 Db 2175 NNN 2234  
 Qy 2453 GGTATCGCTATCGTCTTGCATTCCTTCTGCTGAGCTTTCACTACGCTGTGATTTGGT 2512  
 Db 2235 NNN 2294  
 Qy 2513 CAACAGATGTTCAATGATGATCACACAGATATGAAACAAGAGATGGAACGCTGCT 2572  
 Db 2295 NNN 2354  
 Qy 2573 CAAGATGGCAACTATTTCTTCAACCGCACCTTTGCATCGAGGCAACATGAAGCTAT 2632  
 Db 2355 NNN 2414  
 Qy 2633 GGCATGAGCCCAAGTACTATTTCCAGAGGCTGGAACATCTTCACTTATTCGT 2692  
 Db 2415 AGCATGATCTCCCAACAATTAATTTCAAGAGGTTGGAACATTTTNCGATTAATTTGT 2474  
 Qy 2693 GGCCTATCGCTATTTGGAATCGAGGCTCGAGGGGTCCAGGGTGTGCCGATTTGCGTTC 2752  
 Db 2475 CTCCTCAATTTATGGAATCTGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2534  
 Qy 2753 CTTTCATGCTGCTGATTAATCAACTGCGCAAGTCTTGGCCCACTTAATTAATCAT 2812  
 Db 2535 NNN 2594  
 Qy 2813 TTGATTTATGAGACGACATGGGCGTTTGGGTAATCTGACATTTGTACTTTGCATAT 2872  
 Db 2595 CAAGATTTATGGAATTCAGTGGGTGCTGGGCACTTCACTGCTGCGCATATAT 2854  
 Qy 2873 CATCTCATCTTGGCGGTGATGGAATGCAACTGTTCGAAAGAAATATCATGA---TCA 2929

Db 2655 TGTCTTCACTTTCCGCTGCTGCGGATGCACTCTTTGGAAAAAGCTAACAAAGATGTGT 2714  
QY 2930 CAAGGACCGCTTTCCGATGCGCACTGCGCGCTGGAACCTTCAACGACTTATGCAAG 2989  
Db 2715 CTGCAAGATCAACCAAGACTGTGAACCTCCCTGCTGCAATATGATGACTTTTTCATTC 2774  
QY 2990 CTTCAAGATCGTGTCCGGGTGCTGCGGAGAAATGATGAGTCCATGAGGAGCACTGCAAT 3049  
Db 2775 CTTCTCATTTGTCTTTCGAGTGTGTGCGGAGTGTGATGAGAACATGAGGAGCACTGCAAT 2834  
QY 3050 GTACGCTG---GGCGATGCTCTGCAATCCCTCTTCTTGCCACCGCTGTCACTCGGCA 3106  
Db 2835 GGAAGTGGAGCGCAAGCCATGTGCTCATGTCTTATGATGTGATGTGATGATGCA 2894  
QY 3107 TCTTGTGATCTTAACCTTTTCTTAAGCTTGTCTTTGTCTTCAATTTGGCTCATGCTT 3166  
Db 2895 CTTGTGTGTCTGAACCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2954  
QY 3167 ATCAGGCGGCACTGCGGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 3226  
Db 2955 GGTCTGCAAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 3005  
QY 3227 CCGATTTAAAGTTGGGTTAAGCTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTA 3286  
Db 3006 CCGTATCAAGAGAGGTGTGCTGCTGCAACCAATGAGTGCAGCTTCACTGAGGCGCA 3065  
QY 3287 ATTGACAAATCAAAATGATGATCAACCATGAGTGAAGAGCAACCAAGATCAGTTGAT 3346  
Db 3066 CTTTAAGCAGCTGAGGCGCATGA-----GGTGAAGCTCTGATGATGATGAT 3114  
QY 3347 TTGGAGCGAAGACATGTGTGCAACCAAGTGTGCGGCAAGAGATGCTGCGGCA 3406  
Db 3115 -----GAAAAAAGGCGCAACTGTATGCGCAATCAACCGGTGCAAGATCAACCGGA 3167  
QY 3407 CGGCTCATCAAGAGGAGTCAAGAGCAGACGCAACTGAGTGTGCGGCTCGGAGTGC 3466  
Db 3168 TGGCGACTTCCAGAAAGATGCGAATG-----3193  
QY 3467 GATGAAATTCAGATCAACGCGCATGAAACCAACAGCCGAGAAATCCAAATATCT 3526  
Db 3194 -----GCAACACAGCGGCAATGCGACAGGCTGAGAGAGATCACTCATGATGN 3242  
QY 3527 AAATTAACGACATGATTTGGCAATCAATTAACCAACAGATGATGATGATGATGATGATG 3586  
Db 3243 NNACCAACNNNTCTTATCAACCAACCA-----ACTTACGTGTGC 3283  
QY 3587 GCTAAACATAGAGTTTGTCTTACAGACGACATGCGACGATTAATCATATG 3646  
Db 3284 NGNTAACCATTTGCTG-----GNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3320  
QY 3647 TAGCCATAGATGACCATTCAGAGACGAGAGCCACAGGCGCGCGAGACATGCA 3706  
Db 3321 NNN 3380  
QY 3707 GGGCGAGAGAACGCGACGCAAGAGATTTAGTCTGACGAGGATCTGAGCA 3766  
Db 3381 TGACACAGCTCTCTTGAAGAGACCATTTGATTAACCAAGAGTGAAGAGGTCCC 3440  
QY 3767 GGAAGGCGATGCGAGAGGCGCGCTGACGAGTGTATCATTTATTCAGACAGCA 3826  
Db 3441 TGTGAAACAGCGTGAAGAAATCTTGG-----3466  
QY 3827 GGAATATCTGATGATATATCACTGCTGCTGCGGATTCGTAATTAAGAAATTTCC 3886  
Db 3467 -----ATCCAGATGCTGCTTCAAGAGGTTGTGTCCAGCGGTTCAA 3509  
QY 3887 GATCTTAAGCGGTGACATGCTGCGCTCTGCAAGATGAGGCAATTTAGACTGAA 3946  
Db 3510 GTGCTGCGAGGTCAACATTCAGAGAGGCTAGGCAAGTCTTGTGTGATCTCTGCGAAAC 3569  
QY 3947 AACTTTCAATTAATTAAGAAATTAATTTTGAAGACGCTGTATCACTATGATTTAAT 4006  
Db 3570 CTGCTTCTCATGTGTGAGCAACGTGTTTGAAGCTTCACTATCTTCAATGATTTGCT 3629

QY 4007 GAGTACTTAGCTTTGGCATTTAGAAATGTACATCTGCCAACAAGACCATACTGAGGA 4066  
Db 3630 GAGCAGTGGCGCTGCGCTTGGAGACATCTACATTTAGAGAGAGAAAGACCATCTGCAC 3689  
QY 4067 TATTTTATCTATTAATGAGACAAATTTACGGTTATATCTTCTTGAATATGATCA 4126  
Db 3690 CATCTGGAATATGCTGACAAAGTCTTCACTATATCTTATCTTGAATATGATCA 3749  
QY 4127 GTGTGCGCTGCGCTTCAAGTGTACTTCAACCAACGCGTGTGTGCTGATTCGT 4186  
Db 3750 GTGAGACGCTTATGCTGCTGCAAGTCTTCAACCAACGCGTGTGTGCTGATTCGT 3809  
QY 4187 GATGTCTATGATATGCTTATCAACTTGTGCTTCACTGTTGAGCTGTGATATCA 4246  
Db 3810 CATGTGTGCTTNN 3869  
QY 4247 AGCTTCAAGACTATGCAACGTTAAGACACTGAGACACTACGTCATGCTCCGAT 4306  
Db 3870 NNN 3929  
QY 4307 GCAAGGCAATGAGGCTGCTGTTATGCTGTGTAACGCTATACCTTCAATCT 4366  
Db 3930 NNN 3989  
QY 4367 GCTATTGTGTCTTAAATTTTGGCTAATTTTGGCTAATTTTGGCTAATTTTGGCT 4426  
Db 3990 NNN 4049  
QY 4427 TGAATAATTTTAAATGCGAGACATGATGCGACAGAGC-----TCAGC 4472  
Db 4050 GGGAAAGTACCAACNNCTGCTTAAATGAGACTTCCGAAATCCGATTTGAATGGAATGT 4109  
QY 4473 CACGATCATACCAATGCAATGCTGCGAGAGCGAGACTA-----CACGTGGT 4525  
Db 4110 CAACATTAATACTGATGTGAAGAGCTTATGAGAGGAGCAATATACAGATGAGTGA 4169  
QY 4526 GAATTCAGATGAATTTGATCATGTAGTAAAGCTATGCTGTCTTCCAGTGGC 4585  
Db 4170 GAACTGAAATCACTNNGACATGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 4229  
QY 4586 CACCTTCAAGGCTGATCAATCATGACATGATGATGATGATGATGATGATGATGATGAT 4645  
Db 4230 NNN 4289  
QY 4646 GCAACCAATTCGTAACGAAACATCTAATGATTTATTTGATTTCTTCACTAT 4705  
Db 4290 GCAGCTAAGTATGAGACATATCTAATGATCTATCTTGTCTATCTTCACTATCT 4349  
QY 4706 TGAATCTTTTCACTCAATCTGTTCAATGTTGTTTCAATGATTTTAAAGAGCA 4765  
Db 4350 CGGCTCTTCTTCACTCAATCTGTTCAATGTTGTTTCAATGATTTTAAAGAGCA 4409  
QY 4766 AAAAAAAGCAGTGTGATCAATGATAATGTTTATGATGAGAGATCAGAAAAAGTACTA 4825  
Db 4410 AAAAAAAGTGTGAGG---TCAGACATCTTCAAGACGAAAGACAGAAAGTACTA 4466  
QY 4826 TAACTGTAAGAAAGATGAGCTTAAAAACCATTTAAAGCATTTCAAGCAAGGTG 4885  
Db 4467 CAATGCAATGAAAAAAGCTGAGCTCAAGAAAGCAGAAACCTATTCCTGCGCTTGN 4526  
QY 4886 GCGACCAAGCAATGCTTTGAATATGTAACCGATAAGAAATGATATATCTAT 4945  
Db 4527 NNN 4586  
QY 4946 GTATATCATTTGCTGAACATGTTCACTGACCTCGATGCTTGAAGAGTGTGAGAC 5005  
Db 4587 NNN 4646  
QY 5006 GTATTAACGCGCTCTAGCATCTCAATGCAATGCTATTTGATTTTCAATTTCCGAATG 5065  
Db 4647 NNNNGAGACATCTNN 4706

5066 TCTATTAATAATTCCTGCTTACGATATCACTATTATTTAGAGCCAGGAATTTATTTGA 5125  
 4707 TGTGCTCAAAATGTTTGCTGAGGCAATTCCTTCAATTCAGTCTGGAACATTTTNA 4766  
 5126 TGTAGTATGTCATTTTATTCATCTTGTAGTCTTGTACTTACGATATTTATTCAGAAATA 5185  
 4767 CTGCTGTATGATCACTCTCCANN 4826  
 5186 CTGCTGTGCGGACCTCTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5245  
 4827 CTGCTGTGCGGACCTCTGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4886  
 5246 ACTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5305  
 4887 NNNNATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4946  
 5306 GGGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5365  
 4947 TGCCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5006  
 5366 CATGCTGTTTCATGACGTTGAG 5425  
 5007 GATGTCGAATTTTGTGATGTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5066  
 5426 GACCTTTGCGAGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5485  
 5067 GACATTTGCGAGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5126  
 5486 TGTACTGAGAGCCATTTATCA-----TGAGAGAGATGAGATGAGATGAGATGAGATGAGATG 5536  
 5127 CCTGCTGCTGCGACATCTTAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5186  
 5537 CAAGAGGCTATCCGGGCAATTTGT 5596  
 5187 GAGTGGCTTTAAAGGAGATTTGT 5246  
 5597 CCTAGTTAAGCTTTTGT 5656  
 5247 CATATCAATCTCTTCTTAAATGTTGT 5306  
 5657 TAGTCAGGCGCACCGAG 5716  
 5307 CAGGTGATCCAG 5366  
 5717 TGAATCTGCGAGAGATTTGT 5776  
 5367 TGAATCTGCGAGAGATTTGT 5426  
 5777 CGAATTCCTGAGAGATTTGT 5836  
 5427 AGACTTTGCAATGCTTGTGAGNNNNCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5486  
 5837 CATATCAATGAGATTTGT 5896  
 5487 CATGCTATGATCTGCGAG 5546  
 5897 CGCCCTTCAAGAGAGATTTGT 5956  
 5547 TGCCCTTCAAGAGAGAGATTTGT 5606  
 5957 TGTGTGAG-----ATAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6010  
 5607 GGAAGAG 5666  
 6011 GCTGTGCGTCAAGAGAGATTTGT 6054  
 5667 ACTGTGTGCAAG 5710

RESULT 5  
 BM632901 673 bp mRNA linear EST 26-FEB-2002  
 LOCUS  
 DEFINITION 1700067505389 A.Gam.ad.cdNA1 Anopheles gambiae cdNA clone

19600449633036 5', mRNA sequence.  
 BM632901  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Anopheles gambiae (African malaria mosquito)  
 Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 673)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
 Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: N001004ABY row: C column: 18  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1..673  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449633036"  
 /dev\_stage="Adult"  
 /lab\_host="MDH10b"  
 /clone\_lib="A.Gam.ad.cdNA1"  
 /note="Vector: pSPori1; Site 1: SalI; Site 2: NotI; whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSPori 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."

ORIGIN  
 Query Match 6.2%; Score 406.8; DB 4; Length 673;  
 Best Local Similarity 77.1%; Pred. No. 5.2e-94;  
 Matches 495; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

3608 CTTAAG 3667  
 32 CTTAAG 91  
 3668 CAG 3727  
 92 TAAAG 151  
 3728 CAG 3787  
 152 CAG 211  
 3788 CCGGCTGAG 3847  
 212 TCTCTGAG 271  
 3848 AGCTGATGAG 3907  
 272 GGGGAG 331  
 3908 CTCGCCGTTCTGAG 3967  
 332 CGGCCGTTCTGAG 391  
 3968 TAAATATTTTGAAG 4027  
 392 TAAATATTTTGAAG 451

```

QY      4028 AGAAGATGATCATCTGGCCAGAAAGCCCATCTGCAGGATATTTTAACTATATGAGCAG 4087
DB      452 CGAAGATGATCATCTTCACAGCGCCCAATCTTCAAGATATTTTAACTATATGAGATCG 511
QY      4088 AATATTACAGGTATATTTCTTTGGAAATATGTAATCAAGTGGTGGCGCTCGGCTTCAA 4147
DB      512 AATTTCACAGTATCTTTTATAGAGATGTTATCAATATGTTAGCTTTAGTTTAA 571
QY      4148 AGTGAATCTTCAACAGCGGTGGTGGTGGCTGCATTCGATTTGCATGATGCTAT 4207
DB      572 AGATATATTTTACAAAGCTTGGTGGCTGATTTTCAATATGATGATGATCTTGAAT 631
QY      4208 CAATCTGCTGCTTCACTTGTGAGCTGGTGGTATTCAGC 4249
DB      632 AAATCTGATGCTTCACTTGTGAGCTGGTGGTATTCAGC 673

RESULT 6
BU729409      866 bp      mRNA      linear      EST 09-MAR-2004
LOCUS      BU729409 MF015DA cDNA Oryzias latipes cDNA clone MF015DA005d18 5',
DEFINITION      mRNA sequence.
ACCESSION      BU729409
VERSION      BU729409.1 GI:45296721
KEYWORDS      EST.
SOURCE      Oryzias latipes (Japanese medaka)
ORGANISM      Oryzias latipes
REFERENCE      Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
AUTHORS      Medaka EST Project in Takeda's lab
JOURNAL      Unpublished (2001)
COMMENT      Contact: Tadasi Shin-i
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshini@genes.nig.ac.jp.
              Location/Qualifiers
                1. 866
                /organism="Oryzias latipes"
                /mol_type="mRNA"
                /strain="Hd-rR"
                /db_xref="taxon:8090"
                /clone="MF015DA005d18"
                /sex="mixture of female and male"
                /tissue type="whole embryo"
                /dev_stage="organogenesis stage 35"
                /clone_lib="MF015DA cDNA"

FEATURES
source

```

## ORIGIN

Query Match 5.1%; Score 334.6; DB 4; Length 866;  
 Best local Similarity 63.0%; Pred. No. 3.6e-75;  
 Matches 539; Conservative 0; Mismatches 305; Indels 12; Gaps 1;

```

QY      5011 ACCGGCTCTAGACATCTCAATGCATATGCTAGTATTTTACGTTCCGAATGCTAT 5070
DB      10 ACAAGATCTCTACTGATCAACCTGTTTTCATGTGCTCTTACTCGGGAAATGTTTC 69
QY      5071 TAAATATTCGTTTACGATATTCATATTTTATGAGCAGCATATTTATTTAGATGTAG 5130
DB      70 TCAAAATATATCTCTCGCGCACTATTTACTTACATTCGCTGGAACATCTTTGATTTG 129
QY      5131 TAGTTCATATTTATTCATCTTGTAGTCTTGTACTTAGCAGATATATTCAGAAATGACTTCG 5190
DB      130 TGTGTGATGATCTTTGATGTAGTATGTTTATTCAGGAAGTCAATCGAATATCTTGG 189
QY      5191 TGTGCGGACCTGCTCGAGAGTGTGTGGCGAAAGTGGCCGTGTCTTCGACTGG 5250

```

```

DB      190 TGTCCCAACCTGTTTCAGATGATTCGCACTAGACAGATTTGGATCTCCCTGTA 249
QY      5251 TGAAGGAGCCCAAGGGCATTTGAGACATGCTCTTTCGCTGGCCATGTCGTCGGCCC 5310
DB      250 TTAAGGCCCAAGGGCATTTGAGACGCTTCTTTCGCTTGAATGATGCTCTTCCTGCC 309
QY      5311 TGTTCACATCTGCCCTGCTGCTTCCCTGATGATGATCACTTTGGCATTTTCGCAATG 5370
DB      310 TGTTTAACAATAGGCTCTTCTTCTTCTGATGATGATGATGATGATGATGATGAT 369
QY      5371 CGTTCTTCATGACAGTGAAGAGAGAGAGGAGCATTAACAGCTTACAATTCAGAGCT 5430
DB      370 CCAACTTGCATACATGTAAGAAAAAGATCAGGATGAGACATGTTCAATTTTGAGACCT 429
QY      5431 TTGGCCAGAGCATGATCTGCTCTTTCAGATGTCAGCTGACCGGTTGGATGTGTAC 5490
DB      430 TGGGAAACATGATGATCTGTTTTCAGATCAACGCTCTGCTGGTGGATGAGCTTTC 489
QY      5491 TGGAGCCATTTATCA-----TGAGGAAGCATGCGATCCACCCGACAGCAGA 5538
DB      490 TGTCTCAATTAAGTGAACAAAGAGAACTGATCTGTACAGCCAACTGAGACCCAGGCA 549
QY      5539 AAGGCTATCCGGGCAATGTGTTCAGCGACCGTGAATTAAGTTTCTCTCTCATACC 5598
DB      550 ACACTACAAAGCAACTGTGGGAACCCATCAGTGGCATATTTTTCACACTACA 609
QY      5599 TAGTTAAGCTTTTGTATGATTAATATGATTAATGATCTGCTCATCTTCGAACTATA 5658
DB      610 TCAATCTTTCCTTTCATAGTGTCAATGATGATGATGATGATGATGATGATGATGAT 669
QY      5659 GTGAGGCCACAGAGACGTGCAAGAGGGCTTAACGACGACGACGACGACGACGACGAC 5718
DB      670 GTGTGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
QY      5719 AGATCTGAGCAATTCGATTCGAGAGGAGCCAGTACATGATGATGATGATGATGAT 5778
DB      730 AGGTGTGGAGAGAGCTTTGATTCAGAGCGCACACAGTTTGTGAGATCTGATGATCT 789
QY      5779 AATTCCTGAGAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5838
DB      790 ACTTTCAGATCTCTAGACCCACCACTGCGGATGCCAAGCTTAACGATTCANCTGG 849
QY      5839 TATCGATGACATACC 5854
DB      850 TTTCAATGATCTGCC 865

```

RESULT 7  
 BI509823 537 bp mRNA linear EST 08-APR-2002  
 LOCUS BI170021A10E09.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170021A10E09 5', mRNA sequence.  
 DEFINITION  
 ACCESSION BI509823  
 VERSION BI509823.1 GI:15360197  
 KEYWORDS  
 SOURCE Apis mellifera (honey bee)  
 ORGANISM Apis mellifera

REFERENCE  
 AUTHORS Whitefield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L., Pardinas, U., Robertson, H.M., Soares, B. and Robinson, G.E.  
 TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee  
 JOURNAL Genome Res. 12 (4), 555-566 (2002)  
 MEDLINE 21932240  
 PUBMED 11932240  
 COMMENT Contact: Gene E. Robinson  
 Department of Entomology  
 University of Illinois  
 505 S. Goodwin Ave., Urbana, IL 61801, USA  
 Tel: 217 265 0309

Fax: 217 244 3499

Email: [genetobi@life.uiuc.edu](mailto:genetobi@life.uiuc.edu)

This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR primers

FORWARD: TAATACGACTCCTAATAGG

BACKWARD: ATTAACCTCCTAATAG

Plate: BB170021A10 row: B column: 09

Seq primer: AGCGATACCAATTTACACAGGA

High quality sequence stop: 537.

## FEATURES

source

```
1. 537
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB170021A10E09"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/note="Organ: brain; Vector: pT773-Pac; Site 1: EcorI;
Site 2: NotI; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."
```

## ORIGIN

```
Query Match      5.0%; Score 327; DB 4; Length 537;
Best Local Similarity 75.7%; Pred. No. 2.9e-73;
Matches 405; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 5134 TTGTCATTTTATTCATCTTAAAGTCTTGTACTTAAAGATATTCAGAGTACTTCTGTGT 5193
DB 3 TTTTCATTTTGCATATTTAGTCTGCTTCAAGATATTTAGAGAGTACTTCTGTAT 62
QY 5194 CGCCGACCTCTCTCGAGTGTGCTGTGGGAAAGTGGCCGCTCTTCTTGAAGTGTGA 5253
DB 63 CGCCAAATCTCTCTGTAGTAAAGGTCGCAAAAGTCGTCGTCTCTGACTCTGTGA 122
QY 5254 AGGAGCGCAAGGGATTCGACATCTCTCGGCTTGGCGATGTGCGCGCCCTGT 5313
DB 123 AAGGTGCGCAAGGGATTCGAACTCTTCTTTCGCTTGGCGATGTGCTTACACCTCT 182
QY 5314 TCAACATCTGCTCTGCTGCTTCTGATCATTTTGCATTTTGGCGATGTGCT 5373
DB 183 TCAATATTTGCTTACTTCTGTTTGGATGTTTATCTTGGCATATTTGGATGTGCT 242
QY 5374 TCTTCATGACGTGAAGAGAGAGCGGCAATTAAGCATCTTAACTTCAAGACTTTG 5433
DB 243 TCTTCATGACGTGAAGAGATTAAGAGCGGATGACATGTGTACATTTTAAACGTTG 302
QY 5434 GCGAGACATGATCTGCTCTTTCAGATGTGAGATGACGCGGTGGATGTGATCTGG 5493
DB 303 GACAGTCGATGATATTTGCTATTTCAAGATGTAAGCTCGGTGGTGGACGCTGTCTTG 362
QY 5494 ACCGCAATTAATGAGAGAGATGATGATCCAGCGAGAGAGAGAGAGATCCGGGCA 5553
DB 363 ACCGCAATTAATGAGAGAGATGATGATCCAGCGAGAGAGAGAGATGATCCGGGCA 422
QY 5554 ATTGTGTTTACGCAAGCTTGAATTAAGCTTCTCTCACTTACCTTAAAGTCTTT 5613
DB 423 ATTGTGTTTCTTACGCAAGCTTGAATTAAGCTTCTCTCACTTACCTTAAAGTCTTT 482
QY 5614 TGATAGTTATTAATGATGATGCTGTCTGATCTCGAGAACTATAGTACGCGCAC 5668
```

DB

483 TAATCGCATTAATAATGATGATGCTGTCTGATCTTGGAGATTAATTCACAGCAC 537

RESULT 8  
CN527280

LOCUS

DEFINITION CN527280 829 bp mRNA linear EST 29-APR-2004  
IMAGE:30653177 5', mRNA sequence.

ACCESSION

VERSION CN527280.1 GI:46855436

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

The following repetitive elements were found in this cDNA
sequence: 502-571, >(CAT)n#simple_repeat
Seq primer: pYX-5.

Location/Qualifiers
1. 829
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30653177"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP HB0"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTAATGAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
```

## FEATURES

source

```
Query Match      4.9%; Score 321.4; DB 7; Length 829;
Best Local Similarity 63.5%; Pred. No. 9.6e-72;
Matches 526; Conservative 0; Mismatches 292; Indels 10; Gaps 2;

QY 5086 TACGATATCACTATTTATTTAGAGCAATTTATTTGATGATGTTGCTATTTAT 5145
DB 3 TGGCCCACTATTTACTTACCAAGAGTGAACATCTTCGATTTCTGTGTATCTCT 62
QY 5146 CCATCTTAGTCTTTTACTTACGATTTATGAGAGATCTGTGTGCGGACCTGTC 5205
DB 63 CCATCTTAGTCTCTCTCTCCGACATCATCAAGAGTACTTCTTCCCAACGCTCT 122
QY 5206 TCCGAGTGTGCGGTGCGCAAGTGGCCGCTGTCTTGCATCTGTCAAGAGGCAAG 5265
```

Db	123	TCCTGTGATCCGTCCTGTGGCCAGGATCGGCGGCATCTCCAGGCTATATCCAGAGGCCAAG	182
Qy	5266	GCATTTCGACACTGCTCTTTCGGCTTGGCCATGTCGTGCGGCGCCCTGTTCAACATCTGCC	5325
Db	183	GGATTTCGACGTTGCTCTTTCGGCCCTCATGATGTCCTCTGCGCCCTCTTCAACATCGGCC	242
Qy	5326	TGCTGCTGTTTCCTGTCATGTTCACTTTTGCGCATTTTTCGGATGTCGTTCTTATGACAG	5385
Db	243	TCCCTCTCTTCTCTGTGATGTTCACTTCACTTCATCTTTCGGATGAGCCAACTTTGCCATGC	302
Qy	5386	TGAGGAGAGAGAGGGGCAATTAAACGACGCTCAACTTCAACACTTTTGCGCCAGACATGA	5445
Db	303	TCAATGAGAGAGGCTGGCATGACACACATGTTCAACTTCCAGACCTTTGCCAAGCATGC	362
Qy	5446	TCCAGCTCTTTCAGATGTCACGTCAAGCCGGTGGGATGATGTACTGACGCGCATTTATCA	5505
Db	363	TGTGCTTTTTCAGATCAACGACGTTCGGCTGGCTGGGATGCGCTCTCAGGCCCATCTCA	422
Qy	5506	ATGAGGAAGCATGCGATCCACCCGACAGCGA-----CAAAGGCTATCCGGGCATTT	5556
Db	423	ACACAGGACCCCTCACTGTGACCCCAACCTGCCCAACAGCAATGGCTCCAGGGGGAATC	482
Qy	5557	GTGTTTCAGGACCGTTGGGAATTAAGTTTCTCTCTCACTACCTGTTATAGCTTTTGA	5616
Db	483	GTGGAGGCCACAGCAGTGGGACCTCTTCTTTCACACCTTAATCATCTCTTCTCTCA	542
Qy	5617	TAGTTATTAATATGATACATGCTGCTGATCTTCGAAATATATGTCAGGCCACGAGACG	5676
Db	543	TCTGTGTCAACATGTACATTTGCCATCATCTTGGAATCTTGAGAACTTCAGTGTGGCCACAGAAAGA	602
Qy	5677	TGCAAGAGGGTCTTAACGACGACGACATACATGATATGATATCTGGACGCAATTCG	5736
Db	603	GCACAGAGGCCCTTGAGCGCAGGATGACCTTCGACATGTTCTATAGATATCTGGAGAAAGTTCG	662
Qy	5737	ATCCGAGAGGGACCCAGTACATATAGCTATGATCAAGTCTCCGAATTCCTCGACGTAATCG	5796
Db	663	ACCGGAGGCCACCCAGTTCAATTGAGTATTTGGCCCTTCCGACTTTGGCGATGCCCT-G	721
Qy	5797	AGCCCCCGCTGCAGATCCACAAACCGAACAGTACAGATCATATCATGATGACATATCCCA	5856
Db	722	TCTGAGACCTCGGATGCGCAAGCCAAACAGATATAGCTCATATATGACCTCGGCCA	781
Qy	5857	TCTGTGCGGTGACCTCATGTACTGTCGCTGCACATCTTCGAGCGCCCTTA	5904
Db	782	TGTGTAGAGGAGGAGCGCATCCACTGTATGAGCATCTCGTTCGCCCTTCA	829
RESULT 9			
AK032187	2802 bp	mRNA	linear
LOCUS			
DEFINITION	Mus musculus adult male olfactory brain cDNA, RIKEN full-length		
VERSION	enriched library, clone:643048L01 product:sodium channel protein		
KEYWORDS	II homolog [rattus norvegicus], full insert sequence.		
SOURCE	AK032187		
ORGANISM	AK032187.1 GI:26328014		
	HTC; CAP trapper.		
	Mus musculus (house mouse)		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PMID	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Ichih, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
MEDLINE	prepare full-length cDNA libraries for rapid discovery of new genes		
PMID	Genome Res. 10 (10), 1617-1630 (2000)		

TITLE	MEDLINE
PUBLISHED	204993374
REFERENCE	11042159
AUTHORS	3
	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
	Kono,H., Akiyama,J., Nishii,K., Katsunai,T., Teshiro,H., Itoh,M.,
	Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
	Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
	Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M.,
	Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Maruyama,S., Kawai,J.,
	Okazaki,Y., Murakatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
TITLE	RIKEN Integrated sequence analysis (RISA) system-364-Format
JOURNAL	sequencing pipeline with 384 multicapillary sequencer
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
PUBLISHED	20530913
REFERENCE	11076861
AUTHORS	4
	The RIKEN Genome Exploration Research Group Phase II Team and the
TITLE	FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409, 685-690 (2001)
AUTHORS	5
	The FANTOM Consortium and the RIKEN Genome Exploration Research
TITLE	Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation
REFERENCE	of 60,770 full-length cDNAs
AUTHORS	Nature 420, 563-573 (2002)
	6 (bases 1 to 2802)
	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
	Fukuda,S., Furuno,M., Hanagimura,T., Hara,A., Hashizume,W.,
	Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
	Horii,F., Imtani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
	Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
	Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
	Nakamura,M., Nishi,K., Nomura,K., Numataki,R., Onno,M., Ohato,N.,
	Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
	Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shitaki,T.,
	Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
	Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
	Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
	Physical and Chemical Research (RIKEN), Laboratory for Genome
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
	RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
	Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
	URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
	Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome
	Encyclopedia Project of Genome Exploration Research Group in Riken
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.
	Division of Experimental Animal Research in Riken contributed to
	prepare mouse tissues.
	Please visit our web site for further details.
	URL: http://genome.gsc.riken.jp/
	URL: http://fantom.gsc.riken.jp/.
FEATURES	Location/Qualifiers
SOURCE	1. .2802
	/organism="Mus musculus"
	/mol type="mRNA"
	/strain="C57BL/6J"
	/db_xref="FANTOM DB:6430408L10"
	/db_xref="taxon:10090"
	/clone="6430408L10"
	/sex="male"
	/tissue type="olfactory brain"
	/clone.lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="adult"
	<1..1215
	/note="unnamed protein product; putative
	sodium channel protein II homolog [Rattus norvegicus]
	[PIR B25019, evidence: FASTY, 100%ID, 12.6%length,
	match=759]"
	/codon_start=1

/protein\_id="BAC27748.1"  
 /db\_xref="GI:26328015"  
 /translation="ITLSTVGMPLAILEKVFSPLEPRVLRARIGLILKIGAKG  
 IRTLLPALMSLPLAFNIGLLPLVMPFIYAFPGSNPXYVREVGIDIMENPEFPGNS  
 MICLFQITTSAGMDGLAPILNSGPDPCDPEKDHGVSSVDCDCGPGTGFVSYII  
 ISFLVVMYIAVILENFSVAESAPLSDDEMEFVEKEDPDATQIIECKLS  
 DPAALDPLPLIAKNKVLITAMDLPWISGRILHLDLFLPFRVILVLESESEMALRI  
 OMERFMAINSKSVYPIITTLKROKOEVAIVORARYRLKOKVKVKSISTYKRD  
 KGKDEGPRIKEDIITDKLNNSTPEKTDVPSPTSPSYDSVTRKPEKREKDKSEK  
 EDKGDIRESEK"

## ORIGIN

Query Match 4.8%; Score 312; DB 3; Length 2802;  
 Best Local Similarity 60.6%; Pred. No. 3.9e-69;  
 Matches 576; Conservative 0; Mismatches 350; Indels 24; Gaps 3;

QY 5137 TCATTTTATCCATCTTAGGCTCTTGTACTTACGATATTTATCGAAGACTTTCGTGCGC 5196  
 DB 2 TCATCTCTCCATCTAGTGAAGATGTTTCTCGCGGAGCTATAGAAAGTATTCGTGCTCC 61  
 QY 5197 CGACCTCTCCGAGTGTGGTGTGGGAAAGTGGCCGCTGCTTGTGACTGCTGAGAG 5256  
 DB 62 CTACCTCTGTCGAGTCACTCGCCCTGGCAGGATTGACGAATCTTACGCTGATCAAG 121  
 QY 5257 GAGCCAAAGGAGTTCGACACTGCTCTCGCGTTGGCCATGCGTGGCCGCTGTTCA 5316  
 DB 122 GCGCCAAAGGAGTTCGACACTGCTCTCGCGTTGGCCATGCGTGGCCGCTGTTCA 181  
 QY 5317 ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5376  
 DB 182 ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241  
 QY 5377 TCATGACAGTGAAG 5436  
 DB 242 TTGGCTACGTTAAAG 301  
 QY 5437 AGAGCATATCTGCTCTTTCAGAGTGTGAGCGTACGCGGTTGGAGTGTGACTGAGAG 5496  
 DB 302 ACAGCATATCTGCTCTTTCAGAGTGTGAGCGTACGCGGTTGGAGTGTGACTGAGAG 361  
 QY 5497 CCATTTATCAATGAG 5548  
 DB 362 CTATACCTAAATAGTGAAG 418  
 QY 5549 -----GGGCAATTTGTGTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5601  
 DB 419 CGGTGAAGGAG 478  
 QY 5602 TTATAGCTTTTGTATGATTAATATATGATGATGATGATGATGATGATGATGATGATG 5661  
 DB 479 TCATATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538  
 QY 5662 AGGCGACCGAG 5721  
 DB 539 TTGCGACAG 598  
 QY 5722 TCTGCGACAGAAATTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5781  
 DB 599 TCTGCGAG 658  
 QY 5782 TCTGCGAG 5841  
 DB 659 TTGCGAG 718  
 QY 5842 CGATGACATATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5901  
 DB 719 CCAATGAG 778  
 QY 5902 TTACGAAAG 5961  
 DB 779 TTACGAAAG 838  
 QY 5962 AG-----ATAGCGGCGCGCGCGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6015

DB 829 AGCGGTCATGAGCTTCCATATCCCTCCAAAGGCTCTTATAGAGAGAGAGAGAGAGAG 898  
 QY 6016 GCGCTCAGCGAG 6065  
 DB 899 AGCGGCAACAG 948

## RESULT 10

BO715936 928 bp mRNA linear EST 16-JUL-2002  
 LOCUS BO715936

DEFINITION AGENCOURT 8294886 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6309535

ACCESSION BO715936

VERSION BO715936.1 GI:21854835

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS 1 (bases 1 to 928)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: Susan D. Sullivan, Ph.D.

cDNA Library Preparation: Resgen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing by: Agencourt Bioscience Corporation

clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LMNL at:

http://image.lnl.gov

Plate: LMNL13730 row: g column: 08

High quality sequence stop: 715.

location/Qualifiers

1..928

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:6309535"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: olfactory epithelium; Vector: pCMV-Sport6.1;

Site\_1: ECKRV; Site\_2: Not; Cloned unidirectionally.

Primer: Oligo dt. Average insert size 2.2 kb. Constructed

by Resgen, Invitrogen Corp. Note: this is a NIH\_MGC

Library."

ORIGIN

Query Match 4.8%; Score 310.4; DB 5; Length 928;  
 Best Local Similarity 62.5%; Pred. No. 7.3e-69;  
 Matches 507; Conservative 0; Mismatches 292; Indels 12; Gaps 1;

QY 5130 GATATGATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5189  
 DB 1 GTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
 QY 5190 GTGTGCGGAG 5249  
 DB 61 GTGTGCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 QY 5250 GTGAG 5309  
 DB 121 ATCAAG 180  
 QY 5310 CTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5369  
 DB 181 CTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 5370 TCGTTCATGACAG 5429  
 DB 241 TCCAACTTGGCTATGTTAAAG 300

QY 5430 TTGGCAGAGCATGATCTCTCTTTCAGATGTGACGCTGACCGGTTGGATGATGTA 5489  
 DB 301 TTGGCAGAGCATGATCTCTCTTTCAGATGTGACGCTGACCGGTTGGATGATGTA 360  
 QY 5490 CTGGAGCCATTTATCAA-----TGAGGAAGCATGCGATCCACCGACGAC 5537  
 DB 361 TTGGCCCATCTCAAGAGTGACCTGCTGATGACCTGATGATCAATTCACCTGGA 420  
 QY 5538 AAAGGCTATCCGGGCAATTTGTGTTCAGCAGCCTGTGAATTAACGTTCTCTCATAC 5597  
 DB 421 AGCTCAGTGAAGGAGACCTGTGGAACCATCTGTGGGATTTCTTTTGTGACGCTAC 480  
 QY 5598 CTGATATTAAGCTTTTGTATGATTTAATATGATGATGCTGTGATTCGAGAACTAT 5657  
 DB 481 ATATCATATATCTTCTCTGTTGTGTGATGATGATGATGATGATGATGATGATGAT 540  
 QY 5658 AGTCAGGCGCACCGAGAGCGTGAAGGCTTAACCGACGACGATGATGATGATGATGAT 5717  
 DB 541 AGCGTTGCCACAGAGAGAGTGAAGCGCCCTGAGTGAAGAGAGAGAGAGAGAGAGAG 600  
 QY 5718 GAGATCTGGCAGCAATTCGATCCGAGGCGACCGACGATGATGATGATGATGATGATG 5777  
 DB 601 GAGGTCGGGAGAGAGTTCGACCTGACCGCACCGATGATGATGATGATGATGATGATG 660  
 QY 5778 GAATTCCTGAGAGTCTGAGAGCGCCGCTGAGATGATGATGATGATGATGATGATGATG 5837  
 DB 661 GATCTTTCAGAGCTCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
 QY 5838 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5897  
 DB 721 ATTGCGATGAGAGCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 5898 GCCCTTACGAGAGCTTCTTGTGCGGAGAG 5928  
 DB 781 GCTTTACAAAGCGGTCCTCGGTGAMAG 811

RESULT 11  
 BM63126 502 bp mRNA linear EST 26-FEB-2002  
 LOCUS 1700687506664 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449642363 5', mRNA sequence.  
 ACCESSION BM63126  
 VERSION BM63126.1 GI:18932637  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;  
 Anopheles.  
 1 (bases 1 to 502)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,  
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HOLTRA@celera.com  
 Plate: NU01004AV7 row: H column: 09  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
 1. 502  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449642363"  
 /dev\_stage="Adult"

/lab\_host="DH10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."

Query Match 4.6%; Score 302; DB 4; Length 502;  
 Best Local Similarity 75.1%; Pred. No. 9.3e-67;  
 Matches 377; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 4681 TATATTCGATTCATCATATTTGATTCCTTTTTCACATCGTCAATTCATTCG 4740  
 DB 1 TGTACTGTGTGTTTATTTATCTTTGGTCAATCTTCACGTTGAATTCATTCATTCG 60  
 QY 4741 TTATCATGATATTTTATGAGCAAAAGAAAAGCAAGTGATCATTTAGAAATGTTCA 4800  
 DB 61 TTTATTTGACAACTTCATGATGAGAAAAGAAAGCTGTGTGATCGCTAGAAATGTTCA 120  
 QY 4801 TGACAGAGATGAGAAAAGTACTATATGATGATGATGATGATGATGATGATGATG 4860  
 DB 121 TGACAGAGATGAGAAAAGTACTATATGATGATGATGATGATGATGATGATGATG 180  
 QY 4861 TAAAGCCATTCGACAGCAAGTGGCGACCAAGCAATATGTTGAATATGTAACCG 4920  
 DB 181 TAAAGCAATTCCTGTCAGAGTGGCGGCTCAAGCAATATTTTGAATATGTAACGA 240  
 QY 4921 ATAGAAATTCATATATATATATATGATGATGATGATGATGATGATGATGATGATG 4980  
 DB 241 ACAGAAAGTTGACATGATATATATATGATGATGATGATGATGATGATGATGATG 300  
 QY 4981 TCGATGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
 DB 301 TCGACACATGACAAACATGAGAACTTTAGTGTGTTGATTAATGATGATGAT 360  
 QY 5041 TCGATGTTATTTTCAGTTCGAGTCTATTAATAATGCTTTAGATGATGATGAT 5100  
 DB 361 TCACTGATATTCAGCAGCGAGATGTTAATGAGATTTTGCACCTGATTCATTA 420  
 QY 5101 TTATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160  
 DB 421 TTATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 QY 5161 TACTTAGCATATTTATCGAGAA 5182  
 DB 481 TTCTAAGTATATCATTTGAAAA 502

RESULT 12  
 CDS01236/c 771 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
 DEFINITION BAC070N13 of DrosBAC library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL101052  
 VERSION AL101052.1 GI:5612663  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
 AUTHORS Direct Submission  
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.ddg.ebi.ac.uk/>. This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaut at CERH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

## FEATURES

### Location/Qualifiers

```
1. .771
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC207N13"
/clone_1fb="DrosBAC"
/plasmid="pBelBAC11"
note="end : Spe"
```

Query Match	4.6%	Score 301.2	DB 9	Length 771
Best Local Similarity	87.5%	Pred No. 1.7e-66		
Matches 300	Conservative 21	Mismatches 21	Indels 0	Gaps 0

QY	5454	TTTCAGATGTCGACCTCAGCCGGTGGATGGGTGTACTGGACGCCATTAATCAGGAA	5513
Db	343	TKGCTGTTGTGCAAGTCGACCGCGTTGGGATGGTGAACGGATATTMTGCAATAGGAA	284
QY	5514	GCATGCCATTCACCCGACAGGCACAAAGGCTATCCGGSCAATTGGGTTCACGACCCTT	5573
Db	283	GCATGCCGATCCACCCGACAGCACAAAGGCTATCCGGGCTMTTGGGTTCACGACCCTT	224
QY	5574	GGAATTAACGTTTCTCTCTCATACCTAGTTAATAACCTTTTGATAGTAATTATGTAC	5633
Db	223	GGAATTAACGTTTCTCTCTTTTAACCTMTATATAATTTTTTGTGTTTTTTTAATMTGTAAC	164
QY	5634	ATTGCTGCATTTCTCGAAGACTATATGTCAAGCCACCCAGAGACGTGCAAGAGGCTTAAC	5693
Db	163	ATTGCTKTWTWTWTWTYYKAGAACTATATGTCAAGCCACCCAGAGACGTGCAAGAGGCTTTAAC	104
QY	5694	GACGACGACTACGACATGTACTATAGATCTGGCAGCAATTGCATCCGGAGGGCACCAG	5753
Db	103	GACGACGACTACGACATGTACTATAGATCTGGCAGCAATTGCATCCGGAGGGCACCAG	44
QY	5754	TACATACGCTATGATCAGCTGTCGGAATTTCTGAGCGTACTGG	5796
Db	43	TACATACGCTATGATCAGCTGTMTGATTTCTGAGCAGGTCCTG	1

RESULT 13						
BC029489						
LOCUS	BC029489	1777 bp	mRNA	linear	HTC 16-MAY-2002	
DEFINITION	Homo sapiens, clone IMAGE:5278436,					
ACCESSION	BC029489					
VERSION	BC029489.1	GI:20809571				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 1777) Strausberg,R. Direct Submission					
AUTHORS						
TITLE						
JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian					

REMARK	COMMENT
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	Contact: MGC help desk

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGR) & Shitaki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.bhgc.stanford.edu>  
Contact: (Dickson, Mark, [medepax1@stanford.edu](mailto:medepax1@stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAP Plate: 48 Row: h Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10337596  
This clone has the following problem: frame shifted.

### Location/Qualifiers

```
1. 1777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5278436"
/tissue_type="Brain, hypothalamus"
/clone_id="NH MGC_96"
/lab_host="DH10B"
/notes="Vector: pBluescript"
```

Query March	4.5%;	Score 292.2;	DB 3	Length 1777;
Best Local Similarity	56.2%;	Pred. No. 4.9e-64;		
Matches 698;	Conservative 0;	Mismatches 473;	Indels 72;	Gaps 5

Qy	193	AAAAA	CAAAA	AGAA	AAATCCG	TATAT	ATACG	AGAG	ACG	AGATGA	AGAGTCC	CAAC	CCG	ATC
Db	342	AGAA	AGCTAA	AGAG	CCCAA	CAGAA	CCGAA	CCGAA	GTAG	AGATGA	TGAAAA	TGGCC	CAAA	GC
Qy	253	CTA	CACTTGA	CAG	GGTGTG	CCAA	TAC	CTT	TGAT---	TG	CAG	GGC	AGT	CCG
Db	402	CAAA	CAGTGA	CTTG	GAAG	CAG	AAAAATCT	CTTC	ATTTAT	TGAA	GACAT	TCT	CTC	AG
Qy	310	AATT	GGCTC	CAC	TCTCT	TG	AGAT	ATTC	ATCT	AC	AGAT	TGTA	CTG	ATCG
Db	462	AGAT	GGGT	AGT	AGCCCT	TG	AGAG	AT	TG	CA	CCCT	ACT	TA	GT
Qy	370	TAGT	TGTA	CAAA	AG	AAAA	AT	T	TTTT	TG	CC	TTTT	CG	AT
Db	522	TAGT	ATTTAA	TAA	GG	AAAG	CAATCT	CTG	ATTC	AGT	GC	CA	CCCT	CTT
Qy	430	TG	ATCCAT	CAATCC	GATAC	GTG	TGG	CCATTTA	CA	TTCT	ATG	ATC	ATTA	TTTT
Db	582	TA	ACTCC	CTTCA	ACC	CTAT	TAGA	AAAT	TAG	ATAT	TAG	ATTTG	GT	CA
Qy	490	CC	CTAT	CA	TATCA	CA	CAAT	TTCT	GTCA	ATC	ATC	ATG	ATAT	TG
Db	642	AT	ATG	CTCAT	TAT	TG	TG	CA	ATTTCTTA	CCAA	CTGT	ATTTAT	AT	CA
Qy	550	C---	C	AG	GT	TG	AT	GC	AT	TG	AT	TA	TA	TA
Db	702	CAG	ATCG	ACAA	GAAT	TG	TGA	AT	AT	CTTTA	CAG	AAATTTA	CTTT	AA
Qy	607	TTAA	AG	TATG	GCAC	GAG	TTTCA	TTTAT	TATG	CCG	TTA	CTAT	CTTA	AG
Db	762	TT	AAAA	AT	ACTT	GCA	GGG	CTTT	GT	TTA	GA	ATTTCA	CTTT	AC
Qy	667	ATT	GG	CTG	GA	CTT	GT	AT	AT	TAG	CTT	AT	TG	AT
Db	822	ATT	GG	TG	GA	TTTCA	CA	GT	CA	TTT	TG	AT	TG	CA
Qy	727	AT	CTAG	AC	GC	CTG	CA	AG	TTA	GG	TG	CTG	CA	GC
Db	882	AT	GT	CT	AG	GT	TGA	AA	CA	TTT	CA	GT	CA	ATTC
Qy	787	CAG	CTTGA	AC	CA	TG	TG	CG	CG	CTCA	TG	CA	TG	CA
Db	942	CA	GG	CTG	AA	GC	AT	TTG	TG	GG	GG	CTG	AT	TC
Qy	847	TT	AT	CT	GA	CA	AT	TTT	CT	CG	AT	TTG	CG	CT

```

Db      1002 TGAATCTTGACGCTGCTCTGCTAAGAGCTGTTGCGCTAATAGATGTCAGTTGTCATGG 1061
QY      907 GCGTGTCTACCGAGAAATGCATCAAGAAGTTCCCGCTGACGGTCTCTGGG----- 957
Db      1062 GCAACCTACGAAATTAATATGTTTGCAATGAGCCTCCAGATTAATCTCTTGGAAATTAATA 1121
QY      958 -----GCATCTGA 966
Db      1122 TCATCTCTCTTTAACAATTCATGATGAGATGCTACTCTTCAATAGACACTGA 1181
QY      967 CCGACGAACTGGGACTATCAATGCAATGCAATGCTCAATGGTATTCGAGACGAGG 1026
Db      1182 GCATATTTAATCTGGAGATATATGAGATTAATAAGTCACTTTATTTTATTTAGAGGGG 1241
QY      1027 GCATCTATTTCCGTATATGGGCAATATATCCGCTGGGGCAATGAGACGAGATTAAG 1086
Db      1242 AAAATGATGCTCTGCTTTGTCGCAACGCTCAATGAGGCGAGTCTGGAAGATACA 1301
QY      1087 TGTGCTGACAGGGGTTTGTCCGAAATCCGAATTAATGCTACACAGCTTCGATTCGTTG 1146
Db      1302 TCTGTGTGAAGG---CTGTAGAAACCCCAACTATGCTACAGAGCTTTGACACCTTTA 1358
QY      1147 GATGGCTTTCCTGTCGCCCTTCGCTGATGACACAGACTTCTGGAGAGATCTGTACC 1206
Db      1359 GTTGGGCTTTTGTCTTATTTGCTCTCATGACTCAAGACTTCTGGGAAAACCTTTATC 1418
QY      1207 AGCTGCTGTGGCGCGCGCGGACATGACATGCTCTTTATAGTATCATCTTCC 1266
Db      1419 AACTGACACTACGCTGCTGCGGAAAACGTAACATATTTTGTGCTGCTATTTTCT 1478
QY      1267 TAGCTTCATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATGCTATGAGCAAT 1326
Db      1479 TGGGCTCATTTCTATTAATTAATTTGATCTTGGCTGTGTCGTCATGAGCTTATGAGAA- 1537
QY      1327 TCGAAGGAAGGCCGGAAGGAAGAGGCTGCCGAAAGAGAGG 1369
Db      1538 --CAGATCAGGCCACATTTGGAAGAGGCTGACAGAGAGAGC 1578

```

```

RESULT 14
LOCUS   CB520657 768 bp mRNA linear EST 09-JUL-2003
DEFINITION
UI-M-GIO-cel-n-19-0-UI.r1 NIH BMAP_GIO Mus musculus cDNA clone
CB520657
IMAGE:6840500 5', mRNA sequence.
ACCESSION
CB520657.1 GI:29354012
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 768)
NIN-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straussberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

```

Seq primer: pYX-5.

FEATURES  
source

Location/Qualifiers  
1..768  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6840500"

```

/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIN BMAP_GIO"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

```

#### ORIGIN

Query Match 4.4%; Score 288; DB 6; Length 768;  
Best Local Similarity 62.4%; Pred. No. 4,7e-63;  
Matches 472; Conservative 0; Mismatches 272; Indels 12; Gaps 1;

```

QY      5036 GAAATTCGATGTTATTTTCAGTTCGAAATGCTATTAATAAATTCGCTTAAGATATCA 5095
Db      13 GGTATTCATCGTCTCTTCTACTGGGAGTTTGTCTGAAGCTCATCTCTCAGATCTA 72
QY      5096 CTATTTATTTGACGATGAAATTTATTTGATGATGATGATGATGATGATGATGATGATG 5155
Db      73 CTACTTCACGATTTGGTGAACATCTTGACTTTGTGGTGGATGATGATGATGATGATGATG 132
QY      5156 TCTTGTACTTACGATATTTATGAGAAGTCTTGTGTCGCGGACCTGCTCCGATGGT 5215
Db      133 AATGTTCTTGTGTCGATGATGAGAAGTATTTGTGTCTCTCACTCTGTTCCGATCAT 192
QY      5216 GCGTGTGCGAAGAGGGCGGTCGCTGACGATGAGAGGAGGCAAGGGCATTCGGAC 5275
Db      193 CCGCTGCGCAGAGATTTGACGATCTTACGCTGATCAAGGCGCAAGGGATTCGAC 252
QY      5276 ACTGCTCTTGGCTTGGCCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGTT 5335
Db      253 GCTGCTCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
QY      5336 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5395
Db      313 CCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 372
QY      5396 GAGCGCATTTAAGAGCTGTAACATTTCAAGACTTTGAGCGCAGAGATGATGCTGCTT 5455
Db      373 GCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
QY      5456 TGAATGTCGACGTGACCGCGTGGGATGATGATGATGATGATGATGATGATGATGATG 5506
Db      433 CCAATTCACACCTCTGCGGGCTGGGATGATGATGATGATGATGATGATGATGATGATG 492
QY      5507 ---TAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5563
Db      493 TCTTACTGTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 552
QY      5564 AGCGACCTTGAATTAAGTTTCTCTCACTACTTACTTAAAGCTTTTGAATGATAT 5623
Db      553 CCCATCTGTGGGATTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATG 612
QY      5624 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5683
Db      613 GAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 672
QY      5684 GGGTCTAACGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5743
Db      673 GCCCTAGTAGAGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 732

```

QY 5744 GGGACCCAGTACATAGCTATGATCAGCTGCGCA 5779  
 DB 733 CGCCACNCAGTTCATAGAGTCTGCAAGCTCTCTGA 768  
 RESULT 15  
 LOCUS BM650999  
 DEFINITION 170006873J2939 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 1960049620245 5', mRNA sequence.  
 ACCESSION BM650999  
 VERSION BM650999.1 GI:18950510  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 688)  
 Holt R.A., Lin J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
 Charlab, R., Collins, P.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004NBZ row: N column: 19  
 Seq primer: M13 Reverse.  
 FEATURES  
 source  
 location/Qualifiers  
 1..688  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="1960049620245"  
 /dev\_stage="Adult"  
 /lab\_host="DH10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI. Whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mt4.org)."  
 ORIGIN  
 Query Match 4.3%; Score 281.6; DB 4; Length 688;  
 Best Local Similarity 68.7%; Pred. No. 2.1e-61;  
 Matches 445; Conservative 0; Mismatches 124; Indels 79; Gaps 1;  
 QY 4389 TGGCTAATTTTGGCATATGAGGTGTACAGCTTTTGTGGAAATATTTTAAGTGCAG 4448  
 DB 38 TGGCTAATTTTGGCATATGAGGTGTGTGCTGGCAATCTTCAAGTGTG 97  
 4449 GACATGATGGCAGAACTCAGCCAGATCATATCCAAATCGCAATCGCTGCGAGAGC 4508  
 DB 98 GATAAATAATAAAGCTACATTAAGTCAAGAAATTAACGATGTAAATGCTTGGCAAGCC 157  
 QY 4509 GAGAACTACAGCTGGGTGAATTCAGCAATGAATTCATCATGTGTAAGCGGTATCTG 4568  
 DB 158 GAAAACTAATTCATGGGAAATTCACCAATGAATTCGATCATGTAGTAAAGCAATATTG 217  
 QY 4569 TGCCTTTTCAAGTGGCAGCCTTCAAGGCTGATATCAATCAAGATCAAGATGCTATGAT 4628  
 DB 218 TGTCTGTTTCAAGTACCAATTCAGAGATGATACAAATTAAGACATGCTATTGAT 277  
 QY 4629 TCACGAG----- 4635  
 DB 278 TCTAGAGAGCTAAGTTTGTAAATAGACTTATATAAACAATGTGTAACAATTTAAACT 337

QY 4636 -----AGTGGACAAAGAACCAATTCGTGAAGCAAT 4669  
 DB 338 ACATTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 397  
 QY 4670 CTACATGATTTATATTTGATTTCTTCATCATATTTGATTCCTTTTCAAGCTCATCT 4729  
 DB 398 CTACATGATTTCTGATCTTTGCTTTCTTTATTTATCTTTGGTCAATTTCTTCAAGTGAATCT 457  
 QY 4730 GTTCATTTGTTTATTCATTTGATTAATTTAATGACCAAAAGAAAAAGCAGGTGATCAT 4789  
 DB 458 ATTCAATGTTTATTAATTTGACAACTTCATTAAGACAAAAAGCAGGTGATCGCT 517  
 QY 4790 AGAAATGTTCTAGACAGAAAGTCAAGAAAGTACTATTAATGCTATGAAAAAGAGGCTC 4849  
 DB 518 AGAAATGTTCTAGACAGAAAGTCAAGAAAGTACTATTAATGCTATGAAAAAGAGGCTC 577  
 QY 4850 TAAAAACCATTAATAAGCATTCACAAAGTGGGCAACCAAGCAATAGTCTTTGA 4909  
 DB 578 GAAGAACTCTTAAGCAATTCCTCGTCAAGGTGGGCTCAAGCAATAGTCTTTGA 637  
 QY 4910 AATAGTAAACGATTAAGAAATTCATTAATCATTAATGTTTATTCATTTG 4957  
 DB 638 AATAGTAAACGATTAAGAAATTCATTAATCATTAATGTTTATTCATTTG 685

Search completed: May 9, 2005, 17:32:47  
 Job time: 18883 secs

**This Page Blank (uspto)**